

09-05-00

Express Mail No.: EK916750942US
Docket No.: 787CIP2C

Box 50

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE
PATENT APPLICATION TRANSMITTAL UNDER 37 CFR 1.53

BOX PATENT APPLICATION
Assistant Commissioner for Patents
Washington, D.C. 20231

Sir:

Transmitted herewith for filing is the patent application of

Inventor(s): Y. Tom Tang, Chenghua Liu, Vinod Asundi, Ping Zhou, Jie Zhang, Feiyan Ren,
Qing A. Zhao, Aidong J. Xue, Tom Wehrman, Jian-Rui Wang, Radoje T. Drmanac

Title: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

1. Type of application

- ☒ This is a new application for a
- ☒ Utility patent.
- ☐ Design patent.
- ☒ This is a continuation-in-part application of prior application no. 09/560,875 filed April 27, 2000, Attorney Docket No. 787CIP, which is a continuation-in-part application of prior application no. 09/496,914 filed February 03, 2000, Attorney Docket No. 787.

2. Application Papers Enclosed

1	Title Page		
121	Pages of Specification (excluding Claims, Abstract, Drawings & Sequence Listing)		
4	Page(s) of Claims		
1	Page(s) of Abstract		
0	Sheet(s) of Drawings (Figs. X-X)	<input type="checkbox"/> Formal	<input type="checkbox"/> Informal
575	Page(s) of Sequence Listing		

CERTIFICATION UNDER 37 CFR 1.10

I hereby certify that this Patent Application Transmittal and the documents referred to as enclosed therewith are being deposited with the United States Postal Service on **September 01, 2000**, in an envelope addressed to the Assistant Commissioner for Patents, Washington, D.C. 20231 utilizing the "Express Mail Post Office to Addressee" service of the United States Postal Service under Mailing Label No. EK916750942US


Annya Dushine

3. Oath or Declaration

- ☐ Enclosed
 - ☐ Executed by (check all applicable boxes)
 - ☐ Inventor(s)
 - ☐ Legal representative of inventors(s) (37 CFR 1.42 or 1.43)
 - ☐ Joint inventor or person showing a proprietary interest on behalf of inventor who refused to sign or cannot be reached
 - ☐ The petition required by 37 CFR 1.47 and the statement required by 37 CFR 1.47 are enclosed. See Item 5D below for fee.
- ☒ Unexecuted – the undersigned attorney or agent is authorized to file this application on behalf of the applicant(s). An executed declaration will follow.

4. Additional Papers Enclosed

- ☐ Preliminary Amendment
- ☐ Information Disclosure Statement
- ☐ Declaration of Biological Deposit
- ☒ Computer readable copy of sequence listing containing nucleotide and/or amino acid sequence
- ☒ Statement Under 37 CFR § 1.821
- ☒ Paper copy of sequence listing identical to computer copy (575 pages)
- ☐ Microfiche computer program
- ☒ Verified statement claiming small entity status under 37 CFR 1.9 and 1.27
- ☐ Associate Power of Attorney
- ☐ Verified translation of a non-English patent application
- ☒ Return receipt postcard
- ☐ Other _____

5. Priority Applications Under 35 USC 119

Certified copies of applications from which priority under 35 USC 119 is claimed are listed below and

- ☐ are attached.
- ☐ will follow.

6. **Filing Fee Calculation (37 CFR 1.16)**

A. ☒ **Utility Application**

CLAIMS AS FILED – INCLUDING PRELIMINARY AMENDMENT (IF ANY)						
			SMALL ENTITY		OTHER THAN A SMALL ENTITY	
	NO. FILED	NO. EXTRA	RATE	FEE	RATE	FEE
BASIC FEE				\$345.00		\$690.00
TOTAL	30-20	= 10	X 9 =	\$90.00	X 18 =	\$0.00
INDEP.	3-3	= 0	X 39 =	\$0.00	X 78 =	\$0.00
<input checked="" type="checkbox"/> First Presentation of Multiple Dependent Claim			+ 130 =	\$130.00	+ 260 =	\$0.00
FILING FEE:				\$565.00	OR	\$0.00

B. ☐ **Design Application (\$155.00/\$310.00)** Filing Fee: \$ _____

C. ☐ **Plant Application (\$240.00/\$480.00)** Filing Fee: \$ _____

D. **Other fees**

☐ Recording Assignment [Fee -- \$40.00 per assignment] \$ _____

☐ Other \$ _____

TOTAL FEES \$ 565.00

7. Method of Payments of Fees

- ☐ Enclosed check
- ☒ Charge Deposit Account No. 501169. A duplicate copy of this transmittal is enclosed
- ☐ Not enclosed

8. Deposit Account and Refund Authorization

The Commissioner is hereby authorized to charge payment of any additional fees due or credit any overpayment to Deposit Account No. 501169. A duplicate copy of this transmittal is enclosed.

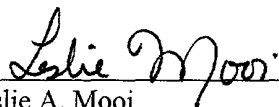
Please refund any overpayment to Hyseq, Inc. at the address below.

Please direct all future correspondence to Leslie A. Mooi at the address below.

Respectfully submitted,

Date: September 01, 2000

By:



Leslie A. Mooi
Attorney for Applicants
Registration No.: 37,047
HYSEQ, INC.
670 Almanor Avenue
Sunnyvale, CA 94085
(408) 524-8100
(408) 524-8145 (Telefacsimile)

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant(s) or Patentee(s): Y. Tom Tang, Chenghua Liu, Vinod Asundi, Ping Zhou, Jie Zhang, Feiyan Ren, Qing A. Zhao, Aidong J. Xue, Tom Wehrman, Jian-Rui Wang, Radoje T. Drmanac

Application No. or Patent No.: Not Yet Assigned

Filed or Issued: Herewith

For: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

**VERIFIED STATEMENT (DECLARATION) CLAIMING SMALL ENTITY STATUS
(37 CFR § 1.9(f) AND 1.27(c)) - SMALL BUSINESS CONCERN**

I hereby declare that I am

- ☐ The owner of the small business concern identified below:
☒ An official of the small business concern empowered to act on behalf of the concern identified below:

NAME OF CONCERN: HYSEQ, INC.
ADDRESS: 670 Almanor Avenue
Sunnyvale, CA 94085

I hereby declare that the above-identified small business concern qualifies as a small business concern as defined in 13 CFR § 121.12, and reproduced in 37 CFR § 1.9(d), for purposes of paying reduced fees under § 41(a) and (b) of Title 35, United States Code, in that the number of employees of the concern, including those of its affiliates, does not exceed 500 persons. For purposes of this statement, (1) the number of employees of the business concern is the average over the previous fiscal year of the concern of the persons employed on a full-time, part-time or temporary basis during each of the pay periods of the fiscal year, and (2) concerns are affiliates of each other when either, directly or indirectly, one concern controls or has the power to control the other, or a third party or parties controls or has the power to control both.

I hereby declare that rights under contract or law have been conveyed to, and remain with, the small business concern identified above with regard to the invention, entitled NOVEL NUCLEIC ACIDS AND POLYPEPTIDES by inventors Y. Tom Tang, Chenghua Liu, Vinod Asundi, Ping Zhou, Jie Zhang, Feiyan Ren, Qing A. Zhao, Aidong J. Xue, Tom Wehrman, Jian-Rui Wang, Radoje T. Drmanac, et al. described in

- ☒ The specification filed herewith.
☐ Application Serial No. [], filed [Date].
☐ Patent No. [], issued [Date].

If the rights held by the above identified small business concern are not exclusive, each individual, concern or organization having rights to the invention is listed below¹ and no rights to the invention are held by any person, other than the inventor, who could not qualify as a small business concern under 37 CFR § 1.9(c), or by any concern which would not qualify as a small business concern under 37 CFR § 1.9(d) or a nonprofit organization under 37 CFR § 1.9(e).

Full Name: _____

Address: _____

() Individual () Small Business Concern () Nonprofit Organization

I acknowledge the duty to file, in this application or patent, notification of any change in status resulting in loss of entitlement to small entity status prior to paying, or at the time of paying, the earliest of the issue fee or any maintenance fee due after the date on which status as a small entity is no longer appropriate (37 CFR § 1.28(b)).

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under § 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application, any patent issuing thereon, or any patent to which this verified statement is directed.

Name of person signing: Mark E. Gitter

Title of person
other than owner: Chief Financial Officer

Address of person signing: HYSEQ, INC.
670 Almanor Avenue
Sunnyvale, CA 94085

Signature: _____

Date: _____

¹NOTE: Separate verified statements are required from each named person, concern or organization having rights to the invention averring to their status as small entities. (37 CFR § 1.27)

Our Ref. No.: 787CIP2C



NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

09654936 090100

Express Mail Label No.: EK916750942US

NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

1. CROSS REFERENCE TO RELATED APPLICATIONS

5 This application is a continuation-in-part application of U.S. Application Serial No. 09/560,875, filed April 27, 2000, Attorney Docket No. 787CIP, which in turn is a continuation-in-part application of U.S. Application Serial No. 09/496,914, filed February 03, 2000, both of which are incorporated herein by reference in their entirety.

10 2. BACKGROUND OF THE INVENTION

2.1 TECHNICAL FIELD

 The present invention provides novel polynucleotides and proteins encoded by such polynucleotides, along with uses for these polynucleotides and proteins, for
15 example in therapeutic, diagnostic and research methods.

2.2 BACKGROUND

 Technology aimed at the discovery of protein factors (including e.g., cytokines, such as lymphokines, interferons, CSFs, chemokines, and interleukins) has matured
20 rapidly over the past decade. The now routine hybridization cloning and expression cloning techniques clone novel polynucleotides "directly" in the sense that they rely on information directly related to the discovered protein (i.e., partial DNA/amino acid sequence of the protein in the case of hybridization cloning; activity of the protein in the case of expression cloning). More recent "indirect" cloning techniques such as
25 signal sequence cloning, which isolates DNA sequences based on the presence of a now well-recognized secretory leader sequence motif, as well as various PCR-based or low stringency hybridization-based cloning techniques, have advanced the state of the art by making available large numbers of DNA/amino acid sequences for proteins that are known to have biological activity, for example, by virtue of their secreted nature in the

case of leader sequence cloning, by virtue of their cell or tissue source in the case of PCR-based techniques, or by virtue of structural similarity to other genes of known biological activity.

Identified polynucleotide and polypeptide sequences have numerous applications in, for example, diagnostics, forensics, gene mapping; identification of mutations responsible for genetic disorders or other traits, to assess biodiversity, and to produce many other types of data and products dependent on DNA and amino acid sequences.

3. SUMMARY OF THE INVENTION

The compositions of the present invention include novel isolated polypeptides, novel isolated polynucleotides encoding such polypeptides, including recombinant DNA molecules, cloned genes or degenerate variants thereof, especially naturally occurring variants such as allelic variants, antisense polynucleotide molecules, and antibodies that specifically recognize one or more epitopes present on such polypeptides, as well as hybridomas producing such antibodies.

The compositions of the present invention additionally include vectors, including expression vectors, containing the polynucleotides of the invention, cells genetically engineered to contain such polynucleotides and cells genetically engineered to express such polynucleotides.

The present invention relates to a collection or library of at least one novel nucleic acid sequence assembled from expressed sequence tags (ESTs) isolated mainly by sequencing by hybridization (SBH), and in some cases, sequences obtained from one or more public databases. The invention relates also to the proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins. These nucleic acid sequences are designated as SEQ ID NO: 1 – 164 and are provided in the Sequence Listing. In the nucleic acids provided in the Sequence Listing, A is adenosine; C is cytosine; G is guanosine; T is thymine; and N is any of the four bases. In the amino acids provided in the Sequence Listing, * corresponds to the stop codon.

The nucleic acid sequences of the present invention also include, nucleic acid sequences that hybridize to the complement of SEQ ID NO: 1 – 164 under stringent hybridization conditions; nucleic acid sequences which are allelic variants or species homologues of any of the nucleic acid sequences recited above, or nucleic acid sequences that encode a peptide comprising a specific domain or truncation of the peptides encoded by SEQ ID NO: 1 – 164. A polynucleotide comprising a nucleotide sequence having at least 90% identity to an identifying sequence of SEQ ID NO: 1 – 164 or a degenerate variant or fragment thereof. The identifying sequence can be 100 base pairs in length.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO: 1 – 164. The sequence information can be a segment of any one of SEQ ID NO: 1 – 164 that uniquely identifies or represents the sequence information of SEQ ID NO: 1 – 164.

A collection as used in this application can be a collection of only one polynucleotide. The collection of sequence information or identifying information of each sequence can be provided on a nucleic acid array. In one embodiment, segments of sequence information is provided on a nucleic acid array to detect the polynucleotide that contains the segment. The array can be designed to detect full-match or mismatch to the polynucleotide that contains the segment. The collection can also be provided in a computer-readable format.

This invention also includes the reverse or direct complement of any of the nucleic acid sequences recited above; cloning or expression vectors containing the nucleic acid sequences; and host cells or organisms transformed with these expression vectors.

Nucleic acid sequences (or their reverse or direct complements) according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology, such as use as hybridization probes, use as primers for PCR, use in an array, use in computer-readable media, use in sequencing full-length genes, use for chromosome and gene mapping, use in the recombinant production of protein, and use in the generation of anti-sense DNA or RNA, their chemical analogs and the like.

In a preferred embodiment, the nucleic acid sequences of SEQ ID NO: 1-164 or novel segments or parts of the nucleic acids of the invention are used as primers in

expression assays that are well known in the art. In a particularly preferred embodiment, the nucleic acid sequences of SEQ ID NO: 1-164 or novel segments or parts of the nucleic acids provided herein are used in diagnostics for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as

5 expressed sequence tags for physical mapping of the human genome.

The isolated polynucleotides of the invention include, but are not limited to, a polynucleotide comprising any one of the nucleotide sequences set forth in the SEQ ID NO: 1-164; a polynucleotide comprising any of the full length protein coding sequences of the SEQ ID NO: 1-164; and a polynucleotide comprising any of the nucleotide
10 sequences of the mature protein coding sequences of the SEQ ID NO: 1-164. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent hybridization conditions to (a) the complement of any one of the nucleotide sequences set forth in the SEQ ID NO: 1-164; (b) a nucleotide sequence encoding any one of the amino acid sequences set forth in the
15 Sequence Listing; (c) a polynucleotide which is an allelic variant of any polynucleotides recited above; (d) a polynucleotide which encodes a species homolog (e.g. orthologs) of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of any of the polypeptides comprising an amino acid sequence set forth in the Sequence Listing.

20 The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising any of the amino acid sequences set forth in the Sequence Listing; or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides with biological activity that are encoded by (a) any of the polynucleotides having a nucleotide sequence set forth in the SEQ ID NO: 1-164; or (b)
25 polynucleotides that hybridize to the complement of the polynucleotides of (a) under stringent hybridization conditions. Biologically or immunologically active variants of any of the polypeptide sequences in the Sequence Listing, and "substantial equivalents" thereof (e.g., with at least about 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98% or 99% amino acid sequence identity) that preferably retain biological activity are also contemplated. The
30 polypeptides of the invention may be wholly or partially chemically synthesized but are

preferably produced by recombinant means using the genetically engineered cells (e.g. host cells) of the invention.

The invention also provides compositions comprising a polypeptide of the invention. Polypeptide compositions of the invention may further comprise an
5 acceptable carrier, such as a hydrophilic, e.g., pharmaceutically acceptable, carrier.

The invention also provides host cells transformed or transfected with a polynucleotide of the invention.

The invention also relates to methods for producing a polypeptide of the invention comprising growing a culture of the host cells of the invention in a suitable
10 culture medium under conditions permitting expression of the desired polypeptide, and purifying the polypeptide from the culture or from the host cells. Preferred embodiments include those in which the protein produced by such process is a mature form of the protein.

Polynucleotides according to the invention have numerous applications in a
15 variety of techniques known to those skilled in the art of molecular biology. These techniques include use as hybridization probes, use as oligomers, or primers, for PCR, use for chromosome and gene mapping, use in the recombinant production of protein, and use in generation of anti-sense DNA or RNA, their chemical analogs and the like. For example, when the expression of an mRNA is largely restricted to a particular cell
20 or tissue type, polynucleotides of the invention can be used as hybridization probes to detect the presence of the particular cell or tissue mRNA in a sample using, *e.g.*, *in situ* hybridization.

In other exemplary embodiments, the polynucleotides are used in diagnostics as expressed sequence tags for identifying expressed genes or, as well known in the art
25 and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The polypeptides according to the invention can be used in a variety of conventional procedures and methods that are currently applied to other proteins. For example, a polypeptide of the invention can be used to generate an antibody that
30 specifically binds the polypeptide. Such antibodies, particularly monoclonal antibodies,

are useful for detecting or quantitating the polypeptide in tissue. The polypeptides of the invention can also be used as molecular weight markers, and as a food supplement.

Methods are also provided for preventing, treating, or ameliorating a medical condition which comprises the step of administering to a mammalian subject a
5 therapeutically effective amount of a composition comprising a polypeptide of the present invention and a pharmaceutically acceptable carrier.

In particular, the polypeptides and polynucleotides of the invention can be utilized, for example, in methods for the prevention and/or treatment of disorders involving aberrant protein expression or biological activity.

10 The present invention further relates to methods for detecting the presence of the polynucleotides or polypeptides of the invention in a sample. Such methods can, for example, be utilized as part of prognostic and diagnostic evaluation of disorders as recited herein and for the identification of subjects exhibiting a predisposition to such conditions. The invention provides a method for detecting the polynucleotides of the
15 invention in a sample, comprising contacting the sample with a compound that binds to and forms a complex with the polynucleotide of interest for a period sufficient to form the complex and under conditions sufficient to form a complex and detecting the complex such that if a complex is detected, the polynucleotide of interest is detected. The invention also provides a method for detecting the polypeptides of the invention in
20 a sample comprising contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex and detecting the formation of the complex such that if a complex is formed, the polypeptide is detected.

The invention also provides kits comprising polynucleotide probes and/or
25 monoclonal antibodies, and optionally quantitative standards, for carrying out methods of the invention. Furthermore, the invention provides methods for evaluating the efficacy of drugs, and monitoring the progress of patients, involved in clinical trials for the treatment of disorders as recited above.

The invention also provides methods for the identification of compounds that
30 modulate (i.e., increase or decrease) the expression or activity of the polynucleotides

and/or polypeptides of the invention. Such methods can be utilized, for example, for the identification of compounds that can ameliorate symptoms of disorders as recited herein. Such methods can include, but are not limited to, assays for identifying compounds and other substances that interact with (*e.g.*, bind to) the polypeptides of the invention. The invention provides a method for identifying a compound that binds to the polypeptides of the invention comprising contacting the compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and detecting the complex by detecting the reporter gene sequence expression such that if expression of the reporter gene is detected the compound the binds to a polypeptide of the invention is identified.

The methods of the invention also provides methods for treatment which involve the administration of the polynucleotides or polypeptides of the invention to individuals exhibiting symptoms or tendencies. In addition, the invention encompasses methods for treating diseases or disorders as recited herein comprising administering compounds and other substances that modulate the overall activity of the target gene products. Compounds and other substances can effect such modulation either on the level of target gene/protein expression or target protein activity.

The polypeptides of the present invention and the polynucleotides encoding them are also useful for the same functions known to one of skill in the art as the polypeptides and polynucleotides to which they have the closest homology (set forth in Table 1). If no homology is set forth for a sequence, then the polypeptides and polynucleotides of the present invention are useful for a variety of applications, as described herein, including use in arrays for detection.

4. DETAILED DESCRIPTION OF THE INVENTION

4.1 DEFINITIONS

It must be noted that as used herein and in the appended claims, the singular forms "a", "an" and "the" include plural references unless the context clearly dictates otherwise.

The term "active" refers to those forms of the polypeptide which retain the biologic and/or immunologic activities of any naturally occurring polypeptide. According to the invention, the terms "biologically active" or "biological activity" refer to a protein or peptide having structural, regulatory or biochemical functions of a naturally occurring molecule. Likewise "immunologically active" or "immunological activity" refers to the capability of the natural, recombinant or synthetic polypeptide to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

The term "activated cells" as used in this application are those cells which are engaged in extracellular or intracellular membrane trafficking, including the export of secretory or enzymatic molecules as part of a normal or disease process.

The terms "complementary" or "complementarity" refer to the natural binding of polynucleotides by base pairing. For example, the sequence 5'-AGT-3' binds to the complementary sequence 3'-TCA-5'. Complementarity between two single-stranded molecules may be "partial" such that only some of the nucleic acids bind or it may be "complete" such that total complementarity exists between the single stranded molecules. The degree of complementarity between the nucleic acid strands has significant effects on the efficiency and strength of the hybridization between the nucleic acid strands.

The term "embryonic stem cells (ES)" refers to a cell that can give rise to many differentiated cell types in an embryo or an adult, including the germ cells. The term "germ line stem cells (GSCs)" refers to stem cells derived from primordial stem cells that provide a steady and continuous source of germ cells for the production of gametes. The term "primordial germ cells (PGCs)" refers to a small population of cells set aside from other cell lineages particularly from the yolk sac, mesenteries, or gonadal ridges during embryogenesis that have the potential to differentiate into germ cells and other cells. PGCs are the source from which GSCs and ES cells are derived

The PGCs, the GSCs and the ES cells are capable of self-renewal. Thus these cells not only populate the germ line and give rise to a plurality of terminally differentiated cells that comprise the adult specialized organs, but are able to regenerate themselves.

The term "expression modulating fragment," EMF, means a series of
5 nucleotides which modulates the expression of an operably linked ORF or another EMF.

As used herein, a sequence is said to "modulate the expression of an operably linked sequence" when the expression of the sequence is altered by the presence of the EMF. EMFs include, but are not limited to, promoters, and promoter modulating
10 sequences (inducible elements). One class of EMFs are nucleic acid fragments which induce the expression of an operably linked ORF in response to a specific regulatory factor or physiological event.

The terms "nucleotide sequence" or "nucleic acid" or "polynucleotide" or "oligonucleotide" are used interchangeably and refer to a heteropolymer of nucleotides
15 or the sequence of these nucleotides. These phrases also refer to DNA or RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent the sense or the antisense strand, to peptide nucleic acid (PNA) or to any DNA-like or RNA-like material. It is contemplated that where the polynucleotide is RNA, the T (thymine) in the sequences provided herein may be substituted with U
20 (uracil). Generally, nucleic acid segments provided by this invention may be assembled from fragments of the genome and short oligonucleotide linkers, or from a series of oligonucleotides, or from individual nucleotides, to provide a synthetic nucleic acid which is capable of being expressed in a recombinant transcriptional unit comprising regulatory elements derived from a microbial or viral operon, or a eukaryotic gene.

25 The terms "oligonucleotide fragment" or a "polynucleotide fragment", "portion," or "segment" or "probe" or "primer" are used interchangeably and refer to a sequence of nucleotide residues which are at least about 5 nucleotides, more preferably at least about 7 nucleotides, more preferably at least about 9 nucleotides, more preferably at least about 11 nucleotides and most preferably at least about 17
30 nucleotides. The fragment is preferably less than about 500 nucleotides, preferably less

than about 200 nucleotides, more preferably less than about 100 nucleotides, more preferably less than about 50 nucleotides and most preferably less than 30 nucleotides. Preferably the probe is from about 6 nucleotides to about 200 nucleotides, preferably from about 15 to about 50 nucleotides, more preferably from about 17 to 30 nucleotides and most preferably from about 20 to 25 nucleotides. Preferably the fragments can be used in polymerase chain reaction (PCR), various hybridization procedures or microarray procedures to identify or amplify identical or related parts of mRNA or DNA molecules. A fragment or segment may uniquely identify each polynucleotide sequence of the present invention. Preferably the fragment comprises a sequence substantially similar to any one of SEQ ID NOs:1-164.

Probes may, for example, be used to determine whether specific mRNA molecules are present in a cell or tissue or to isolate similar nucleic acid sequences from chromosomal DNA as described by Walsh et al. (Walsh, P.S. et al., 1992, PCR Methods Appl 1:241-250). They may be labeled by nick translation, Klenow fill-in reaction, PCR, or other methods well known in the art. Probes of the present invention, their preparation and/or labeling are elaborated in Sambrook, J. et al., 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY; or Ausubel, F.M. et al., 1989, Current Protocols in Molecular Biology, John Wiley & Sons, New York NY, both of which are incorporated herein by reference in their entirety.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NOs: 1-164. The sequence information can be a segment of any one of SEQ ID NOs: 1-164 that uniquely identifies or represents the sequence information of that sequence of SEQ ID NO: 1-164. One such segment can be a twenty-mer nucleic acid sequence because the probability that a twenty-mer is fully matched in the human genome is 1 in 300. In the human genome, there are three billion base pairs in one set of chromosomes. Because 4^{20} possible twenty-mers exist, there are 300 times more twenty-mers than there are base pairs in a set of human chromosome. Using the same analysis, the probability for a seventeen-mer to be fully matched in the human genome is approximately 1 in 5. When these

segments are used in arrays for expression studies, fifteen-mer segments can be used. The probability that the fifteen-mer is fully matched in the expressed sequences is also approximately one in five because expressed sequences comprise less than approximately 5 % of the entire genome sequence.

5 Similarly, when using sequence information for detecting a single mismatch, a segment can be a twenty-five mer. The probability that the twenty-five mer would appear in a human genome with a single mismatch is calculated by multiplying the probability for a full match ($1/4^{25}$) times the increased probability for mismatch at each nucleotide position (3×25). The probability that an eighteen mer with a single mismatch can be
10 detected in an array for expression studies is approximately one in five. The probability that a twenty-mer with a single mismatch can be detected in a human genome is approximately one in five.

The term "open reading frame," ORF, means a series of nucleotide triplets coding for amino acids without any termination codons and is a sequence translatable
15 into protein.

The terms "operably linked" or "operably associated" refer to functionally related nucleic acid sequences. For example, a promoter is operably associated or operably linked with a coding sequence if the promoter controls the transcription of the coding sequence. While operably linked nucleic acid sequences can be contiguous and
20 in the same reading frame, certain genetic elements e.g. repressor genes are not contiguously linked to the coding sequence but still control transcription/translation of the coding sequence.

The term "pluripotent" refers to the capability of a cell to differentiate into a number of differentiated cell types that are present in an adult organism. A pluripotent
25 cell is restricted in its differentiation capability in comparison to a totipotent cell.

The terms "polypeptide" or "peptide" or "amino acid sequence" refer to an oligopeptide, peptide, polypeptide or protein sequence or fragment thereof and to naturally occurring or synthetic molecules. A polypeptide "fragment," "portion," or "segment" is a stretch of amino acid residues of at least about 5 amino acids, preferably
30 at least about 7 amino acids, more preferably at least about 9 amino acids and most

preferably at least about 17 or more amino acids. The peptide preferably is not greater than about 200 amino acids, more preferably less than 150 amino acids and most preferably less than 100 amino acids. Preferably the peptide is from about 5 to about 200 amino acids. To be active, any polypeptide must have sufficient length to display biological and/or immunological activity.

The term "naturally occurring polypeptide" refers to polypeptides produced by cells that have not been genetically engineered and specifically contemplates various polypeptides arising from post-translational modifications of the polypeptide including, but not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation and acylation.

The term "translated protein coding portion" means a sequence which encodes for the full length protein which may include any leader sequence or any processing sequence.

The term "mature protein coding sequence" means a sequence which encodes a peptide or protein without a signal or leader sequence. The peptide may have been produced by processing in the cell which removes any leader/signal sequence. The peptide may be produced synthetically or the protein may have been produced using a polynucleotide only encoding for the mature protein coding sequence.

The term "derivative" refers to polypeptides chemically modified by such techniques as ubiquitination, labeling (e.g., with radionuclides or various enzymes), covalent polymer attachment such as pegylation (derivatization with polyethylene glycol) and insertion or substitution by chemical synthesis of amino acids such as ornithine, which do not normally occur in human proteins.

The term "variant"(or "analog") refers to any polypeptide differing from naturally occurring polypeptides by amino acid insertions, deletions, and substitutions, created using, *e.g.*, recombinant DNA techniques. Guidance in determining which amino acid residues may be replaced, added or deleted without abolishing activities of interest, may be found by comparing the sequence of the particular polypeptide with that of homologous peptides and minimizing the number of amino acid sequence

changes made in regions of high homology (conserved regions) or by replacing amino acids with consensus sequence.

Alternatively, recombinant variants encoding these same or similar polypeptides may be synthesized or selected by making use of the "redundancy" in the genetic code.

- 5 Various codon substitutions, such as the silent changes which produce various restriction sites, may be introduced to optimize cloning into a plasmid or viral vector or expression in a particular prokaryotic or eukaryotic system. Mutations in the polynucleotide sequence may be reflected in the polypeptide or domains of other peptides added to the polypeptide to modify the properties of any part of the
- 10 polypeptide, to change characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate.

- Preferably, amino acid "substitutions" are the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, *i.e.*, conservative amino acid replacements. "Conservative" amino acid substitutions may be
- 15 made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues involved. For example, nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine; polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine; positively
- 20 charged (basic) amino acids include arginine, lysine, and histidine; and negatively charged (acidic) amino acids include aspartic acid and glutamic acid. "Insertions" or "deletions" are preferably in the range of about 1 to 20 amino acids, more preferably 1 to 10 amino acids. The variation allowed may be experimentally determined by systematically making insertions, deletions, or substitutions of amino acids in a
- 25 polypeptide molecule using recombinant DNA techniques and assaying the resulting recombinant variants for activity.

- Alternatively, where alteration of function is desired, insertions, deletions or non-conservative alterations can be engineered to produce altered polypeptides. Such alterations can, for example, alter one or more of the biological functions or
- 30 biochemical characteristics of the polypeptides of the invention. For example, such

alterations may change polypeptide characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate. Further, such alterations can be selected so as to generate polypeptides that are better suited for expression, scale up and the like in the host cells chosen for expression. For example, cysteine residues can
5 be deleted or substituted with another amino acid residue in order to eliminate disulfide bridges.

The terms "purified" or "substantially purified" as used herein denotes that the indicated nucleic acid or polypeptide is present in the substantial absence of other biological macromolecules, *e.g.*, polynucleotides, proteins, and the like. In one
10 embodiment, the polynucleotide or polypeptide is purified such that it constitutes at least 95% by weight, more preferably at least 99% by weight, of the indicated biological macromolecules present (but water, buffers, and other small molecules, especially molecules having a molecular weight of less than 1000 daltons, can be present).

The term "isolated" as used herein refers to a nucleic acid or polypeptide separated from at least one other component (*e.g.*, nucleic acid or polypeptide) present with the nucleic acid or polypeptide in its natural source. In one embodiment, the nucleic acid or polypeptide is found in the presence of (if anything) only a solvent, buffer, ion, or other component normally present in a solution of the same. The terms
15 "isolated" and "purified" do not encompass nucleic acids or polypeptides present in their natural source.
20

The term "recombinant," when used herein to refer to a polypeptide or protein, means that a polypeptide or protein is derived from recombinant (*e.g.*, microbial, insect, or mammalian) expression systems. "Microbial" refers to recombinant
25 polypeptides or proteins made in bacterial or fungal (*e.g.*, yeast) expression systems. As a product, "recombinant microbial" defines a polypeptide or protein essentially free of native endogenous substances and unaccompanied by associated native glycosylation. Polypeptides or proteins expressed in most bacterial cultures, *e.g.*, *E. coli*, will be free of glycosylation modifications; polypeptides or proteins expressed in yeast will have a
30 glycosylation pattern in general different from those expressed in mammalian cells.

The term "recombinant expression vehicle or vector" refers to a plasmid or phage or virus or vector, for expressing a polypeptide from a DNA (RNA) sequence. An expression vehicle can comprise a transcriptional unit comprising an assembly of (1) a genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers, (2) a structural or coding sequence which is transcribed into mRNA and translated into protein, and (3) appropriate transcription initiation and termination sequences. Structural units intended for use in yeast or eukaryotic expression systems preferably include a leader sequence enabling extracellular secretion of translated protein by a host cell. Alternatively, where recombinant protein is expressed without a leader or transport sequence, it may include an amino terminal methionine residue. This residue may or may not be subsequently cleaved from the expressed recombinant protein to provide a final product.

The term "recombinant expression system" means host cells which have stably integrated a recombinant transcriptional unit into chromosomal DNA or carry the recombinant transcriptional unit extrachromosomally. Recombinant expression systems as defined herein will express heterologous polypeptides or proteins upon induction of the regulatory elements linked to the DNA segment or synthetic gene to be expressed. This term also means host cells which have stably integrated a recombinant genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers. Recombinant expression systems as defined herein will express polypeptides or proteins endogenous to the cell upon induction of the regulatory elements linked to the endogenous DNA segment or gene to be expressed. The cells can be prokaryotic or eukaryotic.

The term "secreted" includes a protein that is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence when it is expressed in a suitable host cell. "Secreted" proteins include without limitation proteins secreted wholly (*e.g.*, soluble proteins) or partially (*e.g.*, receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins that are transported across the membrane of the endoplasmic reticulum. "Secreted" proteins are also intended to include proteins containing

non-typical signal sequences (e.g. Interleukin-1 Beta, see Krasney, P.A. and Young, P.R. (1992) Cytokine 4(2):134 -143) and factors released from damaged cells (e.g. Interleukin-1 Receptor Antagonist, see Arend, W.P. et. al. (1998) Annu. Rev. Immunol. 16:27-55)

5 Where desired, an expression vector may be designed to contain a "signal or leader sequence" which will direct the polypeptide through the membrane of a cell. Such a sequence may be naturally present on the polypeptides of the present invention or provided from heterologous protein sources by recombinant DNA techniques.

10 The term "stringent" is used to refer to conditions that are commonly understood in the art as stringent. Stringent conditions can include highly stringent conditions (i.e., hybridization to filter-bound DNA in 0.5 M NaHPO₄, 7% sodium dodecyl sulfate (SDS), 1 mM EDTA at 65°C, and washing in 0.1X SSC/0.1% SDS at 68°C), and moderately stringent conditions (i.e., washing in 0.2X SSC/0.1% SDS at 42°C). Other exemplary hybridization conditions are described herein in the examples.

15 In instances of hybridization of deoxyoligonucleotides, additional exemplary stringent hybridization conditions include washing in 6X SSC/0.05% sodium pyrophosphate at 37°C (for 14-base oligonucleotides), 48°C (for 17-base oligos), 55°C (for 20-base oligonucleotides), and 60°C (for 23-base oligonucleotides).

20 As used herein, "substantially equivalent" can refer both to nucleotide and amino acid sequences, for example a mutant sequence, that varies from a reference sequence by one or more substitutions, deletions, or additions, the net effect of which does not result in an adverse functional dissimilarity between the reference and subject sequences. Typically, such a substantially equivalent sequence varies from one of those listed herein by no more than about 35% (*i.e.*, the number of individual residue
25 substitutions, additions, and/or deletions in a substantially equivalent sequence, as compared to the corresponding reference sequence, divided by the total number of residues in the substantially equivalent sequence is about 0.35 or less). Such a sequence is said to have 65% sequence identity to the listed sequence. In one embodiment, a substantially equivalent, *e.g.*, mutant, sequence of the invention varies
30 from a listed sequence by no more than 30% (70% sequence identity); in a variation of

this embodiment, by no more than 25% (75% sequence identity); and in a further variation of this embodiment, by no more than 20% (80% sequence identity) and in a further variation of this embodiment, by no more than 10% (90% sequence identity) and in a further variation of this embodiment, by no more than 5% (95% sequence identity). Substantially equivalent, *e.g.*, mutant, amino acid sequences according to the invention preferably have at least 80% sequence identity with a listed amino acid sequence, more preferably at least 90% sequence identity. Substantially equivalent nucleotide sequences of the invention can have lower percent sequence identities, taking into account, for example, the redundancy or degeneracy of the genetic code.

Preferably, nucleotide sequence has at least about 65% identity, more preferably at least about 75% identity, and most preferably at least about 95% identity. For the purposes of the present invention, sequences having substantially equivalent biological activity and substantially equivalent expression characteristics are considered substantially equivalent. For the purposes of determining equivalence, truncation of the mature sequence (*e.g.*, via a mutation which creates a spurious stop codon) should be disregarded. Sequence identity may be determined, *e.g.*, using the Jotun Hein method (Hein, J. (1990) *Methods Enzymol.* 183:626-645). Identity between sequences can also be determined by other methods known in the art, *e.g.* by varying hybridization conditions.

The term "totipotent" refers to the capability of a cell to differentiate into all of the cell types of an adult organism.

The term "transformation" means introducing DNA into a suitable host cell so that the DNA is replicable, either as an extrachromosomal element, or by chromosomal integration. The term "transfection" refers to the taking up of an expression vector by a suitable host cell, whether or not any coding sequences are in fact expressed. The term "infection" refers to the introduction of nucleic acids into a suitable host cell by use of a virus or viral vector.

As used herein, an "uptake modulating fragment," UMF, means a series of nucleotides which mediate the uptake of a linked DNA fragment into a cell. UMFs can be readily identified using known UMFs as a target sequence or target motif with the

computer-based systems described below. The presence and activity of a UMF can be confirmed by attaching the suspected UMF to a marker sequence. The resulting nucleic acid molecule is then incubated with an appropriate host under appropriate conditions and the uptake of the marker sequence is determined. As described above, a UMF will increase the frequency of uptake of a linked marker sequence.

Each of the above terms is meant to encompass all that is described for each, unless the context dictates otherwise.

4.2 NUCLEIC ACIDS OF THE INVENTION

Nucleotide sequences of the invention are set forth in the Sequence Listing.

The isolated polynucleotides of the invention include a polynucleotide comprising the nucleotide sequences of the SEQ ID NO: 1 – 164; a polynucleotide encoding any one of the peptide sequences of SEQ ID NO:1 – 164; and a polynucleotide comprising the nucleotide sequence encoding the mature protein coding sequence of the polynucleotides of any one of SEQ ID NO: 1 - 164. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent conditions to (a) the complement of any of the nucleotides sequences of the SEQ ID NO: 1 – 164; (b) nucleotide sequences encoding any one of the amino acid sequences set forth in the Sequence Listing; (c) a polynucleotide which is an allelic variant of any polynucleotide recited above; (d) a polynucleotide which encodes a species homolog of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of the polypeptides of SEQ ID NO: 1- 164. Domains of interest may depend on the nature of the encoded polypeptide; e.g., domains in receptor-like polypeptides include ligand-binding, extracellular, transmembrane, or cytoplasmic domains, or combinations thereof; domains in immunoglobulin-like proteins include the variable immunoglobulin-like domains; domains in enzyme-like polypeptides include catalytic and substrate binding domains; and domains in ligand polypeptides include receptor-binding domains.

The polynucleotides of the invention include naturally occurring or wholly or partially synthetic DNA, e.g., cDNA and genomic DNA, and RNA, e.g., mRNA. The polynucleotides may include all of the coding region of the cDNA or may represent a portion of the coding region of the cDNA.

- 5 The present invention also provides genes corresponding to the cDNA sequences disclosed herein. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other
- 10 sources of genomic materials. Further 5' and 3' sequence can be obtained using methods known in the art. For example, full length cDNA or genomic DNA that corresponds to any of the polynucleotides of the SEQ ID NO: 1 - 164 can be obtained by screening appropriate cDNA or genomic DNA libraries under suitable hybridization conditions using any of the polynucleotides of the SEQ ID NO: 1 - 164 or a portion thereof as a probe.
- 15 Alternatively, the polynucleotides of the SEQ ID NO: 1 - 164 may be used as the basis for suitable primer(s) that allow identification and/or amplification of genes in appropriate genomic DNA or cDNA libraries.

The nucleic acid sequences of the invention can be assembled from ESTs and sequences (including cDNA and genomic sequences) obtained from one or more public

20 databases, such as dbEST, gbpri, and UniGene. The EST sequences can provide identifying sequence information, representative fragment or segment information, or novel segment information for the full-length gene.

The polynucleotides of the invention also provide polynucleotides including nucleotide sequences that are substantially equivalent to the polynucleotides recited

25 above. Polynucleotides according to the invention can have, *e.g.*, at least about 65%, at least about 70%, at least about 75%, at least about 80%, more typically at least about 90%, and even more typically at least about 95%, sequence identity to a polynucleotide recited above.

Included within the scope of the nucleic acid sequences of the invention are

30 nucleic acid sequence fragments that hybridize under stringent conditions to any of the

nucleotide sequences of the SEQ ID NO: 1 - 164, or complements thereof, which fragment is greater than about 5 nucleotides, preferably 7 nucleotides, more preferably greater than 9 nucleotides and most preferably greater than 17 nucleotides. Fragments of, e.g. 15, 17, or 20 nucleotides or more that are selective for (i.e. specifically

5 hybridize to any one of the polynucleotides of the invention) are contemplated. Probes capable of specifically hybridizing to a polynucleotide can differentiate polynucleotide sequences of the invention from other polynucleotide sequences in the same family of genes or can differentiate human genes from genes of other species, and are preferably based on unique nucleotide sequences.

10 The sequences falling within the scope of the present invention are not limited to these specific sequences, but also include allelic and species variations thereof. Allelic and species variations can be routinely determined by comparing the sequence provided in SEQ ID NO: 1 - 164, a representative fragment thereof, or a nucleotide sequence at least 90% identical, preferably 95% identical, to SEQ ID NOs: 1 - 164 with a sequence from

15 another isolate of the same species. Furthermore, to accommodate codon variability, the invention includes nucleic acid molecules coding for the same amino acid sequences as do the specific ORFs disclosed herein. In other words, in the coding region of an ORF, substitution of one codon for another codon that encodes the same amino acid is expressly contemplated.

20 The nearest neighbor result for the nucleic acids of the present invention, including SEQ ID NOs: 1 - 164, can be obtained by searching a database using an algorithm or a program. Preferably, a BLAST which stands for Basic Local Alignment Search Tool is used to search for local sequence alignments (Altschul, S.F. J Mol. Evol. 36 290-300 (1993) and Altschul S.F. et al. J. Mol. Biol. 21:403-410 (1990)). Alternatively a FASTA

25 version 3 search against Genpept, using Fastxy algorithm.

Species homologs (or orthologs) of the disclosed polynucleotides and proteins are also provided by the present invention. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous or related to that encoded by the polynucleotides.

5 The nucleic acid sequences of the invention are further directed to sequences which encode variants of the described nucleic acids. These amino acid sequence variants may be prepared by methods known in the art by introducing appropriate nucleotide changes into a native or variant polynucleotide. There are two variables in the construction of amino acid sequence variants: the location of the mutation and the
10 nature of the mutation. Nucleic acids encoding the amino acid sequence variants are preferably constructed by mutating the polynucleotide to encode an amino acid sequence that does not occur in nature. These nucleic acid alterations can be made at sites that differ in the nucleic acids from different species (variable positions) or in highly conserved regions (constant regions). Sites at such locations will typically be
15 modified in series, *e.g.*, by substituting first with conservative choices (*e.g.*, hydrophobic amino acid to a different hydrophobic amino acid) and then with more distant choices (*e.g.*, hydrophobic amino acid to a charged amino acid), and then deletions or insertions may be made at the target site. Amino acid sequence deletions generally range from about 1 to 30 residues, preferably about 1 to 10 residues, and are
20 typically contiguous. Amino acid insertions include amino- and/or carboxyl-terminal fusions ranging in length from one to one hundred or more residues, as well as intrasequence insertions of single or multiple amino acid residues. Intrasequence insertions may range generally from about 1 to 10 amino residues, preferably from 1 to 5 residues. Examples of terminal insertions include the heterologous signal sequences
25 necessary for secretion or for intracellular targeting in different host cells and sequences such as FLAG or poly-histidine sequences useful for purifying the expressed protein.

In a preferred method, polynucleotides encoding the novel amino acid sequences are changed via site-directed mutagenesis. This method uses oligonucleotide sequences
30 to alter a polynucleotide to encode the desired amino acid variant, as well as sufficient

adjacent nucleotides on both sides of the changed amino acid to form a stable duplex on either side of the site of being changed. In general, the techniques of site-directed mutagenesis are well known to those of skill in the art and this technique is exemplified by publications such as, Edelman et al., *DNA* 2:183 (1983). A versatile and efficient method for producing site-specific changes in a polynucleotide sequence was published by Zoller and Smith, *Nucleic Acids Res.* 10:6487-6500 (1982). PCR may also be used to create amino acid sequence variants of the novel nucleic acids. When small amounts of template DNA are used as starting material, primer(s) that differs slightly in sequence from the corresponding region in the template DNA can generate the desired amino acid variant. PCR amplification results in a population of product DNA fragments that differ from the polynucleotide template encoding the polypeptide at the position specified by the primer. The product DNA fragments replace the corresponding region in the plasmid and this gives a polynucleotide encoding the desired amino acid variant.

A further technique for generating amino acid variants is the cassette mutagenesis technique described in Wells et al., *Gene* 34:315 (1985); and other mutagenesis techniques well known in the art, such as, for example, the techniques in Sambrook et al., supra, and *Current Protocols in Molecular Biology*, Ausubel et al. Due to the inherent degeneracy of the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be used in the practice of the invention for the cloning and expression of these novel nucleic acids. Such DNA sequences include those which are capable of hybridizing to the appropriate novel nucleic acid sequence under stringent conditions.

Polynucleotides encoding preferred polypeptide truncations of the invention can be used to generate polynucleotides encoding chimeric or fusion proteins comprising one or more domains of the invention and heterologous protein sequences.

The polynucleotides of the invention additionally include the complement of any of the polynucleotides recited above. The polynucleotide can be DNA (genomic, cDNA, amplified, or synthetic) or RNA. Methods and algorithms for obtaining such polynucleotides are well known to those of skill in the art and can include, for example,

methods for determining hybridization conditions that can routinely isolate polynucleotides of the desired sequence identities.

In accordance with the invention, polynucleotide sequences comprising the mature protein coding sequences corresponding to any one of SEQ ID NO: 1-164, or
5 functional equivalents thereof, may be used to generate recombinant DNA molecules that direct the expression of that nucleic acid, or a functional equivalent thereof, in appropriate host cells. Also included are the cDNA inserts of any of the clones identified herein.

A polynucleotide according to the invention can be joined to any of a variety of
10 other nucleotide sequences by well-established recombinant DNA techniques (see Sambrook J et al. (1989) Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY). Useful nucleotide sequences for joining to polynucleotides include an assortment of vectors, e.g., plasmids, cosmids, lambda phage derivatives, phagemids, and the like, that are well known in the art. Accordingly, the invention
15 also provides a vector including a polynucleotide of the invention and a host cell containing the polynucleotide. In general, the vector contains an origin of replication functional in at least one organism, convenient restriction endonuclease sites, and a selectable marker for the host cell. Vectors according to the invention include
20 expression vectors, replication vectors, probe generation vectors, and sequencing vectors. A host cell according to the invention can be a prokaryotic or eukaryotic cell and can be a unicellular organism or part of a multicellular organism.

The present invention further provides recombinant constructs comprising a nucleic acid having any of the nucleotide sequences of the SEQ ID NOs: 1 - 164 or a fragment thereof or any other polynucleotides of the invention. In one embodiment, the
25 recombinant constructs of the present invention comprise a vector, such as a plasmid or viral vector, into which a nucleic acid having any of the nucleotide sequences of the SEQ ID NOs: 1 - 164 or a fragment thereof is inserted, in a forward or reverse orientation. In the case of a vector comprising one of the ORFs of the present invention, the vector may further comprise regulatory sequences, including for
30 example, a promoter, operably linked to the ORF. Large numbers of suitable vectors

and promoters are known to those of skill in the art and are commercially available for generating the recombinant constructs of the present invention. The following vectors are provided by way of example. Bacterial: pBs, phagescript, PsiX174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene); pTrc99A, pKK223-3, 5 pKK233-3, pDR540, pRIT5 (Pharmacia). Eukaryotic: pWLneo, pSV2cat, pOG44, PXTI, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia).

The isolated polynucleotide of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman et al., *Nucleic Acids Res.* 19, 4485-4490 (1991), in order to produce the 10 protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, *Methods in Enzymology* 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the 15 protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters 20 include lacI, lacZ, T3, T7, gpt, lambda PR, and trc. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art. Generally, recombinant expression vectors will include origins of replication and selectable markers permitting 25 transformation of the host cell, e.g., the ampicillin resistance gene of *E. coli* and *S. cerevisiae* TRP1 gene, and a promoter derived from a highly-expressed gene to direct transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), a-factor, acid phosphatase, or heat shock proteins, among others. The heterologous 30 structural sequence is assembled in appropriate phase with translation initiation and

termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an amino terminal identification peptide imparting desired characteristics, *e.g.*, stabilization or simplified purification of expressed recombinant product. Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation and termination signals in operable reading phase with a functional promoter. The vector will comprise one or more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and to, if desirable, provide amplification within the host. Suitable prokaryotic hosts for transformation include *E. coli*, *Bacillus subtilis*, *Salmonella typhimurium* and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*, although others may also be employed as a matter of choice.

As a representative but non-limiting example, useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM 1 (Promega Biotech, Madison, WI, USA). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed. Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is induced or derepressed by appropriate means (*e.g.*, temperature shift or chemical induction) and cells are cultured for an additional period. Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

Polynucleotides of the invention can also be used to induce immune responses. For example, as described in Fan et al., *Nat. Biotech.* 17:870-872 (1999), incorporated herein by reference, nucleic acid sequences encoding a polypeptide may be used to generate antibodies against the encoded polypeptide following topical administration of naked plasmid DNA or following injection, and preferably intramuscular injection of

the DNA. The nucleic acid sequences are preferably inserted in a recombinant expression vector and may be in the form of naked DNA.

4.3 HOSTS

5 The present invention further provides host cells genetically engineered to contain the polynucleotides of the invention. For example, such host cells may contain nucleic acids of the invention introduced into the host cell using known transformation, transfection or infection methods. The present invention still further provides host cells genetically engineered to express the polynucleotides of the invention, wherein such
10 polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in the cell.

Knowledge of nucleic acid sequences allows for modification of cells to permit, or increase, expression of endogenous polypeptide. Cells can be modified (e.g., by homologous recombination) to provide increased polypeptide expression by replacing,
15 in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the polypeptide at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the encoding sequences. See, for example, PCT International Publication No. WO94/12650, PCT International Publication No. WO92/20808, and PCT International Publication No.
20 WO91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., *ada*, *dhfr*, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the coding sequence, amplification of the marker DNA by standard selection
25 methods results in co-amplification of the desired protein coding sequences in the cells.

The host cell can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic host cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the recombinant construct into the host cell can be effected by calcium phosphate transfection, DEAE, dextran mediated
30 transfection, or electroporation (Davis, L. et al., *Basic Methods in Molecular Biology*

(1986)). The host cells containing one of the polynucleotides of the invention, can be used in conventional manners to produce the gene product encoded by the isolated fragment (in the case of an ORF) or can be used to produce a heterologous protein under the control of the EMF.

- 5 Any host/vector system can be used to express one or more of the ORFs of the present invention. These include, but are not limited to, eukaryotic hosts such as HeLa cells, Cv-1 cell, COS cells, 293 cells, and Sf9 cells, as well as prokaryotic host such as *E. coli* and *B. subtilis*. The most preferred cells are those which do not normally express the particular polypeptide or protein or which expresses the polypeptide or
- 10 protein at low natural level. Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, et
- 15 al., in *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor, New York (1989), the disclosure of which is hereby incorporated by reference.

- Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described by Gluzman, *Cell* 23:175 (1981). Other
- 20 cell lines capable of expressing a compatible vector are, for example, the C127, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60,
- 25 U937, HaK or Jurkat cells. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, enhancer, splice,
- 30 and polyadenylation sites may be used to provide the required nontranscribed genetic

elements. Recombinant polypeptides and proteins produced in bacterial culture are usually isolated by initial extraction from cell pellets, followed by one or more salting-out, aqueous ion exchange or size exclusion chromatography steps. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps. Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents.

Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or insects or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains, *Candida*, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli*, *Bacillus subtilis*, *Salmonella typhimurium*, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequence include polyadenylation

signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, *e.g.*, inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the host cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (*gpt*) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

4.4 POLYPEPTIDES OF THE INVENTION

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising: the amino acid sequences set forth as any one of SEQ ID NO: 1-164 or an amino acid sequence encoded by any one of the nucleotide sequences SEQ ID NOs: 1 - 164 or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides preferably with biological or immunological activity that are encoded by: (a) a polynucleotide having any one of the nucleotide sequences set forth in the SEQ ID NOs: 1 - 164 or (b) polynucleotides encoding any one of the amino acid sequences set forth as SEQ ID NO: 1-164 or (c) polynucleotides that hybridize to the complement of the polynucleotides of either (a) or (b) under stringent hybridization conditions. The invention also provides biologically active or immunologically active variants of any of the amino acid sequences set forth as SEQ ID NO: 1-164 or the corresponding full length or mature protein; and "substantial equivalents" thereof (e.g., with at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, typically at least about 95%, more typically at least about 98%, or most typically at least about 99% amino acid identity) that retain biological activity. Polypeptides encoded by allelic variants may have a similar, increased, or decreased activity compared to polypeptides comprising SEQ ID NO: 1-164.

Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H. U. Saragovi, et al., *Bio/Technology* 10, 773-778 (1992) and in R. S. McDowell, et al., *J. Amer. Chem. Soc.* 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites.

The present invention also provides both full-length and mature forms (for example, without a signal sequence or precursor sequence) of the disclosed proteins.

The protein coding sequence is identified in the sequence listing by translation of the

disclosed nucleotide sequences. The mature form of such protein may be obtained by expression of a full-length polynucleotide in a suitable mammalian cell or other host cell. The sequence of the mature form of the protein is also determinable from the amino acid sequence of the full-length form. Where proteins of the present invention are membrane bound, soluble forms of the proteins are also provided. In such forms, part or all of the regions causing the proteins to be membrane bound are deleted so that the proteins are fully secreted from the cell in which it is expressed.

Protein compositions of the present invention may further comprise an acceptable carrier, such as a hydrophilic, *e.g.*, pharmaceutically acceptable, carrier.

The present invention further provides isolated polypeptides encoded by the nucleic acid fragments of the present invention or by degenerate variants of the nucleic acid fragments of the present invention. By "degenerate variant" is intended nucleotide fragments which differ from a nucleic acid fragment of the present invention (*e.g.*, an ORF) by nucleotide sequence but, due to the degeneracy of the genetic code, encode an identical polypeptide sequence. Preferred nucleic acid fragments of the present invention are the ORFs that encode proteins.

A variety of methodologies known in the art can be utilized to obtain any one of the isolated polypeptides or proteins of the present invention. At the simplest level, the amino acid sequence can be synthesized using commercially available peptide synthesizers. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. This technique is particularly useful in producing small peptides and fragments of larger polypeptides. Fragments are useful, for example, in generating antibodies against the native polypeptide. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The polypeptides and proteins of the present invention can alternatively be purified from cells which have been altered to express the desired polypeptide or

protein. As used herein, a cell is said to be altered to express a desired polypeptide or protein when the cell, through genetic manipulation, is made to produce a polypeptide or protein which it normally does not produce or which the cell normally produces at a lower level. One skilled in the art can readily adapt procedures for introducing and
5 expressing either recombinant or synthetic sequences into eukaryotic or prokaryotic cells in order to generate a cell which produces one of the polypeptides or proteins of the present invention.

The invention also relates to methods for producing a polypeptide comprising growing a culture of host cells of the invention in a suitable culture medium, and
10 purifying the protein from the cells or the culture in which the cells are grown. For example, the methods of the invention include a process for producing a polypeptide in which a host cell containing a suitable expression vector that includes a polynucleotide of the invention is cultured under conditions that allow expression of the encoded polypeptide. The polypeptide can be recovered from the culture, conveniently from the
15 culture medium, or from a lysate prepared from the host cells and further purified. Preferred embodiments include those in which the protein produced by such process is a full length or mature form of the protein.

In an alternative method, the polypeptide or protein is purified from bacterial cells which naturally produce the polypeptide or protein. One skilled in the art can
20 readily follow known methods for isolating polypeptides and proteins in order to obtain one of the isolated polypeptides or proteins of the present invention. These include, but are not limited to, immunochromatography, HPLC, size-exclusion chromatography, ion-exchange chromatography, and immuno-affinity chromatography. See, *e.g.*, Scopes, *Protein Purification: Principles and Practice*, Springer-Verlag (1994);
25 Sambrook, et al., in *Molecular Cloning: A Laboratory Manual*; Ausubel et al., *Current Protocols in Molecular Biology*. Polypeptide fragments that retain biological/immunological activity include fragments comprising greater than about 100 amino acids, or greater than about 200 amino acids, and fragments that encode specific protein domains.

001050-09100

The purified polypeptides can be used in *in vitro* binding assays which are well known in the art to identify molecules which bind to the polypeptides. These molecules include but are not limited to, for e.g., small molecules, molecules from combinatorial libraries, antibodies or other proteins. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

In addition, the peptides of the invention or molecules capable of binding to the peptides may be complexed with toxins, e.g., ricin or cholera, or with other compounds that are toxic to cells. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for SEQ ID NO: 1-164.

The protein of the invention may also be expressed as a product of transgenic animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications, in the peptide or DNA sequence, can be made by those skilled in the art using known techniques. Modifications of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, e.g., U.S. Pat. No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein. Regions of the protein that are important for the protein function can be determined by various methods known in the art including the alanine-scanning method which involved systematic substitution of single or strings of amino acids with alanine,

followed by testing the resulting alanine-containing variant for biological activity. This type of analysis determines the importance of the substituted amino acid(s) in biological activity. Regions of the protein that are important for protein function may be determined by the eMATRIX program.

5 Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and are useful for screening or other immunological methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are encompassed by the present invention.

10 The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, *e.g.*, Invitrogen, San Diego, Calif., U.S.A. (the MaxBat™ kit), and such methods
15 are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

20 The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (*i.e.*, from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over
25 such affinity resins as concanavalin A-agarose, heparin-toyopearl™ or Cibacrom blue 3GA Sepharose™; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

30 Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein,

such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX), or as a His tag. Kits for expression and purification of such fusion proteins are commercially available from New England BioLab (Beverly, Mass.), Pharmacia (Piscataway, N.J.) and Invitrogen, respectively. The protein can also be
5 tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("FLAG®") is commercially available from Kodak (New Haven, Conn.).

Finally, one or more reverse-phase high performance liquid chromatography (RP- HPLC) steps employing hydrophobic RP-HPLC media, *e.g.*, silica gel having
10 pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

15 The polypeptides of the invention include analogs (variants). This embraces fragments, as well as peptides in which one or more amino acids has been deleted, inserted, or substituted. Also, analogs of the polypeptides of the invention embrace fusions of the polypeptides or modifications of the polypeptides of the invention, wherein the polypeptide or analog is fused to another moiety or moieties, *e.g.*, targeting
20 moiety or another therapeutic agent. Such analogs may exhibit improved properties such as activity and/or stability. Examples of moieties which may be fused to the polypeptide or an analog include, for example, targeting moieties which provide for the delivery of polypeptide to pancreatic cells, *e.g.*, antibodies to pancreatic cells, antibodies to immune cells such as T-cells, monocytes, dendritic cells, granulocytes,
25 etc., as well as receptor and ligands expressed on pancreatic or immune cells. Other moieties which may be fused to the polypeptide include therapeutic agents which are used for treatment, for example, immunosuppressive drugs such as cyclosporin, SK506, azathioprine, CD3 antibodies and steroids. Also, polypeptides may be fused to immune modulators, and other cytokines such as alpha or beta interferon.

30

4.4.1 DETERMINING POLYPEPTIDE AND POLYNUCLEOTIDE IDENTITY AND SIMILARITY

Preferred identity and/or similarity are designed to give the largest match between the sequences tested. Methods to determine identity and similarity are codified in computer programs including, but are not limited to, the GCG program package, including GAP (Devereux, J., et al., Nucleic Acids Research 12(1):387 (1984); Genetics Computer Group, University of Wisconsin, Madison, WI), BLASTP, BLASTN, BLASTX, FASTA (Altschul, S.F. et al., J. Molec. Biol. 215:403-410 (1990), PSI-BLAST (Altschul S.F. et al., Nucleic Acids Res. vol. 25, pp. 3389-3402, herein incorporated by reference), eMatrix software (Wu et al., J. Comp. Biol., vol. 6, pp. 219-235 (1999), herein incorporated by reference), eMotif software (Nevill-Manning et al, ISMB-97, vol 4, pp. 202-209, herein incorporated by reference) and the Kyte-Doolittle hydrophobicity prediction algorithm (J. Mol Biol, 157, pp. 105-31 (1982), incorporated herein by reference). The BLAST programs are publicly available from the National Center for Biotechnology Information (NCBI) and other sources (BLAST Manual, Altschul, S., et al. NCB NLM NIH Bethesda, MD 20894; Altschul, S., et al., J. Mol. Biol. 215:403-410 (1990).

4.5 GENE THERAPY

Mutations in the polynucleotides of the invention gene may result in loss of normal function of the encoded protein. The invention thus provides gene therapy to restore normal activity of the polypeptides of the invention; or to treat disease states involving polypeptides of the invention. Delivery of a functional gene encoding polypeptides of the invention to appropriate cells is effected *ex vivo*, *in situ*, or *in vivo* by use of vectors, and more particularly viral vectors (e.g., adenovirus, adeno-associated virus, or a retrovirus), or *ex vivo* by use of physical DNA transfer methods (e.g., liposomes or chemical treatments). See, for example, Anderson, Nature, supplement to vol. 392, no. 6679, pp.25-20 (1998). For additional reviews of gene therapy technology see Friedmann, Science, 244: 1275-1281 (1989); Verma, Scientific American: 68-84 (1990); and Miller, Nature, 357: 455-460 (1992). Introduction of any

one of the nucleotides of the present invention or a gene encoding the polypeptides of the present invention can also be accomplished with extrachromosomal substrates (transient expression) or artificial chromosomes (stable expression). Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes. Alternatively, it is contemplated that in other human disease states, preventing the expression of or inhibiting the activity of polypeptides of the invention will be useful in treating the disease states. It is contemplated that antisense therapy or gene therapy could be applied to negatively regulate the expression of polypeptides of the invention.

Other methods inhibiting expression of a protein include the introduction of antisense molecules to the nucleic acids of the present invention, their complements, or their translated RNA sequences, by methods known in the art. Further, the polypeptides of the present invention can be inhibited by using targeted deletion methods, or the insertion of a negative regulatory element such as a silencer, which is tissue specific.

The present invention still further provides cells genetically engineered *in vivo* to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in the cell. These methods can be used to increase or decrease the expression of the polynucleotides of the present invention.

Knowledge of DNA sequences provided by the invention allows for modification of cells to permit, increase, or decrease, expression of endogenous polypeptide. Cells can be modified (e.g., by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the protein at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the desired protein encoding sequences. See, for example, PCT International Publication No. WO 94/12650, PCT International Publication No. WO 92/20808, and PCT International Publication No. WO 91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., *ada*, *dhfr*, and the multifunctional CAD

gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the desired protein coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequences include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, *e.g.*, inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of

cells in which the exogenous DNA has integrated into the cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker
5 flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

10 The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is
15 incorporated by reference herein in its entirety.

4.6 TRANSGENIC ANIMALS

In preferred methods to determine biological functions of the polypeptides of the invention in vivo, one or more genes provided by the invention are either over
20 expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals.
25 Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably

non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of a promoter of the polynucleotides of the invention is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

The polynucleotides of the present invention also make possible the development, through, e.g., homologous recombination or knock out strategies, of animals that fail to express polypeptides of the invention or that express a variant polypeptide. Such animals are useful as models for studying the *in vivo* activities of polypeptide as well as for studying modulators of the polypeptides of the invention.

In preferred methods to determine biological functions of the polypeptides of the invention *in vivo*, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of the polynucleotides of the invention promoter is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

4.7 USES AND BIOLOGICAL ACTIVITY

The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified herein. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA). The mechanism underlying the particular condition or pathology will dictate whether the polypeptides of the invention, the polynucleotides of the invention or modulators (activators or inhibitors) thereof would be beneficial to the subject in need of treatment. Thus, "therapeutic compositions of the invention" include compositions comprising isolated polynucleotides (including recombinant DNA molecules, cloned genes and degenerate variants thereof) or polypeptides of the invention (including full length protein, mature protein and truncations or domains thereof), or compounds and other substances that modulate the overall activity of the target gene products, either at the level of target gene/protein expression or target protein activity. Such modulators include polypeptides, analogs, (variants), including fragments and fusion proteins, antibodies and other binding proteins; chemical compounds that directly or indirectly activate or inhibit the polypeptides of the invention (identified, e.g., via drug screening assays as described herein); antisense polynucleotides and polynucleotides suitable for triple helix

formation; and in particular antibodies or other binding partners that specifically recognize one or more epitopes of the polypeptides of the invention.

The polypeptides of the present invention may likewise be involved in cellular activation or in one of the other physiological pathways described herein.

5

4.7.1 RESEARCH USES AND UTILITIES

The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for
10 tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as
15 probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein
20 antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to
25 identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The polypeptides provided by the present invention can similarly be used in assays to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as
30 a reagent (including the labeled reagent) in assays designed to quantitatively determine

levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding polypeptide is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E. F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S. L. and A. R. Kimmel eds., 1987.

4.7.2 NUTRITIONAL USES

Polynucleotides and polypeptides of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the polypeptide or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the polypeptide or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

4.7.3 CYTOKINE AND CELL PROLIFERATION/DIFFERENTIATION ACTIVITY

A polypeptide of the present invention may exhibit activity relating to cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell

populations. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor-dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of therapeutic compositions of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+(preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e, CMK, HUVEC, and Caco. Therapeutic compositions of the invention can be used in the following:

- 10 Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli, et al., I. Immunol. 149:3778-3783, 1992; Bowman et al., I. Immunol. 152:1756-1761, 1994.
- 15 Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A. M. and Shevach, E. M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human interleukin- γ , Schreiber, R. D. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.
- 20 Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L. S. and Lipsky, P. E. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al., Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad.
- 30

- Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse and human interleukin 6--Nordan, R. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Aced. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11--Bennett, F.,
- 5 Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9--Ciarletta, A., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.
- 10 Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W Strober, Pub. Greene Publishing
- 15 Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

20

4.7.4 STEM CELL GROWTH FACTOR ACTIVITY

- A polypeptide of the present invention may exhibit stem cell growth factor activity and be involved in the proliferation, differentiation and survival of pluripotent and totipotent stem cells including primordial germ cells, embryonic stem cells,
- 25 hematopoietic stem cells and/or germ line stem cells. Administration of the polypeptide of the invention to stem cells *in vivo* or *ex vivo* is expected to maintain and expand cell populations in a totipotent or pluripotent state which would be useful for re-engineering damaged or diseased tissues, transplantation, manufacture of bio-pharmaceuticals and the development of bio-sensors. The ability to produce large
- 30 quantities of human cells has important working applications for the production of

human proteins which currently must be obtained from non-human sources or donors, implantation of cells to treat diseases such as Parkinson's, Alzheimer's and other neurodegenerative diseases; tissues for grafting such as bone marrow, skin, cartilage, tendons, bone, muscle (including cardiac muscle), blood vessels, cornea, neural cells, gastrointestinal cells and others; and organs for transplantation such as kidney, liver, pancreas (including islet cells), heart and lung.

It is contemplated that multiple different exogenous growth factors and/or cytokines may be administered in combination with the polypeptide of the invention to achieve the desired effect, including any of the growth factors listed herein, other stem cell maintenance factors, and specifically including stem cell factor (SCF), leukemia inhibitory factor (LIF), Flt-3 ligand (Flt-3L), any of the interleukins, recombinant soluble IL-6 receptor fused to IL-6, macrophage inflammatory protein 1-alpha (MIP-1-alpha), G-CSF, GM-CSF, thrombopoietin (TPO), platelet factor 4 (PF-4), platelet-derived growth factor (PDGF), neural growth factors and basic fibroblast growth factor (bFGF).

Since totipotent stem cells can give rise to virtually any mature cell type, expansion of these cells in culture will facilitate the production of large quantities of mature cells. Techniques for culturing stem cells are known in the art and administration of polypeptides of the invention, optionally with other growth factors and/or cytokines, is expected to enhance the survival and proliferation of the stem cell populations. This can be accomplished by direct administration of the polypeptide of the invention to the culture medium. Alternatively, stroma cells transfected with a polynucleotide that encodes for the polypeptide of the invention can be used as a feeder layer for the stem cell populations in culture or in vivo. Stromal support cells for feeder layers may include embryonic bone marrow fibroblasts, bone marrow stromal cells, fetal liver cells, or cultured embryonic fibroblasts (see U.S. Patent No. 5,690,926).

Stem cells themselves can be transfected with a polynucleotide of the invention to induce autocrine expression of the polypeptide of the invention. This will allow for generation of undifferentiated totipotent/pluripotent stem cell lines that are useful

as is or that can then be differentiated into the desired mature cell types. These stable cell lines can also serve as a source of undifferentiated totipotent/pluripotent mRNA to create cDNA libraries and templates for polymerase chain reaction experiments. These studies would allow for the isolation and identification of differentially expressed genes in stem cell populations that regulate stem cell proliferation and/or maintenance.

Expansion and maintenance of totipotent stem cell populations will be useful in the treatment of many pathological conditions. For example, polypeptides of the present invention may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease, accidental damage or genetic disorders. The polypeptide of the invention may be useful for inducing the proliferation of neural cells and for the regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders which involve degeneration, death or trauma to neural cells or nerve tissue. In addition, the expanded stem cell populations can also be genetically altered for gene therapy purposes and to decrease host rejection of replacement tissues after grafting or implantation.

Expression of the polypeptide of the invention and its effect on stem cells can also be manipulated to achieve controlled differentiation of the stem cells into more differentiated cell types. A broadly applicable method of obtaining pure populations of a specific differentiated cell type from undifferentiated stem cell populations involves the use of a cell-type specific promoter driving a selectable marker. The selectable marker allows only cells of the desired type to survive. For example, stem cells can be induced to differentiate into cardiomyocytes (Wobus et al., *Differentiation*, 48: 173-182, (1991); Klug et al., *J. Clin. Invest.*, 98(1): 216-224, (1998)) or skeletal muscle cells (Browder, L. W. In: *Principles of Tissue Engineering* eds. Lanza et al., Academic Press (1997)). Alternatively, directed differentiation of stem cells can be accomplished by culturing the stem cells in the presence of a differentiation factor such as retinoic acid and an antagonist of the polypeptide of the invention which would

inhibit the effects of endogenous stem cell factor activity and allow differentiation to proceed.

In vitro cultures of stem cells can be used to determine if the polypeptide of the invention exhibits stem cell growth factor activity. Stem cells are isolated from any one of various cell sources (including hematopoietic stem cells and embryonic stem cells) and cultured on a feeder layer, as described by Thompson et al. Proc. Natl. Acad. Sci, U.S.A., 92: 7844-7848 (1995), in the presence of the polypeptide of the invention alone or in combination with other growth factors or cytokines. The ability of the polypeptide of the invention to induce stem cells proliferation is determined by colony formation on semi-solid support e.g. as described by Bernstein et al., Blood, 77: 2316-2321 (1991).

4.7.5 HEMATOPOIESIS REGULATING ACTIVITY

A polypeptide of the present invention may be involved in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell disorders. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with

transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either *in-vivo* or *ex-vivo* (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

Therapeutic compositions of the invention can be used in the following:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M. G. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, N.Y. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I. K. and Briddell, R. A. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, N.Y. 1994; Neben et al., Experimental Hematology 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R. E. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, N.Y. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, N.Y. 1994; Long term culture initiating cell assay, Sutherland, H. J. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, N.Y. 1994.

4.7.6 TISSUE GROWTH ACTIVITY

A polypeptide of the present invention also may be involved in bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as in wound healing and tissue repair and replacement, and in healing of burns, incisions and ulcers.

5 A polypeptide of the present invention which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Compositions of a polypeptide, antibody, binding partner, or other modulator of the invention may have prophylactic use in closed as well as open fracture reduction and
10 also in the improved fixation of artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A polypeptide of this invention may also be involved in attracting bone-forming cells, stimulating growth of bone-forming cells, or inducing differentiation of
15 progenitors of bone-forming cells. Treatment of osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes may also be possible using the composition of the invention.

20 Another category of tissue regeneration activity that may involve the polypeptide of the present invention is tendon/ligament formation. Induction of tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a
25 preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of
30 congenital, trauma induced, or other tendon or ligament defects of other origin, and is

also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The compositions of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a composition may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a composition of the invention.

Compositions of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

Compositions of the present invention may also be involved in the generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation

of fibrotic scarring may allow normal tissue to regenerate. A polypeptide of the present invention may also exhibit angiogenic activity.

A composition of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various
5 tissues, and conditions resulting from systemic cytokine damage.

A composition of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

Therapeutic compositions of the invention can be used in the following:

10 Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

15 Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, H. I. and Rovee, D. T., eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

4.7.7 IMMUNE STIMULATING OR SUPPRESSING ACTIVITY

20 A polypeptide of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A polynucleotide of the invention can encode a polypeptide exhibiting such activities. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g.,
25 in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable
30 using a protein of the present invention, including infections by HIV, hepatitis viruses,

herpes viruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, proteins of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

- 5 Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease.
- 10 Such a protein (or antagonists thereof, including antibodies) of the present invention may also to be useful in the treatment of allergic reactions and conditions (*e.g.*, anaphylaxis, serum sickness, drug reactions, food allergies, insect venom allergies, mastocytosis, allergic rhinitis, hypersensitivity pneumonitis, urticaria, angioedema, eczema, atopic dermatitis, allergic contact dermatitis, erythema multiforme, Stevens-
- 15 Johnson syndrome, allergic conjunctivitis, atopic keratoconjunctivitis, venereal keratoconjunctivitis, giant papillary conjunctivitis and contact allergies), such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein (or antagonists thereof) of the present invention. The
- 20 therapeutic effects of the polypeptides or antagonists thereof on allergic reactions can be evaluated by in vivo animals models such as the cumulative contact enhancement test (Lastbom et al., Toxicology 125: 59-66, 1998), skin prick test (Hoffmann et al., Allergy 54: 446-54, 1999), guinea pig skin sensitization test (Vohr et al., Arch. Toxicol. 73: 501-9), and murine local lymph node assay (Kimber et al., J. Toxicol.
- 25 Environ. Health 53: 563-79).

- Using the proteins of the invention it may also be possible to modulate immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited
- 30 by suppressing T cell responses or by inducing specific tolerance in T cells, or both.

Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7)), e.g., preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a therapeutic composition of the invention may prevent cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, a lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular therapeutic compositions in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins in vivo as described in Lenschow et al., Science 257:789-792 (1992) and Turka et al., Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York,

1989, pp. 846-847) can be used to determine the effect of therapeutic compositions of the invention on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block stimulation of T cells can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (e.g., a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response may be useful in cases of viral infection, including systemic viral diseases such as influenza, the common cold, and encephalitis.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells in vitro with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the in vitro activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient,

transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells in vivo.

A polypeptide of the present invention may provide the necessary stimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient mounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (e.g., a cytoplasmic-domain truncated portion) of an MHC class I alpha chain protein and β_2 microglobulin protein or an MHC class II alpha chain protein and an MHC class II beta chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J.

Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., I. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bowman et al., J. Virology 61:1992-1998; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

- 5 Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: In vitro antibody production, Mond, J. J. and Brunswick, M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

- 15 Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

- 20 Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine 182:255-260, 1995; Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

- 25 Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate
- 30

lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al.,
5 Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al.,
10 Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

4.7.8 ACTIVIN/INHIBIN ACTIVITY

A polypeptide of the present invention may also exhibit activin- or
15 inhibin-related activities. A polynucleotide of the invention may encode a polypeptide exhibiting such characteristics. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins and are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a polypeptide of the present invention, alone or in heterodimers with a member of the
20 inhibin family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the polypeptide of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin group, may be useful as a fertility
25 inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, U.S. Pat. No. 4,798,885. A polypeptide of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as, but not limited to, cows, sheep and pigs.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods.

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., *Endocrinology* 91:562-572, 1972; Ling et al., *Nature* 321:779-782, 1986; Vale et al., *Nature* 321:776-779, 1986; Mason et al., *Nature* 318:659-663, 1985; Forage et al., *Proc. Natl. Acad. Sci. USA* 83:3091-3095, 1986.

4.7.9 CHEMOTACTIC/CHEMOKINETIC ACTIVITY

A polypeptide of the present invention may be involved in chemotactic or chemokinetic activity for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Chemotactic and chemokinetic receptor activation can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic compositions (e.g. proteins, antibodies, binding partners, or modulators of the invention) provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

Therapeutic compositions of the invention can be used in the following:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for

movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Marguiles, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25:1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153:1762-1768, 1994.

4.7.10 HEMOSTATIC AND THROMBOLYTIC ACTIVITY

A polypeptide of the invention may also be involved in hemostasis or thrombolysis or thrombosis. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Compositions may be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A composition of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

Therapeutic compositions of the invention can be used in the following:

Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-164, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

4.7.11 CANCER DIAGNOSIS AND THERAPY

Polypeptides of the invention may be involved in cancer cell generation, proliferation or metastasis. Detection of the presence or amount of polynucleotides or polypeptides of the invention may be useful for the diagnosis and/or prognosis of one or more types of cancer. For example, the presence or increased expression of a polynucleotide/polypeptide of the invention may indicate a hereditary risk of cancer, a

precancerous condition, or an ongoing malignancy. Conversely, a defect in the gene or absence of the polypeptide may be associated with a cancer condition. Identification of single nucleotide polymorphisms associated with cancer or a predisposition to cancer may also be useful for diagnosis or prognosis.

5 Cancer treatments promote tumor regression by inhibiting tumor cell proliferation, inhibiting angiogenesis (growth of new blood vessels that is necessary to support tumor growth) and/or prohibiting metastasis by reducing tumor cell motility or invasiveness. Therapeutic compositions of the invention may be effective in adult and pediatric oncology including in solid phase tumors/malignancies, locally advanced
10 tumors, human soft tissue sarcomas, metastatic cancer, including lymphatic metastases, blood cell malignancies including multiple myeloma, acute and chronic leukemias, and lymphomas, head and neck cancers including mouth cancer, larynx cancer and thyroid cancer, lung cancers including small cell carcinoma and non-small cell cancers, breast cancers including small cell carcinoma and ductal carcinoma, gastrointestinal cancers
15 including esophageal cancer, stomach cancer, colon cancer, colorectal cancer and polyps associated with colorectal neoplasia, pancreatic cancers, liver cancer, urologic cancers including bladder cancer and prostate cancer, malignancies of the female genital tract including ovarian carcinoma, uterine (including endometrial) cancers, and solid tumor in the ovarian follicle, kidney cancers including renal cell carcinoma, brain
20 cancers including intrinsic brain tumors, neuroblastoma, astrocytic brain tumors, gliomas, metastatic tumor cell invasion in the central nervous system, bone cancers including osteomas, skin cancers including malignant melanoma, tumor progression of human skin keratinocytes, squamous cell carcinoma, basal cell carcinoma, hemangiopericytoma and Kaposi's sarcoma.

25 Polypeptides, polynucleotides, or modulators of polypeptides of the invention (including inhibitors and stimulators of the biological activity of the polypeptide of the invention) may be administered to treat cancer. Therapeutic compositions can be administered in therapeutically effective dosages alone or in combination with adjuvant cancer therapy such as surgery, chemotherapy, radiotherapy, thermotherapy, and laser
30 therapy, and may provide a beneficial effect, e.g. reducing tumor size, slowing rate of

tumor growth, inhibiting metastasis, or otherwise improving overall clinical condition, without necessarily eradicating the cancer.

The composition can also be administered in therapeutically effective amounts as a portion of an anti-cancer cocktail. An anti-cancer cocktail is a mixture of the

5 polypeptide or modulator of the invention with one or more anti-cancer drugs in addition to a pharmaceutically acceptable carrier for delivery. The use of anti-cancer cocktails as a cancer treatment is routine. Anti-cancer drugs that are well known in the art and can be used as a treatment in combination with the polypeptide or modulator of the invention include: Actinomycin D, Aminoglutethimide, Asparaginase, Bleomycin, 10 Busulfan, Carboplatin, Carmustine, Chlorambucil, Cisplatin (cis-DDP), Cyclophosphamide, Cytarabine HCl (Cytosine arabinoside), Dacarbazine, Dactinomycin, Daunorubicin HCl, Doxorubicin HCl, Estramustine phosphate sodium, Etoposide (V16-213), Floxuridine, 5-Fluorouracil (5-Fu), Flutamide, Hydroxyurea (hydroxycarbamide), Ifosfamide, Interferon Alpha-2a, Interferon Alpha-2b, Leuprolide 15 acetate (LHRH-releasing factor analog), Lomustine, Mechlorethamine HCl (nitrogen mustard), Melphalan, Mercaptopurine, Mesna, Methotrexate (MTX), Mitomycin, Mitoxantrone HCl, Octreotide, Plicamycin, Procarbazine HCl, Streptozocin, Tamoxifen citrate, Thioguanine, Thiotepa, Vinblastine sulfate, Vincristine sulfate, Amsacrine, Azacitidine, Hexamethylmelamine, Interleukin-2, Mitoguazone, 20 Pentostatin, Semustine, Teniposide, and Vindesine sulfate.

In addition, therapeutic compositions of the invention may be used for prophylactic treatment of cancer. There are hereditary conditions and/or environmental situations (e.g. exposure to carcinogens) known in the art that predispose an individual to developing cancers. Under these circumstances, it may be beneficial to treat these 25 individuals with therapeutically effective doses of the polypeptide of the invention to reduce the risk of developing cancers.

In vitro models can be used to determine the effective doses of the polypeptide of the invention as a potential cancer treatment. These *in vitro* models include proliferation assays of cultured tumor cells, growth of cultured tumor cells in soft agar 30 (see Freshney, (1987) Culture of Animal Cells: A Manual of Basic Technique, Wiley-

Liss, New York, NY Ch 18 and Ch 21), tumor systems in nude mice as described in Giovannella et al., J. Natl. Can. Inst., 52: 921-30 (1974), mobility and invasive potential of tumor cells in Boyden Chamber assays as described in Pilkington et al., Anticancer Res., 17: 4107-9 (1997), and angiogenesis assays such as induction of vascularization of the chick chorioallantoic membrane or induction of vascular endothelial cell migration as described in Ribatta et al., Intl. J. Dev. Biol., 40: 1189-97 (1999) and Li et al., Clin. Exp. Metastasis, 17:423-9 (1999), respectively. Suitable tumor cells lines are available, e.g. from American Type Tissue Culture Collection catalogs.

4.7.12 RECEPTOR/LIGAND ACTIVITY

A polypeptide of the present invention may also demonstrate activity as receptor, receptor ligand or inhibitor or agonist of receptor/ligand interactions. A polynucleotide of the invention can encode a polypeptide exhibiting such characteristics. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses. Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley- Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1- 7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA

84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

By way of example, the polypeptides of the invention may be used as a receptor
5 for a ligand(s) thereby transmitting the biological activity of that ligand(s). Ligands may be identified through binding assays, affinity chromatography, dihybrid screening assays, BIAcore assays, gel overlay assays, or other methods known in the art.

Studies characterizing drugs or proteins as agonist or antagonist or partial agonists or a partial antagonist require the use of other proteins as competing ligands.

10 The polypeptides of the present invention or ligand(s) thereof may be labeled by being coupled to radioisotopes, colorimetric molecules or a toxin molecules by conventional methods. ("Guide to Protein Purification" Murray P. Deutscher (ed) Methods in Enzymology Vol. 182 (1990) Academic Press, Inc. San Diego). Examples of radioisotopes include, but are not limited to, tritium and carbon-14 . Examples of
15 colorimetric molecules include, but are not limited to, fluorescent molecules such as fluorescamine, or rhodamine or other colorimetric molecules. Examples of toxins include, but are not limited, to ricin.

4.7.13 DRUG SCREENING

20 This invention is particularly useful for screening chemical compounds by using the novel polypeptides or binding fragments thereof in any of a variety of drug screening techniques. The polypeptides or fragments employed in such a test may either be free in solution, affixed to a solid support, borne on a cell surface or located intracellularly. One method of drug screening utilizes eukaryotic or prokaryotic host
25 cells which are stably transformed with recombinant nucleic acids expressing the polypeptide or a fragment thereof. Drugs are screened against such transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One may measure, for example, the formation of complexes between polypeptides of the invention or fragments and the agent being

tested or examine the diminution in complex formation between the novel polypeptides and an appropriate cell line, which are well known in the art.

Sources for test compounds that may be screened for ability to bind to or modulate (i.e., increase or decrease) the activity of polypeptides of the invention include (1) inorganic and organic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of either random or mimetic peptides, oligonucleotides or organic molecules.

Chemical libraries may be readily synthesized or purchased from a number of commercial sources, and may include structural analogs of known compounds or compounds that are identified as "hits" or "leads" via natural product screening.

The sources of natural product libraries are microorganisms (including bacteria and fungi), animals, plants or other vegetation, or marine organisms, and libraries of mixtures for screening may be created by: (1) fermentation and extraction of broths from soil, plant or marine microorganisms or (2) extraction of the organisms themselves. Natural product libraries include polyketides, non-ribosomal peptides, and (non-naturally occurring) variants thereof. For a review, see *Science* 282:63-68 (1998).

Combinatorial libraries are composed of large numbers of peptides, oligonucleotides or organic compounds and can be readily prepared by traditional automated synthesis methods, PCR, cloning or proprietary synthetic methods. Of particular interest are peptide and oligonucleotide combinatorial libraries. Still other libraries of interest include peptide, protein, peptidomimetic, multiparallel synthetic collection, recombinatorial, and polypeptide libraries. For a review of combinatorial chemistry and libraries created therefrom, see Myers, *Curr. Opin. Biotechnol.* 8:701-707 (1997). For reviews and examples of peptidomimetic libraries, see Al-Obeidi et al., *Mol. Biotechnol.* 9(3):205-23 (1998); Hruby et al., *Curr Opin Chem Biol*, 1(1):114-19 (1997); Dorner et al., *Bioorg Med Chem*, 4(5):709-15 (1996) (alkylated dipeptides).

Identification of modulators through use of the various libraries described herein permits modification of the candidate "hit" (or "lead") to optimize the capacity of the

“hit” to bind a polypeptide of the invention. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

The binding molecules thus identified may be complexed with toxins, e.g., ricin or cholera, or with other compounds that are toxic to cells such as radioisotopes. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for a polypeptide of the invention. Alternatively, the binding molecules may be complexed with imaging agents for targeting and imaging purposes.

4.7.14 ASSAY FOR RECEPTOR ACTIVITY

The invention also provides methods to detect specific binding of a polypeptide e.g. a ligand or a receptor. The art provides numerous assays particularly useful for identifying previously unknown binding partners for receptor polypeptides of the invention. For example, expression cloning using mammalian or bacterial cells, or dihybrid screening assays can be used to identify polynucleotides encoding binding partners. As another example, affinity chromatography with the appropriate immobilized polypeptide of the invention can be used to isolate polypeptides that recognize and bind polypeptides of the invention. There are a number of different libraries used for the identification of compounds, and in particular small molecules, that modulate (*i.e.*, increase or decrease) biological activity of a polypeptide of the invention. Ligands for receptor polypeptides of the invention can also be identified by adding exogenous ligands, or cocktails of ligands to two cells populations that are genetically identical except for the expression of the receptor of the invention: one cell population expresses the receptor of the invention whereas the other does not. The response of the two cell populations to the addition of ligands(s) are then compared. Alternatively, an expression library can be co-expressed with the polypeptide of the invention in cells and assayed for an autocrine response to identify potential ligand(s).

As still another example, BIAcore assays, gel overlay assays, or other methods known in the art can be used to identify binding partner polypeptides, including, (1) organic and inorganic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of random peptides, oligonucleotides or organic molecules.

5 The role of downstream intracellular signaling molecules in the signaling cascade of the polypeptide of the invention can be determined. For example, a chimeric protein in which the cytoplasmic domain of the polypeptide of the invention is fused to the extracellular portion of a protein, whose ligand has been identified, is produced in a host cell. The cell is then incubated with the ligand specific for the extracellular portion
10 of the chimeric protein, thereby activating the chimeric receptor. Known downstream proteins involved in intracellular signaling can then be assayed for expected modifications i.e. phosphorylation. Other methods known to those in the art can also be used to identify signaling molecules involved in receptor activity.

15 **4.7.15 ANTI-INFLAMMATORY ACTIVITY**

 Compositions of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting
20 chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Compositions with such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation intimation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion
25 injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Compositions of the invention may also be useful to treat anaphylaxis and
30 hypersensitivity to an antigenic substance or material. Compositions of this invention

may be utilized to prevent or treat conditions such as, but not limited to, sepsis, acute pancreatitis, endotoxin shock, cytokine induced shock, rheumatoid arthritis, chronic inflammatory arthritis, pancreatic cell damage from diabetes mellitus type 1, graft versus host disease, inflammatory bowel disease, inflammation associated with

5 pulmonary disease, other autoimmune disease or inflammatory disease, an antiproliferative agent such as for acute or chronic myelogenous leukemia or in the prevention of premature labor secondary to intrauterine infections.

4.7.16 LEUKEMIAS

10 Leukemias and related disorders may be treated or prevented by administration of a therapeutic that promotes or inhibits function of the polynucleotides and/or polypeptides of the invention. Such leukemias and related disorders include but are not limited to acute leukemia, acute lymphocytic leukemia, acute myelocytic leukemia, myeloblastic, promyelocytic, myelomonocytic, monocytic, erythroleukemia, chronic

15 leukemia, chronic myelocytic (granulocytic) leukemia and chronic lymphocytic leukemia (for a review of such disorders, see Fishman et al., 1985, Medicine, 2d Ed., J.B. Lippincott Co., Philadelphia).

4.7.17 NERVOUS SYSTEM DISORDERS

20 Nervous system disorders, involving cell types which can be tested for efficacy of intervention with compounds that modulate the activity of the polynucleotides and/or polypeptides of the invention, and which can be treated upon thus observing an indication of therapeutic utility, include but are not limited to nervous system injuries, and diseases or disorders which result in either a disconnection of axons, a diminution

25 or degeneration of neurons, or demyelination. Nervous system lesions which may be treated in a patient (including human and non-human mammalian patients) according to the invention include but are not limited to the following lesions of either the central (including spinal cord, brain) or peripheral nervous systems:

(i) traumatic lesions, including lesions caused by physical injury or associated with surgery, for example, lesions which sever a portion of the nervous system, or compression injuries;

5 (ii) ischemic lesions, in which a lack of oxygen in a portion of the nervous system results in neuronal injury or death, including cerebral infarction or ischemia, or spinal cord infarction or ischemia;

10 (iii) infectious lesions, in which a portion of the nervous system is destroyed or injured as a result of infection, for example, by an abscess or associated with infection by human immunodeficiency virus, herpes zoster, or herpes simplex virus or with Lyme disease, tuberculosis, syphilis;

(iv) degenerative lesions, in which a portion of the nervous system is destroyed or injured as a result of a degenerative process including but not limited to degeneration associated with Parkinson's disease, Alzheimer's disease, Huntington's chorea, or amyotrophic lateral sclerosis;

15 (v) lesions associated with nutritional diseases or disorders, in which a portion of the nervous system is destroyed or injured by a nutritional disorder or disorder of metabolism including but not limited to, vitamin B12 deficiency, folic acid deficiency, Wernicke disease, tobacco-alcohol amblyopia, Marchiafava-Bignami disease (primary degeneration of the corpus callosum), and alcoholic cerebellar degeneration;

20 (vi) neurological lesions associated with systemic diseases including but not limited to diabetes (diabetic neuropathy, Bell's palsy), systemic lupus erythematosus, carcinoma, or sarcoidosis;

(vii) lesions caused by toxic substances including alcohol, lead, or particular neurotoxins; and

25 (viii) demyelinated lesions in which a portion of the nervous system is destroyed or injured by a demyelinating disease including but not limited to multiple sclerosis, human immunodeficiency virus-associated myelopathy, transverse myelopathy or various etiologies, progressive multifocal leukoencephalopathy, and central pontine myelinolysis.

Therapeutics which are useful according to the invention for treatment of a nervous system disorder may be selected by testing for biological activity in promoting the survival or differentiation of neurons. For example, and not by way of limitation, therapeutics which elicit any of the following effects may be useful according to the invention:

- (i) increased survival time of neurons in culture;
- (ii) increased sprouting of neurons in culture or *in vivo*;
- (iii) increased production of a neuron-associated molecule in culture or *in vivo*, *e.g.*, choline acetyltransferase or acetylcholinesterase with respect to motor neurons; or
- (iv) decreased symptoms of neuron dysfunction *in vivo*.

Such effects may be measured by any method known in the art. In preferred, non-limiting embodiments, increased survival of neurons may be measured by the method set forth in Arakawa et al. (1990, J. Neurosci. 10:3507-3515); increased sprouting of neurons may be detected by methods set forth in Pestronk et al. (1980, Exp. Neurol. 70:65-82) or Brown et al. (1981, Ann. Rev. Neurosci. 4:17-42); increased production of neuron-associated molecules may be measured by bioassay, enzymatic assay, antibody binding, Northern blot assay, *etc.*, depending on the molecule to be measured; and motor neuron dysfunction may be measured by assessing the physical manifestation of motor neuron disorder, *e.g.*, weakness, motor neuron conduction velocity, or functional disability.

In specific embodiments, motor neuron disorders that may be treated according to the invention include but are not limited to disorders such as infarction, infection, exposure to toxin, trauma, surgical damage, degenerative disease or malignancy that may affect motor neurons as well as other components of the nervous system, as well as disorders that selectively affect neurons such as amyotrophic lateral sclerosis, and including but not limited to progressive spinal muscular atrophy, progressive bulbar palsy, primary lateral sclerosis, infantile and juvenile muscular atrophy, progressive bulbar paralysis of childhood (Fazio-Londe syndrome), poliomyelitis and the post polio syndrome, and Hereditary Motorsensory Neuropathy (Charcot-Marie-Tooth Disease).

4.7.18 OTHER ACTIVITIES

A polypeptide of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing,

- 5 infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or
- 10 circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, co-factors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders),
- 15 depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as,
- 20 for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

4.7.19 IDENTIFICATION OF POLYMORPHISMS

The demonstration of polymorphisms makes possible the identification of such polymorphisms in human subjects and the pharmacogenetic use of this information for diagnosis and treatment. Such polymorphisms may be associated with, e.g., differential predisposition or susceptibility to various disease states (such as disorders involving

30 inflammation or immune response) or a differential response to drug administration,

and this genetic information can be used to tailor preventive or therapeutic treatment appropriately. For example, the existence of a polymorphism associated with a predisposition to inflammation or autoimmune disease makes possible the diagnosis of this condition in humans by identifying the presence of the polymorphism.

- 5 Polymorphisms can be identified in a variety of ways known in the art which all generally involve obtaining a sample from a patient, analyzing DNA from the sample, optionally involving isolation or amplification of the DNA, and identifying the presence of the polymorphism in the DNA. For example, PCR may be used to amplify an appropriate fragment of genomic DNA which may then be sequenced. Alternatively,
- 10 the DNA may be subjected to allele-specific oligonucleotide hybridization (in which appropriate oligonucleotides are hybridized to the DNA under conditions permitting detection of a single base mismatch) or to a single nucleotide extension assay (in which an oligonucleotide that hybridizes immediately adjacent to the position of the polymorphism is extended with one or more labeled nucleotides). In addition,
- 15 traditional restriction fragment length polymorphism analysis (using restriction enzymes that provide differential digestion of the genomic DNA depending on the presence or absence of the polymorphism) may be performed. Arrays with nucleotide sequences of the present invention can be used to detect polymorphisms. The array can comprise modified nucleotide sequences of the present invention in order to detect the nucleotide
- 20 sequences of the present invention. In the alternative, any one of the nucleotide sequences of the present invention can be placed on the array to detect changes from those sequences.

- Alternatively a polymorphism resulting in a change in the amino acid sequence could also be detected by detecting a corresponding change in amino acid sequence of
- 25 the protein, e.g., by an antibody specific to the variant sequence.

4.7.20 ARTHRITIS AND INFLAMMATION

- The immunosuppressive effects of the compositions of the invention against rheumatoid arthritis is determined in an experimental animal model system. The
- 30 experimental model system is adjuvant induced arthritis in rats, and the protocol is

described by J. Holoshitz, et al., 1983, Science, 219:56, or by B. Waksman et al., 1963, Int. Arch. Allergy Appl. Immunol., 23:129. Induction of the disease can be caused by a single injection, generally intradermally, of a suspension of killed Mycobacterium tuberculosis in complete Freund's adjuvant (CFA). The route of injection can vary, but rats may be injected at the base of the tail with an adjuvant mixture. The polypeptide is administered in phosphate buffered solution (PBS) at a dose of about 1-5 mg/kg. The control consists of administering PBS only.

The procedure for testing the effects of the test compound would consist of intradermally injecting killed Mycobacterium tuberculosis in CFA followed by immediately administering the test compound and subsequent treatment every other day until day 24. At 14, 15, 18, 20, 22, and 24 days after injection of Mycobacterium CFA, an overall arthritis score may be obtained as described by J. Holoskitz above. An analysis of the data would reveal that the test compound would have a dramatic affect on the swelling of the joints as measured by a decrease of the arthritis score.

4.8 THERAPEUTIC METHODS

The compositions (including polypeptide fragments, analogs, variants and antibodies or other binding partners or modulators including antisense polynucleotides) of the invention have numerous applications in a variety of therapeutic methods. Examples of therapeutic applications include, but are not limited to, those exemplified herein.

4.8.1 EXAMPLE

One embodiment of the invention is the administration of an effective amount of the polypeptides or other composition of the invention to individuals affected by a disease or disorder that can be modulated by regulating the peptides of the invention. While the mode of administration is not particularly important, parenteral administration is preferred. An exemplary mode of administration is to deliver an intravenous bolus. The dosage of the polypeptides or other composition of the

invention will normally be determined by the prescribing physician. It is to be expected that the dosage will vary according to the age, weight, condition and response of the individual patient. Typically, the amount of polypeptide administered per dose will be in the range of about 0.01µg/kg to 100 mg/kg of body weight, with the preferred dose being about 0.1µg/kg to 10 mg/kg of patient body weight. For parenteral administration, polypeptides of the invention will be formulated in an injectable form combined with a pharmaceutically acceptable parenteral vehicle. Such vehicles are well known in the art and examples include water, saline, Ringer's solution, dextrose solution, and solutions consisting of small amounts of the human serum albumin. The vehicle may contain minor amounts of additives that maintain the isotonicity and stability of the polypeptide or other active ingredient. The preparation of such solutions is within the skill of the art.

4.9 PHARMACEUTICAL FORMULATIONS AND ROUTES OF ADMINISTRATION

A protein or other composition of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources and including antibodies and other binding partners of the polypeptides of the invention) may be administered to a patient in need, by itself, or in pharmaceutical compositions where it is mixed with suitable carriers or excipient(s) at doses to treat or ameliorate a variety of disorders. Such a composition may optionally contain (in addition to protein or other active ingredient and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF,

Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the disease or disorder in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet-derived growth factor (PDGF), transforming growth factors (TGF- α and TGF- β), insulin-like growth factor (IGF), as well as cytokines described herein.

The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or other active ingredient or complement its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein or other active ingredient of the invention, or to minimize side effects. Conversely, protein or other active ingredient of the present invention may be included in formulations of the particular clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent (such as IL-1Ra, IL-1 Hy1, IL-1 Hy2, anti-TNF, corticosteroids, immunosuppressive agents). A protein of the present invention may be active in multimers (e.g., heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

As an alternative to being included in a pharmaceutical composition of the invention including a first protein, a second protein or a therapeutic agent may be concurrently administered with the first protein (e.g., at the same time, or at differing times provided that therapeutic concentrations of the combination of agents is achieved at the treatment site). Techniques for formulation and administration of the compounds of the instant application may be found in "Remington's Pharmaceutical Sciences," Mack Publishing Co., Easton, PA, latest edition. A therapeutically effective dose further refers to that amount of the compound sufficient to result in amelioration of symptoms, *e.g.*, treatment, healing, prevention or amelioration of the relevant medical

condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, a therapeutically effective dose refers to that ingredient alone. When applied to a combination, a therapeutically effective dose refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein or other active ingredient of the present invention is administered to a mammal having a condition to be treated. Protein or other active ingredient of the present invention may be administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co-administered with one or more cytokines, lymphokines or other hematopoietic factors, protein or other active ingredient of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein or other active ingredient of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

4.9.1 ROUTES OF ADMINISTRATION

Suitable routes of administration may, for example, include oral, rectal, transmucosal, or intestinal administration; parenteral delivery, including intramuscular, subcutaneous, intramedullary injections, as well as intrathecal, direct intraventricular, intravenous, intraperitoneal, intranasal, or intraocular injections. Administration of protein or other active ingredient of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or

cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection.

Intravenous administration to the patient is preferred.

Alternately, one may administer the compound in a local rather than systemic manner, for example, via injection of the compound directly into a arthritic joints or in fibrotic tissue, often in a depot or sustained release formulation. In order to prevent the scarring process frequently occurring as complication of glaucoma surgery, the compounds may be administered topically, for example, as eye drops. Furthermore, one may administer the drug in a targeted drug delivery system, for example, in a liposome coated with a specific antibody, targeting, for example, arthritic or fibrotic tissue. The liposomes will be targeted to and taken up selectively by the afflicted tissue.

The polypeptides of the invention are administered by any route that delivers an effective dosage to the desired site of action. The determination of a suitable route of administration and an effective dosage for a particular indication is within the level of skill in the art. Preferably for wound treatment, one administers the therapeutic compound directly to the site. Suitable dosage ranges for the polypeptides of the invention can be extrapolated from these dosages or from similar studies in appropriate animal models. Dosages can then be adjusted as necessary by the clinician to provide maximal therapeutic benefit.

4.9.2 COMPOSITIONS/FORMULATIONS

Pharmaceutical compositions for use in accordance with the present invention thus may be formulated in a conventional manner using one or more physiologically acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. These pharmaceutical compositions may be manufactured in a manner that is itself known, *e.g.*, by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes. Proper formulation is dependent upon the route of administration chosen. When a therapeutically effective amount of protein or other active ingredient of the present

invention is administered orally, protein or other active ingredient of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein or other active ingredient of the present invention, and preferably from about 25 to 90% protein or other active ingredient of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein or other active ingredient of the present invention, and preferably from about 1 to 50% protein or other active ingredient of the present invention.

When a therapeutically effective amount of protein or other active ingredient of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein or other active ingredient of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein or other active ingredient solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein or other active ingredient of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art. For injection, the agents of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks's solution, Ringer's solution, or physiological saline buffer. For

transmucosal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

For oral administration, the compounds can be formulated readily by combining the active compounds with pharmaceutically acceptable carriers well known in the art.

- 5 Such carriers enable the compounds of the invention to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions and the like, for oral ingestion by a patient to be treated. Pharmaceutical preparations for oral use can be obtained from a solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or
- 10 dragee cores. Suitable excipients are, in particular, fillers such as sugars, including lactose, sucrose, mannitol, or sorbitol; cellulose preparations such as, for example, maize starch, wheat starch, rice starch, potato starch, gelatin, gum tragacanth, methyl cellulose, hydroxypropylmethyl-cellulose, sodium carboxymethylcellulose, and/or polyvinylpyrrolidone (PVP). If desired, disintegrating agents may be added, such as
- 15 the cross-linked polyvinyl pyrrolidone, agar, or alginic acid or a salt thereof such as sodium alginate. Dragee cores are provided with suitable coatings. For this purpose, concentrated sugar solutions may be used, which may optionally contain gum arabic, talc, polyvinyl pyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or
- 20 pigments may be added to the tablets or dragee coatings for identification or to characterize different combinations of active compound doses.

- Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a plasticizer, such as glycerol or sorbitol. The push-fit capsules can contain the active ingredients in
- 25 admixture with filler such as lactose, binders such as starches, and/or lubricants such as talc or magnesium stearate and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycols. In addition, stabilizers may be added. All formulations for oral administration should be in dosages suitable for such

administration. For buccal administration, the compositions may take the form of tablets or lozenges formulated in conventional manner.

For administration by inhalation, the compounds for use according to the present invention are conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebuliser, with the use of a suitable propellant, *e.g.*, dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon dioxide or other suitable gas. In the case of a pressurized aerosol the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges of, *e.g.*, gelatin for use in an inhaler or insufflator may be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch. The compounds may be formulated for parenteral administration by injection, *e.g.*, by bolus injection or continuous infusion. Formulations for injection may be presented in unit dosage form, *e.g.*, in ampules or in multi-dose containers, with an added preservative. The compositions may take such forms as suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents.

Pharmaceutical formulations for parenteral administration include aqueous solutions of the active compounds in water-soluble form. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Optionally, the suspension may also contain suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions. Alternatively, the active ingredient may be in powder form for constitution with a suitable vehicle, *e.g.*, sterile pyrogen-free water, before use.

The compounds may also be formulated in rectal compositions such as suppositories or retention enemas, *e.g.*, containing conventional suppository bases such as cocoa butter or other glycerides. In addition to the formulations described

previously, the compounds may also be formulated as a depot preparation. Such long acting formulations may be administered by implantation (for example subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the compounds may be formulated with suitable polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

A pharmaceutical carrier for the hydrophobic compounds of the invention is a co-solvent system comprising benzyl alcohol, a nonpolar surfactant, a water-miscible organic polymer, and an aqueous phase. The co-solvent system may be the VPD co-solvent system. VPD is a solution of 3% w/v benzyl alcohol, 8% w/v of the nonpolar surfactant polysorbate 80, and 65% w/v polyethylene glycol 300, made up to volume in absolute ethanol. The VPD co-solvent system (VPD:5W) consists of VPD diluted 1:1 with a 5% dextrose in water solution. This co-solvent system dissolves hydrophobic compounds well, and itself produces low toxicity upon systemic administration. Naturally, the proportions of a co-solvent system may be varied considerably without destroying its solubility and toxicity characteristics. Furthermore, the identity of the co-solvent components may be varied: for example, other low-toxicity nonpolar surfactants may be used instead of polysorbate 80; the fraction size of polyethylene glycol may be varied; other biocompatible polymers may replace polyethylene glycol, e.g. polyvinyl pyrrolidone; and other sugars or polysaccharides may substitute for dextrose. Alternatively, other delivery systems for hydrophobic pharmaceutical compounds may be employed. Liposomes and emulsions are well known examples of delivery vehicles or carriers for hydrophobic drugs. Certain organic solvents such as dimethylsulfoxide also may be employed, although usually at the cost of greater toxicity. Additionally, the compounds may be delivered using a sustained-release system, such as semipermeable matrices of solid hydrophobic polymers containing the therapeutic agent. Various types of sustained-release materials have been established and are well known by those skilled in the art. Sustained-release capsules may, depending on their chemical nature, release the compounds for a few weeks up to over 100 days. Depending on the chemical nature and the biological

stability of the therapeutic reagent, additional strategies for protein or other active ingredient stabilization may be employed.

The pharmaceutical compositions also may comprise suitable solid or gel phase carriers or excipients. Examples of such carriers or excipients include but are not limited to calcium carbonate, calcium phosphate, various sugars, starches, cellulose derivatives, gelatin, and polymers such as polyethylene glycols. Many of the active ingredients of the invention may be provided as salts with pharmaceutically compatible counter ions. Such pharmaceutically acceptable base addition salts are those salts which retain the biological effectiveness and properties of the free acids and which are obtained by reaction with inorganic or organic bases such as sodium hydroxide, magnesium hydroxide, ammonia, trialkylamine, dialkylamine, monoalkylamine, dibasic amino acids, sodium acetate, potassium benzoate, triethanol amine and the like.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) or other active ingredient(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without

limitation, monoglycerides, diglycerides, sulfatides, lysolecithins, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent Nos. 4,235,871; 4,501,728; 4,837,028; and 4,737,323, all of which are incorporated herein by
5 reference.

The amount of protein or other active ingredient of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of
10 protein or other active ingredient of the present invention with which to treat each individual patient. Initially, the attending physician will administer low doses of protein or other active ingredient of the present invention and observe the patient's response. Larger doses of protein or other active ingredient of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and
15 at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01 μ g to about 100 mg (preferably about 0.1 μ g to about 10 mg, more preferably about 0.1 μ g to about 1 mg) of protein or other active ingredient of the present invention per kg body weight. For compositions of the present invention which
20 are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for
25 delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein or other active ingredient of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the
30 invention. Preferably for bone and/or cartilage formation, the composition would

include a matrix capable of delivering the protein-containing or other active ingredient-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions may be biodegradable and chemically defined calcium sulfate, tricalcium phosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxyapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalcium phosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability. Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate, poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent

useful herein is 0.5-20 wt %, preferably 1-10 wt % based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby

5 providing the protein the opportunity to assist the osteogenic activity of the progenitor cells. In further compositions, proteins or other active ingredients of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming

10 growth factors (TGF- α and TGF- β), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired patients for such treatment with proteins or other active ingredients of the present invention. The dosage regimen of a protein-containing pharmaceutical

15 composition to be used in tissue regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, *e.g.*, amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (*e.g.*, bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other

20 clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays,

25 histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either in vivo or ex vivo into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including,

30 without limitation, in the form of viral vectors or naked DNA). Cells may also be

cultured ex vivo in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced in vivo for therapeutic purposes.

5 **4.9.3 EFFECTIVE DOSAGE**

Pharmaceutical compositions suitable for use in the present invention include compositions wherein the active ingredients are contained in an effective amount to achieve its intended purpose. More specifically, a therapeutically effective amount means an amount effective to prevent development of or to alleviate the existing
10 symptoms of the subject being treated. Determination of the effective amount is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein. For any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from appropriate in vitro assays. For example, a dose can be formulated in animal models to achieve a circulating
15 concentration range that can be used to more accurately determine useful doses in humans. For example, a dose can be formulated in animal models to achieve a circulating concentration range that includes the IC_{50} as determined in cell culture (*i.e.*, the concentration of the test compound which achieves a half-maximal inhibition of the protein's biological activity). Such information can be used to more accurately
20 determine useful doses in humans.

A therapeutically effective dose refers to that amount of the compound that results in amelioration of symptoms or a prolongation of survival in a patient. Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, *e.g.*, for
25 determining the LD_{50} (the dose lethal to 50% of the population) and the ED_{50} (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio between LD_{50} and ED_{50} . Compounds which exhibit high therapeutic indices are preferred. The data obtained from these cell culture assays and animal studies can be used in
30 formulating a range of dosage for use in human. The dosage of such compounds lies

preferably within a range of circulating concentrations that include the ED₅₀ with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. The exact formulation, route of administration and dosage can be chosen by the individual physician in view of the patient's condition. See, *e.g.*, Fingl et al., 1975, in "The Pharmacological Basis of Therapeutics", Ch. 1 p.1. Dosage amount and interval may be adjusted individually to provide plasma levels of the active moiety which are sufficient to maintain the desired effects, or minimal effective concentration (MEC). The MEC will vary for each compound but can be estimated from *in vitro* data. Dosages necessary to achieve the MEC will depend on individual characteristics and route of administration. However, HPLC assays or bioassays can be used to determine plasma concentrations.

Dosage intervals can also be determined using MEC value. Compounds should be administered using a regimen which maintains plasma levels above the MEC for 10-90% of the time, preferably between 30-90% and most preferably between 50-90%. In cases of local administration or selective uptake, the effective local concentration of the drug may not be related to plasma concentration.

An exemplary dosage regimen for polypeptides or other compositions of the invention will be in the range of about 0.01 µg/kg to 100 mg/kg of body weight daily, with the preferred dose being about 0.1 µg/kg to 25 mg/kg of patient body weight daily, varying in adults and children. Dosing may be once daily, or equivalent doses may be delivered at longer or shorter intervals.

The amount of composition administered will, of course, be dependent on the subject being treated, on the subject's age and weight, the severity of the affliction, the manner of administration and the judgment of the prescribing physician.

4.9.4 PACKAGING

The compositions may, if desired, be presented in a pack or dispenser device which may contain one or more unit dosage forms containing the active ingredient. The pack may, for example, comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration.

Compositions comprising a compound of the invention formulated in a compatible pharmaceutical carrier may also be prepared, placed in an appropriate container, and labeled for treatment of an indicated condition.

5 **4.10 ANTIBODIES**

Another aspect of the invention is an antibody that specifically binds the polypeptide of the invention. Such antibodies include monoclonal and polyclonal antibodies, single chain antibodies, chimeric antibodies, bifunctional/bispecific antibodies, humanized antibodies, human antibodies, and complementary determining
10 region (CDR)-grafted antibodies, including compounds which include CDR and/or antigen-binding sequences, which specifically recognize a polypeptide of the invention. Preferred antibodies of the invention are human antibodies which are produced and identified according to methods described in WO93/11236, published June 20, 1993, which is incorporated herein by reference in its entirety. Antibody fragments,
15 including Fab, Fab', F(ab')₂, and F_v, are also provided by the invention. The term "specific for" indicates that the variable regions of the antibodies of the invention recognize and bind polypeptides of the invention exclusively (*i.e.*, able to distinguish the polypeptide of the invention from other similar polypeptides despite sequence identity, homology, or similarity found in the family of polypeptides), but may also
20 interact with other proteins (for example, *S. aureus* protein A or other antibodies in ELISA techniques) through interactions with sequences outside the variable region of the antibodies, and in particular, in the constant region of the molecule. Screening assays to determine binding specificity of an antibody of the invention are well known and routinely practiced in the art. For a comprehensive discussion of such assays, see
25 Harlow et al. (Eds), Antibodies A Laboratory Manual; Cold Spring Harbor Laboratory; Cold Spring Harbor , NY (1988), Chapter 6. Antibodies that recognize and bind fragments of the polypeptides of the invention are also contemplated, provided that the antibodies are first and foremost specific for, as defined above, full length polypeptides of the invention. As with antibodies that are specific for full length polypeptides of the
30 invention, antibodies of the invention that recognize fragments are those which can

distinguish polypeptides from the same family of polypeptides despite inherent sequence identity, homology, or similarity found in the family of proteins. Antibodies of the invention can be produced using any method well known and routinely practiced in the art.

5 Non-human antibodies may be humanized by any methods known in the art. In one method, the non-human CDRs are inserted into a human antibody or consensus antibody framework sequence. Further changes can then be introduced into the antibody framework to modulate affinity or immunogenicity.

10 Antibodies of the invention are useful for, for example, therapeutic purposes (by modulating activity of a polypeptide of the invention), diagnostic purposes to detect or quantitate a polypeptide of the invention, as well as purification of a polypeptide of the invention. Kits comprising an antibody of the invention for any of the purposes described herein are also comprehended. In general, a kit of the invention also includes a control antigen for which the antibody is immunospecific. The invention further
15 provides a hybridoma that produces an antibody according to the invention. Antibodies of the invention are useful for detection and/or purification of the polypeptides of the invention.

20 Polypeptides of the invention may also be used to immunize animals to obtain polyclonal and monoclonal antibodies which specifically react with the protein. Such antibodies may be obtained using either the entire protein or fragments thereof as an immunogen. The peptide immunogens additionally may contain a cysteine residue at the carboxyl terminus, and are conjugated to a hapten such as keyhole limpet hemocyanin (KLH). Methods for synthesizing such peptides are known in the art, for example, as in R. P. Merrifield, J. Amer. Chem. Soc. 85, 2149-2154 (1963); J. L.
25 Krstenansky, et al., FEBS Lett. 211, 10 (1987).

30 Monoclonal antibodies binding to the protein of the invention may be useful diagnostic agents for the immunodetection of the protein. Neutralizing monoclonal antibodies binding to the protein may also be useful therapeutics for both conditions associated with the protein and also in the treatment of some forms of cancer where abnormal expression of the protein is involved. In the case of cancerous cells or

leukemic cells, neutralizing monoclonal antibodies against the protein may be useful in detecting and preventing the metastatic spread of the cancerous cells, which may be mediated by the protein. In general, techniques for preparing polyclonal and monoclonal antibodies as well as hybridomas capable of producing the desired antibody are well known in the art (Campbell, A.M., Monoclonal Antibodies Technology: Laboratory Techniques in Biochemistry and Molecular Biology, Elsevier Science Publishers, Amsterdam, The Netherlands (1984); St. Groth et al., J. Immunol. 35:1-21 (1990); Kohler and Milstein, Nature 256:495-497 (1975)), the trioma technique, the human B-cell hybridoma technique (Kozbor et al., Immunology Today 4:72 (1983); Cole et al., in Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, Inc. (1985), pp. 77-96).

Any animal (mouse, rabbit, *etc.*) which is known to produce antibodies can be immunized with a peptide or polypeptide of the invention. Methods for immunization are well known in the art. Such methods include subcutaneous or intraperitoneal injection of the polypeptide. One skilled in the art will recognize that the amount of the protein encoded by the ORF of the present invention used for immunization will vary based on the animal which is immunized, the antigenicity of the peptide and the site of injection. The protein that is used as an immunogen may be modified or administered in an adjuvant in order to increase the protein's antigenicity. Methods of increasing the antigenicity of a protein are well known in the art and include, but are not limited to, coupling the antigen with a heterologous protein (such as globulin or -galactosidase) or through the inclusion of an adjuvant during immunization.

For monoclonal antibodies, spleen cells from the immunized animals are removed, fused with myeloma cells, such as SP2/0-Ag14 myeloma cells, and allowed to become monoclonal antibody producing hybridoma cells. Any one of a number of methods well known in the art can be used to identify the hybridoma cell which produces an antibody with the desired characteristics. These include screening the hybridomas with an ELISA assay, Western blot analysis, or radioimmunoassay (Lutz et al., Exp. Cell Research. 175:109-124 (1988)). Hybridomas secreting the desired antibodies are cloned and the class and subclass is determined using procedures known

in the art (Campbell, A.M., Monoclonal Antibody Technology: Laboratory
Techniques in Biochemistry and Molecular Biology, Elsevier Science Publishers,
Amsterdam, The Netherlands (1984)). Techniques described for the production of
single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce single chain
5 antibodies to proteins of the present invention.

For polyclonal antibodies, antibody-containing antiserum is isolated from the
immunized animal and is screened for the presence of antibodies with the desired
specificity using one of the above-described procedures. The present invention further
provides the above- described antibodies in delectably labeled form. Antibodies can be
10 delectably labeled through the use of radioisotopes, affinity labels (such as biotin,
avidin, etc.), enzymatic labels (such as horseradish peroxidase, alkaline phosphatase,
etc.) fluorescent labels (such as FITC or rhodamine, etc.), paramagnetic atoms, etc.
Procedures for accomplishing such labeling are well-known in the art, for example, see
(Sternberger, L.A. et al., J. Histochem. Cytochem. 18:315 (1970); Bayer, E.A. et al.,
15 Meth. Enzym. 62:308 (1979); Engval, E. et al., Immunol. 109:129 (1972); Goding,
J.W. J. Immunol. Meth. 13:215 (1976)).

The labeled antibodies of the present invention can be used for *in vitro*, *in vivo*,
and *in situ* assays to identify cells or tissues in which a fragment of the polypeptide of
interest is expressed. The antibodies may also be used directly in therapies or other
20 diagnostics. The present invention further provides the above-described antibodies
immobilized on a solid support. Examples of such solid supports include plastics such
as polycarbonate, complex carbohydrates such as agarose and Sepharose®, acrylic
resins and such as polyacrylamide and latex beads. Techniques for coupling antibodies
to such solid supports are well known in the art (Weir, D.M. et al., "Handbook of
25 Experimental Immunology" 4th Ed., Blackwell Scientific Publications, Oxford,
England, Chapter 10 (1986); Jacoby, W.D. et al., Meth. Enzym. 34 Academic Press,
N.Y. (1974)). The immobilized antibodies of the present invention can be used for *in*
vitro, *in vivo*, and *in situ* assays as well as for immuno-affinity purification of the
proteins of the present invention.

4.11 COMPUTER READABLE SEQUENCES

In one application of this embodiment, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any medium which can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. A skilled artisan can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon a nucleotide sequence of the present invention. As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the presently known methods for recording information on computer readable medium to generate manufactures comprising the nucleotide sequence information of the present invention.

A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable medium. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and Microsoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of data processor structuring formats (*e.g.* text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

By providing any of the nucleotide sequences SEQ ID NOs: 1 - 164 or a representative fragment thereof; or a nucleotide sequence at least 95% identical to any

of the nucleotide sequences of the SEQ ID NOs: 1 - 164 in computer readable form, a skilled artisan can routinely access the sequence information for a variety of purposes. Computer software is publicly available which allows a skilled artisan to access sequence information provided in a computer readable medium. The examples which
5 follow demonstrate how software which implements the BLAST (Altschul et al., J. Mol. Biol. 215:403-410 (1990)) and BLAZE (Brutlag et al., Comp. Chem. 17:203-207 (1993)) search algorithms on a Sybase system is used to identify open reading frames (ORFs) within a nucleic acid sequence. Such ORFs may be protein encoding fragments and may be useful in producing commercially important proteins such as enzymes used
10 in fermentation reactions and in the production of commercially useful metabolites.

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit
15 (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based systems are suitable for use in the present invention. As stated above, the computer-based systems of the present invention comprise a data storage means having stored therein a nucleotide sequence of the present invention and the necessary hardware means and
20 software means for supporting and implementing a search means. As used herein, "data storage means" refers to memory which can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention.

As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of a known sequence which match a particular target sequence or target motif. A variety of known algorithms are
30 disclosed publicly and a variety of commercially available software for conducting

search means are and can be used in the computer-based systems of the present invention. Examples of such software includes, but is not limited to, Smith-Waterman, MacPattern (EMBL), BLASTN and BLASTA (NPOLYPEPTIDEIA). A skilled artisan can readily recognize that any one of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems. As used herein, a "target sequence" can be any nucleic acid or amino acid sequence of six or more nucleotides or two or more amino acids. A skilled artisan can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 300 amino acids, more preferably from about 30 to 100 nucleotide residues. However, it is well recognized that searches for commercially important fragments, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzyme active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

4.12 TRIPLE HELIX FORMATION

In addition, the fragments of the present invention, as broadly described, can be used to control gene expression through triple helix formation or antisense DNA or RNA, both of which methods are based on the binding of a polynucleotide sequence to DNA or RNA. Polynucleotides suitable for use in these methods are preferably 20 to 40 bases in length and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 15241:456 (1988); and Dervan et al., Science 251:1360 (1991))

or to the mRNA itself (antisense - Olmno, J. Neurochem. 56:560 (1991);
Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca
Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA
transcription from DNA, while antisense RNA hybridization blocks translation of an
5 mRNA molecule into polypeptide. Both techniques have been demonstrated to be
effective in model systems. Information contained in the sequences of the present
invention is necessary for the design of an antisense or triple helix oligonucleotide.

4.13 DIAGNOSTIC ASSAYS AND KITS

10 The present invention further provides methods to identify the presence or
expression of one of the ORFs of the present invention, or homolog thereof, in a test
sample, using a nucleic acid probe or antibodies of the present invention, optionally
conjugated or otherwise associated with a suitable label.

In general, methods for detecting a polynucleotide of the invention can comprise
15 contacting a sample with a compound that binds to and forms a complex with the
polynucleotide for a period sufficient to form the complex, and detecting the complex,
so that if a complex is detected, a polynucleotide of the invention is detected in the
sample. Such methods can also comprise contacting a sample under stringent
hybridization conditions with nucleic acid primers that anneal to a polynucleotide of the
20 invention under such conditions, and amplifying annealed polynucleotides, so that if a
polynucleotide is amplified, a polynucleotide of the invention is detected in the sample.

In general, methods for detecting a polypeptide of the invention can comprise
contacting a sample with a compound that binds to and forms a complex with the
polypeptide for a period sufficient to form the complex, and detecting the complex, so
25 that if a complex is detected, a polypeptide of the invention is detected in the sample.

In detail, such methods comprise incubating a test sample with one or more of
the antibodies or one or more of the nucleic acid probes of the present invention and
assaying for binding of the nucleic acid probes or antibodies to components within the
test sample.

Conditions for incubating a nucleic acid probe or antibody with a test sample vary. Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the nucleic acid probe or antibody used in the assay. One skilled in the art will recognize that any one of the commonly available hybridization, amplification or immunological assay formats can readily be adapted to employ the nucleic acid probes or antibodies of the present invention.

Examples of such assays can be found in Chard, T., An Introduction to Radioimmunoassay and Related Techniques, Elsevier Science Publishers, Amsterdam, The Netherlands (1986); Bullock, G.R. et al., Techniques in Immunocytochemistry, Academic Press, Orlando, FL Vol. 1 (1982), Vol. 2 (1983), Vol. 3 (1985); Tijssen, P., Practice and Theory of immunoassays: Laboratory Techniques in Biochemistry and Molecular Biology, Elsevier Science Publishers, Amsterdam, The Netherlands (1985). The test samples of the present invention include cells, protein or membrane extracts of cells, or biological fluids such as sputum, blood, serum, plasma, or urine. The test sample used in the above-described method will vary based on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein extracts or membrane extracts of cells are well known in the art and can be readily be adapted in order to obtain a sample which is compatible with the system utilized.

In another embodiment of the present invention, kits are provided which contain the necessary reagents to carry out the assays of the present invention. Specifically, the invention provides a compartment kit to receive, in close confinement, one or more containers which comprises: (a) a first container comprising one of the probes or antibodies of the present invention; and (b) one or more other containers comprising one or more of the following: wash reagents, reagents capable of detecting presence of a bound probe or antibody.

In detail, a compartment kit includes any kit in which reagents are contained in separate containers. Such containers include small glass containers, plastic containers or strips of plastic or paper. Such containers allows one to efficiently transfer reagents from one compartment to another compartment such that the samples and reagents are

not cross-contaminated, and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another. Such containers will include a container which will accept the test sample, a container which contains the antibodies used in the assay, containers which contain wash reagents (such as phosphate buffered saline, Tris-buffers, etc.), and containers which contain the reagents used to detect the bound antibody or probe. Types of detection reagents include labeled nucleic acid probes, labeled secondary antibodies, or in the alternative, if the primary antibody is labeled, the enzymatic, or antibody binding reagents which are capable of reacting with the labeled antibody. One skilled in the art will readily recognize that the disclosed probes and antibodies of the present invention can be readily incorporated into one of the established kit formats which are well known in the art.

4.14 MEDICAL IMAGING

The novel polypeptides and binding partners of the invention are useful in medical imaging of sites expressing the molecules of the invention (e.g., where the polypeptide of the invention is involved in the immune response, for imaging sites of inflammation or infection). See, e.g., Kunkel et al., U.S. Pat. NO. 5,413,778. Such methods involve chemical attachment of a labeling or imaging agent, administration of the labeled polypeptide to a subject in a pharmaceutically acceptable carrier, and imaging the labeled polypeptide *in vivo* at the target site.

4.15 SCREENING ASSAYS

Using the isolated proteins and polynucleotides of the invention, the present invention further provides methods of obtaining and identifying agents which bind to a polypeptide encoded by an ORF corresponding to any of the nucleotide sequences set forth in the SEQ ID NOs: 1 - 164, or bind to a specific domain of the polypeptide encoded by the nucleic acid. In detail, said method comprises the steps of:

- (a) contacting an agent with an isolated protein encoded by an ORF of the present invention, or nucleic acid of the invention; and
- (b) determining whether the agent binds to said protein or said nucleic acid.

In general, therefore, such methods for identifying compounds that bind to a polynucleotide of the invention can comprise contacting a compound with a polynucleotide of the invention for a time sufficient to form a polynucleotide/compound complex, and detecting the complex, so that if a polynucleotide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Likewise, in general, therefore, such methods for identifying compounds that bind to a polypeptide of the invention can comprise contacting a compound with a polypeptide of the invention for a time sufficient to form a polypeptide/compound complex, and detecting the complex, so that if a polypeptide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Methods for identifying compounds that bind to a polypeptide of the invention can also comprise contacting a compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a receptor gene sequence in the cell, and detecting the complex by detecting reporter gene sequence expression, so that if a polypeptide/compound complex is detected, a compound that binds a polypeptide of the invention is identified.

Compounds identified via such methods can include compounds which modulate the activity of a polypeptide of the invention (that is, increase or decrease its activity, relative to activity observed in the absence of the compound). Alternatively, compounds identified via such methods can include compounds which modulate the expression of a polynucleotide of the invention (that is, increase or decrease expression relative to expression levels observed in the absence of the compound). Compounds, such as compounds identified via the methods of the invention, can be tested using standard assays well known to those of skill in the art for their ability to modulate activity/expression.

The agents screened in the above assay can be, but are not limited to, peptides, carbohydrates, vitamin derivatives, or other pharmaceutical agents. The agents can be selected and screened at random or rationally selected or designed using protein modeling techniques.

For random screening, agents such as peptides, carbohydrates, pharmaceutical agents and the like are selected at random and are assayed for their ability to bind to the protein encoded by the ORF of the present invention. Alternatively, agents may be rationally selected or designed. As used herein, an agent is said to be "rationally selected or designed" when the agent is chosen based on the configuration of the particular protein. For example, one skilled in the art can readily adapt currently available procedures to generate peptides, pharmaceutical agents and the like, capable of binding to a specific peptide sequence, in order to generate rationally designed antipeptide peptides, for example see Hurby et al., Application of Synthetic Peptides: Antisense Peptides," In Synthetic Peptides, A User's Guide, W.H. Freeman, NY (1992), pp. 289-307, and Kaspczak et al., Biochemistry 28:9230-8 (1989), or pharmaceutical agents, or the like.

In addition to the foregoing, one class of agents of the present invention, as broadly described, can be used to control gene expression through binding to one of the ORFs or EMFs of the present invention. As described above, such agents can be randomly screened or rationally designed/selected. Targeting the ORF or EMF allows a skilled artisan to design sequence specific or element specific agents, modulating the expression of either a single ORF or multiple ORFs which rely on the same EMF for expression control. One class of DNA binding agents are agents which contain base residues which hybridize or form a triple helix formation by binding to DNA or RNA. Such agents can be based on the classic phosphodiester, ribonucleic acid backbone, or can be a variety of sulfhydryl or polymeric derivatives which have base attachment capacity.

Agents suitable for use in these methods preferably contain 20 to 40 bases and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Okano, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while

antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide and other DNA binding agents.

5 Agents which bind to a protein encoded by one of the ORFs of the present invention can be used as a diagnostic agent. Agents which bind to a protein encoded by one of the ORFs of the present invention can be formulated using known techniques to generate a pharmaceutical composition.

10 4.16 USE OF NUCLEIC ACIDS AS PROBES

Another aspect of the subject invention is to provide for polypeptide-specific nucleic acid hybridization probes capable of hybridizing with naturally occurring nucleotide sequences. The hybridization probes of the subject invention may be derived from any of the nucleotide sequences SEQ ID NOs: 1 - 164. Because the
15 corresponding gene is only expressed in a limited number of tissues, a hybridization probe derived from any of the nucleotide sequences SEQ ID NOs: 1 - 164 can be used as an indicator of the presence of RNA of cell type of such a tissue in a sample.

Any suitable hybridization technique can be employed, such as, for example, in situ hybridization. PCR as described in US Patents Nos. 4,683,195 and 4,965,188
20 provides additional uses for oligonucleotides based upon the nucleotide sequences. Such probes used in PCR may be of recombinant origin, may be chemically synthesized, or a mixture of both. The probe will comprise a discrete nucleotide sequence for the detection of identical sequences or a degenerate pool of possible sequences for identification of closely related genomic sequences.

25 Other means for producing specific hybridization probes for nucleic acids include the cloning of nucleic acid sequences into vectors for the production of mRNA probes. Such vectors are known in the art and are commercially available and may be used to synthesize RNA probes *in vitro* by means of the addition of the appropriate RNA polymerase as T7 or SP6 RNA polymerase and the appropriate radioactively
30 labeled nucleotides. The nucleotide sequences may be used to construct hybridization

probes for mapping their respective genomic sequences. The nucleotide sequence provided herein may be mapped to a chromosome or specific regions of a chromosome using well known genetic and/or chromosomal mapping techniques. These techniques include in situ hybridization, linkage analysis against known chromosomal markers, hybridization screening with libraries or flow-sorted chromosomal preparations specific to known chromosomes, and the like. The technique of fluorescent in situ hybridization of chromosome spreads has been described, among other places, in Verma et al (1988) Human Chromosomes: A Manual of Basic Techniques, Pergamon Press, New York NY.

Fluorescent *in situ* hybridization of chromosomal preparations and other physical chromosome mapping techniques may be correlated with additional genetic map data. Examples of genetic map data can be found in the 1994 Genome Issue of Science (265:1981f). Correlation between the location of a nucleic acid on a physical chromosomal map and a specific disease (or predisposition to a specific disease) may help delimit the region of DNA associated with that genetic disease. The nucleotide sequences of the subject invention may be used to detect differences in gene sequences between normal, carrier or affected individuals.

4.17 PREPARATION OF SUPPORT BOUND OLIGONUCLEOTIDES

Oligonucleotides, i.e., small nucleic acid segments, may be readily prepared by, for example, directly synthesizing the oligonucleotide by chemical means, as is commonly practiced using an automated oligonucleotide synthesizer.

Support bound oligonucleotides may be prepared by any of the methods known to those of skill in the art using any suitable support such as glass, polystyrene or Teflon. One strategy is to precisely spot oligonucleotides synthesized by standard synthesizers. Immobilization can be achieved using passive adsorption (Inouye & Hondo, (1990) J. Clin. Microbiol. 28(6) 1469-72); using UV light (Nagata *et al.*, 1985; Dahlen *et al.*, 1987; Morrissey & Collins, (1989) Mol. Cell Probes 3(2) 189-207) or by covalent binding of base modified DNA (Keller *et al.*, 1988; 1989); all references being specifically incorporated herein.

Another strategy that may be employed is the use of the strong biotin-streptavidin interaction as a linker. For example, Broude *et al.* (1994) Proc. Natl. Acad. Sci. USA 91(8) 3072-6, describe the use of biotinylated probes, although these are duplex probes, that are immobilized on streptavidin-coated magnetic beads. Streptavidin-coated beads
5 may be purchased from Dynal, Oslo. Of course, this same linking chemistry is applicable to coating any surface with streptavidin. Biotinylated probes may be purchased from various sources, such as, e.g., Operon Technologies (Alameda, CA).

Nunc Laboratories (Naperville, IL) is also selling suitable material that could be used. Nunc Laboratories have developed a method by which DNA can be covalently
10 bound to the microwell surface termed CovaLink NH. CovaLink NH is a polystyrene surface grafted with secondary amino groups (>NH) that serve as bridge-heads for further covalent coupling. CovaLink Modules may be purchased from Nunc Laboratories. DNA molecules may be bound to CovaLink exclusively at the 5'-end by a phosphoramidate bond, allowing immobilization of more than 1 pmol of DNA
15 (Rasmussen *et al.*, (1991) Anal. Biochem. 198(1) 138-42).

The use of CovaLink NH strips for covalent binding of DNA molecules at the 5'-end has been described (Rasmussen *et al.*, (1991). In this technology, a phosphoramidate bond is employed (Chu *et al.*, (1983) Nucleic Acids Res. 11(8) 6513-29). This is beneficial as immobilization using only a single covalent bond is preferred.
20 The phosphoramidate bond joins the DNA to the CovaLink NH secondary amino groups that are positioned at the end of spacer arms covalently grafted onto the polystyrene surface through a 2 nm long spacer arm. To link an oligonucleotide to CovaLink NH via an phosphoramidate bond, the oligonucleotide terminus must have a 5'-end phosphate group. It is, perhaps, even possible for biotin to be covalently bound to CovaLink and
25 then streptavidin used to bind the probes.

More specifically, the linkage method includes dissolving DNA in water (7.5 ng/ul) and denaturing for 10 min. at 95°C and cooling on ice for 10 min. Ice-cold 0.1 M 1-methylimidazole, pH 7.0 (1-MeIm₇), is then added to a final concentration of 10 mM 1-MeIm₇. A ss DNA solution is then dispensed into CovaLink NH strips (75 ul/well)
30 standing on ice.

Carbodiimide 0.2 M 1-ethyl-3-(3-dimethylaminopropyl)-carbodiimide (EDC), dissolved in 10 mM 1-MeIm₇, is made fresh and 25 ul added per well. The strips are incubated for 5 hours at 50°C. After incubation the strips are washed using, e.g., Nunc-Immuno Wash; first the wells are washed 3 times, then they are soaked with washing solution for 5 min., and finally they are washed 3 times (where in the washing solution is 0.4 N NaOH, 0.25% SDS heated to 50°C).

It is contemplated that a further suitable method for use with the present invention is that described in PCT Patent Application WO 90/03382 (Southern & Maskos), incorporated herein by reference. This method of preparing an oligonucleotide bound to a support involves attaching a nucleoside 3'-reagent through the phosphate group by a covalent phosphodiester link to aliphatic hydroxyl groups carried by the support. The oligonucleotide is then synthesized on the supported nucleoside and protecting groups removed from the synthetic oligonucleotide chain under standard conditions that do not cleave the oligonucleotide from the support. Suitable reagents include nucleoside phosphoramidite and nucleoside hydrogen phosphate.

An on-chip strategy for the preparation of DNA probe for the preparation of DNA probe arrays may be employed. For example, addressable laser-activated photodeprotection may be employed in the chemical synthesis of oligonucleotides directly on a glass surface, as described by Fodor *et al.* (1991) Science 251(4995) 767-73, incorporated herein by reference. Probes may also be immobilized on nylon supports as described by Van Ness *et al.* (1991) Nucleic Acids Res. 19(12) 3345-50; or linked to Teflon using the method of Duncan & Cavalier (1988) Anal. Biochem. 169(1) 104-8; all references being specifically incorporated herein.

To link an oligonucleotide to a nylon support, as described by Van Ness *et al.* (1991), requires activation of the nylon surface via alkylation and selective activation of the 5'-amine of oligonucleotides with cyanuric chloride.

One particular way to prepare support bound oligonucleotides is to utilize the light-generated synthesis described by Pease *et al.*, (1994) PNAS USA 91(11) 5022-6, incorporated herein by reference). These authors used current photolithographic techniques to generate arrays of immobilized oligonucleotide probes (DNA chips). These

methods, in which light is used to direct the synthesis of oligonucleotide probes in high-density, miniaturized arrays, utilize photolabile 5'-protected *N*-acyl-deoxynucleoside phosphoramidites, surface linker chemistry and versatile combinatorial synthesis strategies. A matrix of 256 spatially defined oligonucleotide probes may be generated in this manner.

4.18 PREPARATION OF NUCLEIC ACID FRAGMENTS

The nucleic acids may be obtained from any appropriate source, such as cDNAs, genomic DNA, chromosomal DNA, microdissected chromosome bands, cosmid or YAC inserts, and RNA, including mRNA without any amplification steps. For example, Sambrook *et al.* (1989) describes three protocols for the isolation of high molecular weight DNA from mammalian cells (p. 9.14-9.23).

DNA fragments may be prepared as clones in M13, plasmid or lambda vectors and/or prepared directly from genomic DNA or cDNA by PCR or other amplification methods. Samples may be prepared or dispensed in multiwell plates. About 100-1000 ng of DNA samples may be prepared in 2-500 ml of final volume.

The nucleic acids would then be fragmented by any of the methods known to those of skill in the art including, for example, using restriction enzymes as described at 9.24-9.28 of Sambrook *et al.* (1989), shearing by ultrasound and NaOH treatment.

Low pressure shearing is also appropriate, as described by Schriefer *et al.* (1990) Nucleic Acids Res. 18(24) 7455-6, incorporated herein by reference). In this method, DNA samples are passed through a small French pressure cell at a variety of low to intermediate pressures. A lever device allows controlled application of low to intermediate pressures to the cell. The results of these studies indicate that low-pressure shearing is a useful alternative to sonic and enzymatic DNA fragmentation methods.

One particularly suitable way for fragmenting DNA is contemplated to be that using the two base recognition endonuclease, *Cvi*II, described by Fitzgerald *et al.* (1992) Nucleic Acids Res. 20(14) 3753-62. These authors described an approach for the rapid fragmentation and fractionation of DNA into particular sizes that they contemplated to be suitable for shotgun cloning and sequencing.

The restriction endonuclease *Cvi*JI normally cleaves the recognition sequence PuGCPy between the G and C to leave blunt ends. Atypical reaction conditions, which alter the specificity of this enzyme (*Cvi*JI**), yield a quasi-random distribution of DNA fragments from the small molecule pUC19 (2688 base pairs). Fitzgerald *et al.* (1992) quantitatively evaluated the randomness of this fragmentation strategy, using a *Cvi*JI** digest of pUC19 that was size fractionated by a rapid gel filtration method and directly ligated, without end repair, to a lac Z minus M13 cloning vector. Sequence analysis of 76 clones showed that *Cvi*JI** restricts pyGCPy and PuGCPu, in addition to PuGCPy sites, and that new sequence data is accumulated at a rate consistent with random fragmentation.

As reported in the literature, advantages of this approach compared to sonication and agarose gel fractionation include: smaller amounts of DNA are required (0.2-0.5 ug instead of 2-5 ug); and fewer steps are involved (no preligation, end repair, chemical extraction, or agarose gel electrophoresis and elution are needed)

Irrespective of the manner in which the nucleic acid fragments are obtained or prepared, it is important to denature the DNA to give single stranded pieces available for hybridization. This is achieved by incubating the DNA solution for 2-5 minutes at 80-90°C. The solution is then cooled quickly to 2°C to prevent renaturation of the DNA fragments before they are contacted with the chip. Phosphate groups must also be removed from genomic DNA by methods known in the art.

4.19 PREPARATION OF DNA ARRAYS

Arrays may be prepared by spotting DNA samples on a support such as a nylon membrane. Spotting may be performed by using arrays of metal pins (the positions of which correspond to an array of wells in a microtiter plate) to repeated by transfer of about 20 nl of a DNA solution to a nylon membrane. By offset printing, a density of dots higher than the density of the wells is achieved. One to 25 dots may be accommodated in 1 mm², depending on the type of label used. By avoiding spotting in some preselected number of rows and columns, separate subsets (subarrays) may be formed. Samples in one subarray may be the same genomic segment of DNA (or the same gene) from different individuals, or may be different, overlapped genomic clones. Each of the subarrays may

represent replica spotting of the same samples. In one example, a selected gene segment may be amplified from 64 patients. For each patient, the amplified gene segment may be in one 96-well plate (all 96 wells containing the same sample). A plate for each of the 64 patients is prepared. By using a 96-pin device, all samples may be spotted on one 8 x 12
5 cm membrane. Subarrays may contain 64 samples, one from each patient. Where the 96 subarrays are identical, the dot span may be 1 mm² and there may be a 1 mm space between subarrays.

Another approach is to use membranes or plates (available from NUNC, Naperville, Illinois) which may be partitioned by physical spacers e.g. a plastic grid
10 molded over the membrane, the grid being similar to the sort of membrane applied to the bottom of multiwell plates, or hydrophobic strips. A fixed physical spacer is not preferred for imaging by exposure to flat phosphor-storage screens or x-ray films.

The present invention is illustrated in the following examples. Upon consideration of the present disclosure, one of skill in the art will appreciate that many other
15 embodiments and variations may be made in the scope of the present invention. Accordingly, it is intended that the broader aspects of the present invention not be limited to the disclosure of the following examples. The present invention is not to be limited in scope by the exemplified embodiments which are intended as illustrations of single aspects of the invention, and compositions and methods which are functionally equivalent are
20 within the scope of the invention. Indeed, numerous modifications and variations in the practice of the invention are expected to occur to those skilled in the art upon consideration of the present preferred embodiments. Consequently, the only limitations which should be placed upon the scope of the invention are those which appear in the appended claims.

25 All references cited within the body of the instant specification are hereby incorporated by reference in their entirety.

5.0 EXAMPLES

5.1 EXAMPLE 1

Novel Nucleic Acid Sequences Obtained From Various Libraries

A plurality of novel nucleic acids were obtained from cDNA libraries prepared from various human tissues and in some cases isolated from a genomic library derived from human chromosome using standard PCR, SBH sequence signature analysis and Sanger sequencing techniques. The inserts of the library were amplified with PCR using
5 primers specific for the vector sequences which flank the inserts. Clones from cDNA libraries were spotted on nylon membrane filters and screened with oligonucleotide probes (e.g., 7-mers) to obtain signature sequences. The clones were clustered into groups of similar or identical sequences. Representative clones were selected for sequencing.

In some cases, the 5' sequence of the amplified inserts was then deduced using a
10 typical Sanger sequencing protocol. PCR products were purified and subjected to fluorescent dye terminator cycle sequencing. Single pass gel sequencing was done using a 377 Applied Biosystems (ABI) sequencer to obtain the novel nucleic acid sequences. In some cases RACE (Random Amplification of cDNA Ends) was performed to further extend the sequence in the 5' direction.

15 **5.2 EXAMPLE 2**

Novel Nucleic Acids

The novel nucleic acids of the present invention of the invention were assembled from sequences that were obtained from a cDNA library by methods described in Example 1 above, and in some cases sequences obtained from one or more public
20 databases. The nucleic acids were assembled using an EST sequence as a seed. Then a recursive algorithm was used to extend the seed EST into an extended assemblage, by pulling additional sequences from different databases (i.e., Hyseq's database containing EST sequences, dbEST version 114, gb pri 114, and UniGene version 101) that belong to this assemblage. The algorithm terminated when there was no additional sequences from
25 the above databases that would extend the assemblage. Inclusion of component sequences into the assemblage was based on a BLASTN hit to the extending assemblage with BLAST score greater than 300 and percent identity greater than 95%.

Using PHRAP (Univ. of Washington) or CAP4 (Paracel), a full length gene cDNA sequence and its corresponding protein sequence were generated from the

assemblage. Any frame shifts and incorrect stop codons were corrected by hand editing. During editing, the sequence was checked using FASTY and/or BLAST against Genbank (i.e., dbEST version 118, gb pri 118, UniGene version 118, Genepet release 118). Other computer programs which may have been used in the editing process were phredPhrap
5 and Consed (University of Washington) and ed-ready, ed-ext and gc-zip-2 (Hyseq, Inc.). The full-length nucleotide and amino acid sequences, including splice variants resulting from these procedures are shown in the Sequence Listing as SEQ ID NOS:1- 164.

Table 1 shows the various tissue sources of SEQ ID NO: 1-164.

The nearest neighbor results for SEQ ID NO: 1-164 were obtained by a
10 BLASTP version 2.0a1 19MP-WashU search against Genpept release 118, using BLAST algorithm. The nearest neighbor result showed the closest homologue for SEQ ID NO: 1-164 from Genpept (and contains the translated amino acid sequences for which the nucleic acid sequence encodes). The nearest neighbor results for SEQ ID NO: 1-164 are shown in Table 2 below.

15

TABLE 1

TISSUE ORIGIN	RNA SOURCE	HYSEQ LIBRARY NAME	SEQ ID NOS:
adult brain	GIBCO	AB3001	4 13-14 19-20 36-37 50 56 73 76 82 93 95 105 127-128 131 134 137 159
adult brain	GIBCO	ABD003	1-4 14 18 23 27 33 36-39 47 51-52 56 58 63-65 71 73 79 82 90 93-94 98 105-106 109-110 115 121 130-131 135 137 141 144-145 159 164
adult brain	Clontech	ABR001	2 18-20 24 30 34 112 131 140- 141
adult brain	Clontech	ABR006	2-3 9 21 40 45 52 121 137 140 152 164
adult brain	Clontech	ABR008	1-3 6-7 9 14-15 23-25 27-29 33-34 36-40 43 46 52-53 55-56 60 63-64 66 68-69 75 77 79 90 92-93 95 98 100 104 106 110 114 117 119 121 127-132 136 140-150 152 155 159-160 164
adult brain	Clontech	ABR011	68
adult brain	Invitrogen	ABR013	21 24 60 114
adult brain	Invitrogen	ABR014	2-3 162
adult brain	Invitrogen	ABR016	1
adult brain	Invitrogen	ABT004	19-20 26-27 31-35 46 56 63-65 87-90 93 110-111 118 127-128 142-143 152 159
cultured preadipocytes	Stratagene	ADP001	3 68 76 82 121 141 157
adrenal gland	Clontech	ADR002	1 9 13 33 43 51-52 73 79 90 93 97 121 124-125 130
adult heart	GIBCO	AHR001	2-4 9 24 36-37 48-49 52-53 64 71 73-74 76 79 82 93 95-96 101 110-111 121 125-126 130 134-135 137 139-140 142-143 153-154 156 159 162
adult kidney	GIBCO	AKD001	4-12 14 18 23 25 27 31 38 47 51 57-58 68 71 73 76-77 79 82 93 95-96 98 101 104 110-111 121 123 126-128 130-131 134- 135 137 141 147-149 152 155 157 159 163-164
adult kidney	Invitrogen	AKT002	1-2 4 18 23 31 71 76 82-83 100-101 111 121 127-128 137 148-149 159 163-164
adult lung	GIBCO	ALG001	5 25 33 51 68 79 95-96 98 109-110 135 155 159 162
lymph node	Clontech	ALN001	1 3 23 59 73 76 83 121 130 147 155 159
young liver	GIBCO	ALV001	2 30-31 45 52 64 79-81 86 98- 99 101-103 130 133 144-145
adult liver	Invitrogen	ALV002	1 18 27 45 56 79 82 86 90 95- 96 98 126 133 142-143 159
adult ovary	Invitrogen	AOV001	1-8 13-14 17-18 23 27 29-31 35 47-52 57-58 62 64-66 68 71 73 75-76 79 82-85 90 93 96 98

TABLE 1

			100-101 104-105 108-112 115-117 121-123 125 127-128 130-131 135 137 140-145 147 153-156 159 162 164
adult placenta	Clontech	APL001	1 90 93 100 107
placenta	Invitrogen	APL002	3 27 51 56 93 131-132 157 162
adult spleen	GIBCO	ASP001	3-4 16 27 52 64 68 79 90 93 96 111 121 127-128 130 137 140-141 148-149 152 159 162 164
testis	GIBCO	ATS001	1-2 13 18 23 46-47 68 71 73 82 93 96 102-103 109-111 121 123 127-128 130 162
adult bladder	Invitrogen	BLD001	3 24 58 71 79 111 121
bone marrow	Clontech	BMD001	2-5 8 10-12 18 21 23 47 51-52 56 68 73-74 76 82 96 100 104 110 119-121 125 130-132 134 137 140 147 153 155-156 161-162
bone marrow	Clontech	BMD002	1 3-5 9-12 18 21 45 47 52 66 74 76 83 93 112 121 127-128 130-132 137 140 142-143 157 162
bone marrow	Clontech	BMD007	121 162
adult colon	Invitrogen	CLN001	65 95 121 148-150
Mixture of 16 tissues - mRNAs*	Various Vendors	CTL021	162
adult cervix	BioChain	CVX001	1-3 13-14 18 22 44-45 47-49 56 68 70-71 73 82 95 100-101 105 108 111 121 125-128 131-132 135 147 150 153 155-156 159
diaphragm	BioChain	DIA002	82
endothelial cells	Strategene	EDT001	1-4 6-7 13 18 23 26-28 30 36-37 45 51-52 55 58 61-62 64 68-69 71 76 79 82 93 95-96 98 100-101 104 110 119 121 125 127-128 131-132 134 137 140-141 147 150 155 159
fetal brain	Clontech	FBR001	79
fetal brain	Clontech	FBR004	14 21 82 104 121 140
fetal brain	Clontech	FBR006	1-4 6-9 14-15 33-35 42 52 56-57 69 77 79 90 93 98 101 110 114 119 121 124 127-128 130 147 152 160

* The 16 tissue-mRNAs and their vendor source, are as follows: 1) Normal adult brain mRNA (Invitrogen), 2) normal adult kidney mRNA (Invitrogen), 3) normal adult liver mRNA (Invitrogen), 4) normal fetal brain mRNA (Invitrogen), 5) normal fetal kidney mRNA (Invitrogen), 6) normal fetal liver mRNA (Invitrogen), 7) normal fetal skin mRNA (Invitrogen), 8) human adrenal gland mRNA (Clontech), 9) human bone marrow mRNA (Clontech), 10) human leukemia lymphoblastic mRNA (Clontech), 11) human thymus mRNA (Clontech), 12) human lymph node mRNA (Clontech), 13) human spinal cord mRNA (Clontech), 14) human thyroid mRNA (Clontech), 15) human esophagus mRNA (BioChain), 16) human conceptional umbilical cord mRNA (BioChain).

TABLE 1

fetal brain	Invitrogen	FBT002	2-3 27 31 63-65 68 79 82 90 93 127-128 142-143 147 150
fetal heart	Invitrogen	FHR001	3 78
fetal kidney	Clontech	FKD001	52 77 121 130 137 150
fetal kidney	Clontech	FKD002	137
fetal kidney	Invitrogen	FKD007	121
fetal lung	Clontech	FLG001	3 5 68 148-149 159
fetal lung	Invitrogen	FLG003	3 82 93 98 111-112 130 136 138 148-149
fetal lung	Clontech	FLG004	3
fetal liver- spleen	Columbia University	FLS001	1-4 10-12 14 18 21 26-28 33 38 43 45 47 51-53 56-59 64-65 68 71 74 76 79-82 86 90 93 95-96 99 101-103 105 108-112 121-122 125 127-128 130-134 137 139-145 147 150 152 157 162 164
fetal liver- spleen	Columbia University	FLS002	1 3-4 10-13 16 18 25-26 28 39 42 51-52 56 58-59 64 68 71 76 79-83 86 90 93 98-99 101 108- 112 122 125-126 130-134 137 139-140 142-143 147 150 152 155 157 159
fetal liver- spleen	Columbia University	FLS003	4 16 162 164
fetal liver	Invitrogen	FLV001	3-4 16 25 28 31 58 64-65 79- 81 86 93 104 133 147-150 159 162
fetal liver	Clontech	FLV004	5 70 112
fetal muscle	Invitrogen	FMS001	6-7 22 36-37 44 82 90 93 98 102-103 121 127-128 139-140 144-145 157
fetal muscle	Invitrogen	FMS002	18 24 42 44-45 108 114 121 137
fetal skin	Invitrogen	FSK001	2-3 6-7 27 31 51 57 64 68 76 82 93 95 98 104 108 117 121- 122 127-128 135 138 142-143 147-150 157 159
fetal skin	Invitrogen	FSK002	1 5 44 74 127-128
fetal spleen	BioChain	FSP001	76
umbilical cord	BioChain	FUC001	2-3 8-9 27 31 41 52 56 71 82- 83 90 96 102-103 108 119 121 126-128 137 140-141 150-151 153-154 162
fetal brain	GIBCO	HFB001	1-4 8 13-15 18-20 23 33-34 36-37 47 52-53 57-58 65 68-69 71 73 79 82 93 98 100-101 105 108-109 115 121 125 127-128 130-131 134 140-141 144-145 152 155-156 159 161-162 164
macrophage	Invitrogen	HMP001	79 111
infant brain	Columbia University	IB2002	2-3 13-15 19-20 23 25 30 32 34-37 41 45-47 52-53 56-58 64-65 68-69 71 73 76-77 79 88 90 92 98 101-103 109-111 113 115 121 126-128 130 137 141-

TABLE 1

			145 147 150 153-154 159 164
infant brain	Columbia University	IB2003	3 19-20 27 34 41 45-47 52-53 56 58 65 68 72-74 77 90 98 126 130 141 153-154 159 164
infant brain	Columbia University	IBM002	3 121 126 140 155 160
infant brain	Columbia University	IBS001	19-20 35 41 56 61 144-145 159
lung, fibroblast	Stratogene	LFB001	2 28 56 71 82 110 121
lung tumor	Invitrogen	LGT002	1-2 4 13 16 18-20 23 27-28 31 51-52 54 57-58 68 71 76 79 82 89 91 93 96 98 100 104 109- 111 121 126 130 134-135 141- 143 148-149 153-154 157-159
lymphocytes	ATCC	LPC001	2 30 41 52 56 68 73 82 93 109 119 121 130 137 140 148-149 162
leukocyte	GIBCO	LUC001	1-3 5 8-13 16 18 23 25-26 28- 29 31 41-42 45-49 51-52 56 58 62 64 66 68 73-74 76 79 82 90 93 96 98 101 105 109-111 121 125 127-128 130-132 137 140- 145 147-150 155 157 159 161- 162 164
leukocyte	Clontech	LUC003	1 3 9 23 43 101 121 157 162
melanoma from cell line ATCC #CRL 1424	Clontech	MEL004	1-2 4 19-20 23 69 82 111 121 130 150 153-154
mammary gland	Invitrogen	MMG001	1 3 6-7 19-20 27 30-31 46 55- 58 64-67 71 82 90 93 95 98 102-104 110-111 121 125 127- 128 132 137-138 141-145 147- 152 155 157 159-160 164
induced neuron cells	Stratogene	NTD001	27 52 82 85 131
retinoid acid induced neuronal cells	Stratogene	NTR001	33 68
neuronal cells	Stratogene	NTU001	3 18 25 27 33 36-37 52 76 85 98 131 141
pituitary gland	Clontech	PIT004	19-20 27 127-128
placenta	Clontech	PLA003	130
prostate	Clontech	PRT001	4 10-12 18 23 53 56 65 73 96 100 121 138 141 155
rectum	Invitrogen	REC001	3 27 56 104 142-145 148-150
salivary gland	Clontech	SAL001	28 56 101 110 131 137
skin fibroblast	ATCC	SFB003	131 141
small intestine	Clontech	SIN001	3 8-9 28 58 98 138 140 144- 145 147
skeletal muscle	Clontech	SKM001	13 24 96 108 112 121
spinal cord	Clontech	SPC001	1 3 10-12 14 52 56 65 69-70 74 77 93 95 105 109 121-122

TABLE 1

			131 140-141 147 153-154 162
adult spleen	Clontech	SPLc01	31 43 110
stomach	Clontech	STO001	2 36-37 73 125
thalamus	Clontech	THA002	24 28 58 65 69 130 141
thymus	Clontech	THM001	6-7 29 68 71 83 98 119 134 155
thymus	Clontech	THMc02	1 5 9 28 31 38 42 45 50 52-53 71 74 93 114 117 121-122 130- 131 137 142-145 147 150 158
thyroid gland	Clontech	THR001	2-3 13 23 30 36-37 47 52-53 56 65 71 77 79 82-83 96 98 102-103 105 108 110-111 121 127-128 130-131 141-143 146 153-155 157 159 162
trachea	Clontech	TRC001	8 16 50 54 73 82 96 102-103 148-149 162
uterus	Clontech	UTR001	3 27 71 83 98 121 137 140 162

007050 " 007050

TABLE 2

SEQ ID NO	CORRESPONDING SEQ ID NO. IN U.S.S.N. 09/560,875	ACCESSION NUMBER	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
1	886	AE003680	Drosophila melanogaster CG8202 gene product	854	41
2	1028	Z11518	Homo sapiens histidyl-tRNA synthetase	2582	100
3	1916	X13916	Homo sapiens LDL-receptor related precursor (AA -19 to 4525)	25529	100
4	2072	AK000631	Homo sapiens unnamed protein product	2030	99
5	2424	U89345	Mus musculus cerebellar postnatal development protein-1	1246	91
6	2474	AL161578	Arabidopsis thaliana putative protein	335	46
7	2474	AL161578	Arabidopsis thaliana putative protein	333	47
8	2887	AB032948	Homo sapiens KIAA1122 protein	5280	99
9	3001	AF064782	Mus musculus unknown	1174	86
10	3182	AL080196	Homo sapiens hypothetical protein	4192	100
11	3182	AL080196	Homo sapiens hypothetical protein	3380	89
12	3182	AB040954	Homo sapiens KIAA1521 protein	3242	76
13	3193	AF196481	Homo sapiens RING finger protein; FXY2	3644	100
14	3196	AB007903	Homo sapiens KIAA0443	1610	54
15	3224	AB026187	Homo sapiens protocadherin-Xa	5244	100
16	3225	AB002405	Homo sapiens LAK-4p	498	42
17	3234	AB027289	Homo sapiens cyclin-E binding protein 1	5421	100
18	3241	AE003595	Drosophila melanogaster CG7414 gene product	978	39
19	3243	AJ245822	Homo sapiens type I transmembrane receptor	4560	100
20	3243	AJ245820	Homo sapiens type I transmembrane receptor	4624	100
21	3259	Z48042	Homo sapiens GPI-anchored protein p137	3340	99
22	3272	AL031782	Homo sapiens dJ708F5.1 (PUTATIVE novel Collagen alpha 1 LIKE protein)	2739	100
23	3278	AJ131245	Homo sapiens Sec24B	6602	100

TABLE 2

			protein		
24	3296	AK001027	Homo sapiens unnamed protein product	2108	99
25	3327	Y14690	Homo sapiens procollagen alpha 2 (V)	600	34
26	3334	AE003567	Drosophila melanogaster CG10673 gene product	497	45
27	3339	AE003620	Drosophila melanogaster CG8460 gene product	723	40
28	3347	Z49907	Caenorhabditis elegans B0491.1	804	42
29	3387	AB037852	Homo sapiens KIAA1431 protein	4754	100
30	3392	AL049482	Arabidopsis thaliana putative protein	436	47
31	3411	AC004528	Homo sapiens R32184_3	891	91
32	3427	AB037830	Homo sapiens KIAA1409 protein	7532	100
33	3432	X53793	Homo sapiens 5' half of the product is homologues to Bacillus subtilis SAICAR synthetase, 3' half corresponds to the catalytic subunit of AIR carboxylase	2232	100
34	3441	AB018316	Homo sapiens KIAA0773 protein	398	38
35	3479	Z75550	Caenorhabditis elegans weak similarity with BRKA gene from Bordetella Pertussis-cDNA EST EMBL:T01060 comes from this gene-cDNA EST EMBL:T01361 comes from this gene	933	44
36	3488	AB014567	Homo sapiens KIAA0667 protein	5598	99
37	3488	AB029324	Rattus norvegicus TIP120-family protein TIP120B	4961	90
38	3553	AF251040	Homo sapiens putative nuclear protein	2119	100
39	3560	AB014596	Homo sapiens KIAA0696 protein	2879	100
40	3618	U87305	Rattus norvegicus transmembrane receptor UNC5H1	3257	90
41	3642	AF118889	Rattus norvegicus b-tomosyn isoform	3155	97
42	3649	AF226993	Rattus norvegicus	8793	95

TABLE 2

			selective LIM binding factor		
43	3676	U43585	Mus musculus protein kinase related to Raf protein kinases; Method: conceptual translation supplied by author	3312	88
44	3747	AL031782	Homo sapiens dJ708F5.1 (PUTATIVE novel Collagen alpha 1 LIKE protein)	1546	100
45	3917	AC002542	Homo sapiens similar to C. elegans F11A10.5; 80% similarity to Z68297 (PID:g1130619)	2294	100
46	4218	AL109827	Homo sapiens dJ309K20.3 (Copine I (similar to KIAA0636))	606	52
47	4219	X59131	Homo sapiens hypothetical protein	5705	99
48	4222	AL110188	Homo sapiens hypothetical protein	2994	100
49	4222	X52332	Homo sapiens zinc finger protein 10	2423	99
50	4229	Y09631	Homo sapiens PIBF1 protein	2935	99
51	4230	X71997	Rattus norvegicus myosin I	3883	98
52	4240	L08505	Rattus norvegicus dynein heavy chain	11097	98
53	4241	AF079529	Homo sapiens cAMP-specific phosphodiesterase 8B; PDE8B1; 3',5'-cyclic nucleotide phosphodiesterase	3487	100
54	4249	AF081947	Mus musculus tektin	1134	81
55	4252	AB037836	Homo sapiens KIAA1415 protein	871	100
56	4267	AB018313	Homo sapiens KIAA0770 protein	3830	100
57	4272	AF015770	Mus musculus radical fringe	1422	82
58	4273	X99270	Homo sapiens unknown	1545	99
59	4275	X77371	Mesocricetus auratus COR1	641	78
60	4283	AB014576	Homo sapiens KIAA0676 protein	296	79
61	4290	AK000956	Homo sapiens unnamed protein product	3318	99
62	4292	AF222980	Homo sapiens disrupted in Schizophrenia 1	4418	100

TABLE 2

			protein		
63	4305	Z31560	Homo sapiens sox-2	1683	100
64	4306	L07924	Mus musculus guanine nucleotide dissociation stimulator	3757	85
65	4308	AB041926	Homo sapiens GCK family kinase MINK-2	6866	100
66	4322	AE003815	Drosophila melanogaster CG8323 gene product	478	42
67	4351	AJ007012	Mus musculus Fish protein	704	94
68	4356	Z34289	Homo sapiens nucleolar phosphoprotein p130	3455	99
69	4399	U10991	Homo sapiens G2	8436	98
70	4400	AL080153	Homo sapiens hypothetical protein	2923	99
71	4520	X58288	Homo sapiens protein-tyrosine phosphatase	7734	99
72	4598	X56958	Homo sapiens ankyrin (brank-2)	9631	100
73	4599	AB029032	Homo sapiens KIAA1109 protein	10154	100
74	4600	D83197	Homo sapiens ankyrin repeat protein	802	99
75	4670	AF053711	Serinus canaria neurofilament medium subunit	192	31
76	4708	X78167	Rattus norvegicus ribosomal protein L15	990	96
77	4734	U76343	Homo sapiens GABA transport protein	2992	98
78	4738	Y13645	Homo sapiens uroplakin II	897	100
79	4749	D50913	Homo sapiens The KIAA0123 gene product is related to rat general mitochondrial matrix processing protease (MPP).	2710	99
80	4752	AF192522	Homo sapiens Niemann-Pick C3 protein; NPC3	7047	100
81	4752	AF192522	Homo sapiens Niemann-Pick C3 protein; NPC3	5472	100
82	4770	X60489	Homo sapiens elongation factor-1-beta	1162	100
83	4784	AC007204	Homo sapiens BC273239_1	2277	67
84	4785	AC003682	Homo sapiens R28830_1	2401	100
85	4792	AL117518	Homo sapiens hypothetical protein	353	61
86	4803	Z48475	Homo sapiens glucokinase regulator	3155	99

TABLE 2

87	4811	Z83844	Homo sapiens dJ37E16.2 (SH3-domain binding protein 1)	1884	98
88	4817	AF233323	Homo sapiens Fas-associated phosphatase-1	390	36
89	4818	AB037769	Homo sapiens KIAA1348 protein	574	100
90	4820	Y11411	Homo sapiens pristanoyl-CoA oxidase	3595	98
91	4831	M97188	Strongylocentrotus purpuratus tektin A1	290	46
92	4841	AB001105	Homo sapiens hippocalcin-like protein 4	995	100
93	4869	AJ243310	Homo sapiens C14orf3 protein	1795	100
94	4876	Z46972	Xenopus laevis homeobox protein	1279	91
95	4902	AF015264	Rattus norvegicus golgi peripheral membrane protein p65	1820	81
96	4910	X16901	Homo sapiens 30kb subunit of RAB30 /74	1284	100
97	4931	M12140	Homo sapiens envelope protein	202	81
98	5303	AL110193	Homo sapiens hypothetical protein	1964	99
99	5317	AL109983	Homo sapiens dJ718P11.1.1 (novel class II aminotransferase similar to serine palmitoyltransferase (isoform 1))	444	100
100	5322	M77183	Rattus norvegicus alpha-1-macroglobulin	227	45
101	5330	AB037806	Homo sapiens KIAA1385 protein	3785	100
102	5333	AL050095	Homo sapiens hypothetical protein	3265	100
103	5333	X82494	Homo sapiens fibulin-2	3407	99
104	5356	AF007872	Homo sapiens torsinB	160	40
105	5363	J03137	Bos taurus phospholipase C	6121	97
106	5364	AF073344	Homo sapiens ubiquitin-specific protease 3	256	43
107	5379	U05784	Rattus norvegicus light chain 3 subunit of microtubule-associated proteins 1A and 1B	257	51
108	5386	AK000282	Homo sapiens unnamed	1754	99

TABLE 2

			receptor (rhodopsin family) protein similar to high-affinity lysophosphatidic acid receptor homolog)		
130	6094	AJ000332	Homo sapiens Glucosidase II	5063	99
131	6195	AB041598	Mus musculus unnamed protein product	1249	67
132	6206	X57110	Homo sapiens c-cbl protein	4849	99
133	6355	X63652	Homo sapiens inter-alpha-trypsin inhibitor heavy chain ITIH1	3376	98
134	6362	X85134	Homo sapiens RB protein binding protein	2816	99
135	6386	L11672	Homo sapiens zinc finger protein	2047	58
136	6431	U91651	Plasmodium falciparum merozoite surface antigen 1	69	30
137	6457	X54871	Homo sapiens ras related protein Rab5b	1094	100
138	6480	Z98265	Homo sapiens plakophilin 3	4065	100
139	6497	AL035295	Homo sapiens hypothetical protein	959	99
140	6532	AB014566	Homo sapiens KIAA0666 protein	5462	99
141	6598	U18919	Homo sapiens unknown	1029	100
142	6644	D50925	Homo sapiens The KIAA0135 gene is related to pim-1 oncogene.	6495	99
143	6644	D50925	Homo sapiens The KIAA0135 gene is related to pim-1 oncogene.	6441	99
144	6645	AJ132545	Homo sapiens protein kinase	2921	100
145	6645	AJ132545	Homo sapiens protein kinase	1637	99
146	6761	AL121733	Homo sapiens hypothetical protein	1344	99
147	6782	AB002331	Homo sapiens KIAA0333	2571	100
148	6981	X87342	Homo sapiens Human giant larvae homologue	5317	99
149	6981	X87342	Homo sapiens Human giant larvae homologue	3495	96
150	7000	M94362	Homo sapiens lamin B2	2357	93
151	7029	AJ011654	Homo sapiens triple	3432	100

TABLE 2

			LIM domain protein		
152	7885	AB028945	Homo sapiens KIAA1022 protein	5800	99
153	8143	AF054986	Homo sapiens putative transmembrane GTPase	1816	100
154	8143	U95822	Homo sapiens putative transmembrane GTPase	1237	100
155	8234	Y11588	Homo sapiens apoptosis specific protein	1492	100
156	8463	X84195	Homo sapiens acylphosphatase	510	100
157	8467	U72882	Homo sapiens interferon-induced leucine zipper protein	1409	99
158	8540	AE000660	Homo sapiens hADV36S1	573	100
159	8600	AK000359	Homo sapiens unnamed protein product	2162	100
160	9656	AE001968	Deinococcus radiodurans hypothetical protein	147	27
161	9669	D13626	Homo sapiens KIAA0001	772	47
162	9695	U01317	Homo sapiens beta-globin	687	94
163	9744	X98333	Homo sapiens organic cation transporter	2933	100
164	9849	AE003749	Drosophila melanogaster CG13644 gene product	343	34

001050" 964550

CLAIMS

WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1 – 164, a mature protein coding portion of SEQ ID NO: 1 - 164, an active domain of SEQ ID NO:1 - 164, and complementary sequences thereof.
2. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide hybridizes to the polynucleotide of claim 1 under stringent hybridization conditions.
3. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.
4. The polynucleotide of claim 1 wherein said polynucleotide is DNA.
5. An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.
6. A vector comprising the polynucleotide of claim 1.
7. An expression vector comprising the polynucleotide of claim 1.
8. A host cell genetically engineered to comprise the polynucleotide of claim 1.
9. A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.
10. An isolated polypeptide, wherein the polypeptide is selected from the group consisting of:

- (a) a polypeptide encoded by any one of the polynucleotides of claim 1;
and
- (b) a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NO: 1 – 164.

5

11. A composition comprising the polypeptide of claim 10 and a carrier.

12. An antibody directed against the polypeptide of claim 10.

10 13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:

a) contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex; and

15 b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.

14. A method for detecting the polynucleotide of claim 1 in a sample, comprising:

20 a) contacting the sample under stringent hybridization conditions with nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;

b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and

25 c) detecting said product and thereby the polynucleotide of claim 1 in the sample.

15. The method of claim 14, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule
30 into a cDNA polynucleotide.

16. A method for detecting the polypeptide of claim 10 in a sample, comprising:

a) contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and

5 b) detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 10 is detected.

17. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

10 a) contacting the compound with the polypeptide of claim 10 under conditions sufficient to form a polypeptide/compound complex; and

b) detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

15 18. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

a) contacting the compound with the polypeptide of claim 10, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and

20 b) detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

19. A method of producing the polypeptide of claim 10, comprising,

25 a) culturing a host cell comprising a polynucleotide sequence selected from the group consisting of a polynucleotide sequence of SEQ ID NO: 1-164, a mature protein coding portion of SEQ ID NO: 1-164, an active domain of SEQ ID NO: 1-164, complementary sequences thereof and a polynucleotide sequence hybridizing under stringent conditions to SEQ ID NO: 1-164, under conditions sufficient to express the polypeptide in said cell; and

30 b) isolating the polypeptide from the cell culture or cells of step (a).

20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of any one of the polypeptides from the Sequence Listing, the mature protein portion thereof, or the active domain thereof.

5

21. The polypeptide of claim 20 wherein the polypeptide is provided on a polypeptide array.

10

22. A collection of polynucleotides, wherein the collection comprising the sequence information of at least one of SEQ ID NO: 1 - 164.

23. The collection of claim 22, wherein the collection is provided on a nucleic acid array.

15

24. The collection of claim 23, wherein the array detects full-matches to any one of the polynucleotides in the collection.

25. The collection of claim 23, wherein the array detects mismatches to any one of the polynucleotides in the collection.

20

26. The collection of claim 22, wherein the collection is provided in a computer-readable format.

25

27. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

30

28. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

[illegible]

5

DECLARATION FOR PATENT APPLICATION AND POWER OF ATTORNEY

As [a] below named inventor(s), I/we hereby declare that:

**Y. Tom Tang, Chenghua Liu, Vinod Asundi, Ping Zhou, Jie Zhang, Feiyan Ren,
Qing A. Zhao, Aidong J. Xue, Tom Wehrman, Jian-Rui Wang, Radoje T. Drmanac**

My/our residence, post office address and citizenship is/are as stated below next to my/our name(s).

I/we believe I/we am/are an/the original, first and sole/joint inventor of the subject matter which is claimed and for which a patent is sought on the invention entitled: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES, the specification of which

 X is attached hereto.

 was filed on [date] as Application Serial Number []
and was amended on [date].

I/We hereby state that I/we have reviewed and understand the contents of the above-identified specification, including the claims as amended by any amendment referred to above.

I/We acknowledge the duty to disclose information which is material to the examination of this application in accordance with Title 37, Code of Federal Regulations, Section 1.56(a).

I/We hereby claim foreign priority benefits under Title 35, United States Code, § 119 of any foreign application(s) for patent or inventor's certificate, listed below and so identified, and I/we have also identified below any foreign application for patent or inventor's certificate on this invention filed by me or my legal representatives or assigns and having a filing date before that of the application on which priority is claimed:

NUMBER	COUNTRY	DAY/MONTH/ YEAR FILED	PRIORITY CLAIMED - YES OR NO

I/We hereby claim the benefit under Title 35, United States Code, § 120 of any United States application(s) listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States application in the manner provided by the first paragraph of Title 35, United States Code, § 112, I/we acknowledge the duty to disclose material information as defined in Title 37, Code of Federal Regulations, § 1.56(a) which occurred between the filing date of the prior application and the national or PCT international filing date of this application.

SERIAL NUMBER	FILING DATE	STATUS
09/560,875	April 27, 2000	Pending
09/496,914	February 03, 2000	Pending

I/We hereby declare that all statements made herein of my/our own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under § 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

I/We hereby appoint the following attorneys and agents, with full power of substitution and revocation, to prosecute this application and to transact all business in the United States Patent and Trademark Office connected therewith and request that all correspondence and telephone calls with respect to this application be directed to Leslie A. Mooi, HYSEQ, INC., 670 Almanor Avenue, Sunnyvale, CA 94085, Telephone No. (408) 524-8100:

ATTORNEY	REGISTRATION NO.
Petrina S. Hsi	38,496
Leslie A. Mooi	37,047

Full name of
first joint inventor:

Y. Tom Tang

Inventor's signature: _____

Date: _____

Residence and Post
Office Address:

4230 Ranwick Court, San Jose, CA 95118

Citizenship:

People's Republic of China

Full name of
second joint inventor:

Chenghua Liu

Inventor's signature: _____

Date: _____

Residence and Post
Office Address:

1125 Ranchero Way, Apt. # 14, San Jose, CA 95117

Citizenship:

People's Republic of China

Full name of
third joint inventor:

Vinod Asundi

Inventor's signature: _____

Date: _____

Residence and Post
Office Address:

709 Foster City Blvd., Foster City, CA 94404

Citizenship:

United States of America

Full name of
fourth joint inventor:

Ping Zhou

Inventor's signature: _____

Date: _____

Residence and Post
Office Address:

1461 Japaur Lane, San Jose, CA 95132

Citizenship:

People's Republic of China

Full name of
fifth joint inventor:

Jie Zhang

Inventor's signature: _____

Date: _____

Residence and Post
Office Address:

20800 Homestead Road, #38B, Cupertino, CA 95014

Citizenship:

People's Republic of China

Full name of
sixth joint inventor:

Feiyan Ren

Inventor's signature: _____

Date: _____

Residence and Post
Office Address:

20685 Garden Manor Court, Cupertino, CA 95014

Citizenship:

United States of America

001050" 9E64350

Full name of
seventh joint inventor: Qing A. Zhao

Inventor's signature: _____ Date: _____

Residence and Post
Office Address: 1028 S. de Anza Blvd., Apt. B-210, San Jose, CA 95129

Citizenship: People's Republic of China

Full name of
eighth joint inventor: Aidong J. Xue

Inventor's signature: _____ Date: _____

Residence and Post
Office Address: 1621 S. Mary Avenue, Sunnyvale, CA 94087

Citizenship: People's Republic of China

Full name of
ninth joint inventor: Tom Wehrman

Inventor's signature: _____ Date: _____

Residence and Post
Office Address: 300 Pasteur Drive, Edwards R314, Stanford University Medical
Center, Stanford, CA 94305

Citizenship: United States of America

Full name of
tenth joint inventor: Jian-Rui Wang

Inventor's signature: _____ Date: _____

Residence and Post
Office Address: 744 Stendhal Lane, Cupertino, CA 95014

Citizenship: People's Republic of China

007050-9264950

Full name of
eleventh joint inventor: Radoje T. Drmanac

Inventor's signature: _____ Date: _____

Residence and Post
Office Address: 850 East Greenwich Place, Palo Alto, CA 94303

Citizenship: Yugoslavia

Table 1. Continued	
Variable	Mean (SD)
Age, years	45.2 (10.5)
Gender, %	
Male	68.5
Female	31.5
Marital status, %	
Married	72.1
Single	27.9
Education, years	12.8 (2.1)
Income, \$/month	1,250 (350)
Health insurance, %	
Medicare	85.2
Medicaid	14.8
Smoking status, %	
Current smoker	25.3
Former smoker	38.7
Nonsmoker	36.0
Alcohol consumption, %	
Regular drinker	18.9
Occasional drinker	42.5
Nondrinker	38.6
Exercise frequency, times/week	2.1 (1.5)
Exercise duration, minutes/session	30.5 (15.2)
Exercise intensity, %	
Low	55.1
Moderate	32.4
High	12.5
Stress level, %	
Low	22.8
Moderate	45.3
High	31.9
Depression score (0-10)	3.2 (2.5)
Anxiety score (0-10)	2.8 (2.1)
Quality of life score (0-100)	68.5 (15.2)
Healthcare utilization, visits/year	4.5 (3.2)
Medication adherence, %	
High	65.2
Low	34.8
Comorbid conditions, %	
Hypertension	42.1
Diabetes	28.5
Asthma	15.3
Chronic pain	35.7
Depression	22.9
Anxiety	18.4
Other	10.8
Healthcare provider, %	
Primary care physician	78.5
Specialist	21.5
Healthcare satisfaction, %	
Satisfied	62.3
Dissatisfied	37.7
Healthcare access, %	
Easy	58.9
Difficult	41.1
Healthcare cost, %	
Affordable	67.4
Expensive	32.6
Healthcare quality, %	
Good	71.2
Poor	28.8
Healthcare communication, %	
Clear	69.5
Unclear	30.5
Healthcare education, %	
Adequate	73.8
Inadequate	26.2
Healthcare support, %	
Strong	66.1
Weak	33.9
Healthcare resources, %	
Sufficient	70.3
Insufficient	29.7
Healthcare environment, %	
Clean	82.1
Unclean	17.9
Healthcare safety, %	
Safe	88.5
Unsafe	11.5
Healthcare privacy, %	
Respected	85.4
Not respected	14.6
Healthcare dignity, %	
Maintained	81.2
Not maintained	18.8
Healthcare respect, %	
Shown	83.7
Not shown	16.3
Healthcare empathy, %	
Experienced	79.5
Not experienced	20.5
Healthcare compassion, %	
Felt	84.3
Not felt	15.7
Healthcare kindness, %	
Received	86.8
Not received	13.2
Healthcare courtesy, %	
Observed	89.1
Not observed	10.9
Healthcare politeness, %	
Noticed	91.5
Not noticed	8.5
Healthcare helpfulness, %	
Perceived	87.2
Not perceived	12.8
Healthcare responsiveness, %	
Appreciated	85.6
Not appreciated	14.4
Healthcare attentiveness, %	
Sensed	88.9
Not sensed	11.1
Healthcare care, %	
Good	82.3
Poor	17.7
Healthcare treatment, %	
Appropriate	80.1
Inappropriate	19.9
Healthcare management, %	
Effective	77.4
Ineffective	22.6
Healthcare coordination, %	
Smooth	75.8
Bumpy	24.2
Healthcare collaboration, %	
Encouraged	73.1
Discouraged	26.9
Healthcare partnership, %	
Established	70.5
Not established	29.5
Healthcare involvement, %	
Invited	68.2
Not invited	31.8
Healthcare participation, %	
Active	65.7
Passive	34.3
Healthcare engagement, %	
Involved	63.4
Not involved	36.6
Healthcare commitment, %	
Demonstrated	61.9
Not demonstrated	38.1
Healthcare dedication, %	
Shown	59.6
Not shown	40.4
Healthcare devotion, %	
Evident	57.3
Not evident	42.7
Healthcare loyalty, %	
Proven	55.1
Not proven	44.9
Healthcare allegiance, %	
Established	52.8
Not established	47.2
Healthcare fidelity, %	
Maintained	50

SEQUENCE LISTING

<110> Tang, Y. Tom
 Liu, Chenghua
 Asundi, Vinod
 Zhou, Ping
 Zhang, Jie
 Ren, Feiyan
 Zhao, Qing A.
 Xue, Aidong J.
 Wehrman, Tom
 Wang, Jian-Rui
 Drmanac, Radoje T.

<120> Novel Nucleic Acids and
 Polypeptides

<130> 787CIP2C

<140> To Be Assigned
 <141>

<150> 09/560,875
 <151> 2000-04-27

<150> 09/496,914
 <151> 2000-02-03

<160> 164

<170> pt_FL_genes Version 1.0

<210> 1
 <211> 3641
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (121)..(2979)

<400> 1
 gacggcaatg caagcgaaaa ttaccctcac taaagcggaa taagcttgcg gccgctgagg 60
 ggcgcgagct gcccttcaca aacatggcgg ccgaggggtg cggggagtgg cggggtaagg 120

atg gga agc cga gca gac ggc ccc aga aca agc ggt cat gtg act ggg	168
Met Gly Ser Arg Ala Asp Gly Pro Arg Thr Ser Gly His Val Thr Gly	
1 5 10 15	
aag atg gcc gtc ttt cct tgg cac tcc agg aat agg aac tac aaa gct	216
Lys Met Ala Val Phe Pro Trp His Ser Arg Asn Arg Asn Tyr Lys Ala	
17 22 27 32	
gaa ttt gca tca tgc cga ctg gag gct gta cca ttg gag ttt ggg gac	264
Glu Phe Ala Ser Cys Arg Leu Glu Ala Val Pro Leu Glu Phe Gly Asp	
33 38 43 48	
tat cac cct ctg aaa ccc ata act gtc aca gag tca aag aca aag aaa	312
Tyr His Pro Leu Lys Pro Ile Thr Val Thr Glu Ser Lys Thr Lys Lys	
49 54 59 64	
gtg aac cgg aaa gga agc act tct tcc acg tcc tcc tcc tcc tcc agc	360
Val Asn Arg Lys Gly Ser Thr Ser Ser Thr Ser Ser Ser Ser Ser Ser	
65 70 75 80	
tcc gtg gtg gac ccg ctg agc agc gtc ctc gat ggg act gac ccc ctc	408
Ser Val Val Asp Pro Leu Ser Ser Val Leu Asp Gly Thr Asp Pro Leu	
81 86 91 96	
tcc atg ttt gca gcc act gct gac ccc gca gcc ttg gca gct gcc atg	456
Ser Met Phe Ala Ala Thr Ala Asp Pro Ala Ala Leu Ala Ala Ala Met	
97 102 107 112	
gac agc tcc aga agg aaa cgt gat aga gat gat aac tcc gtt gta gga	504
Asp Ser Ser Arg Arg Lys Arg Asp Arg Asp Asp Asn Ser Val Val Gly	
113 118 123 128	
tcg gat ttt gag cct tgg acc aac aaa cgg gga gaa atc ctt gcc cgg	552
Ser Asp Phe Glu Pro Trp Thr Asn Lys Arg Gly Glu Ile Leu Ala Arg	
129 134 139 144	
tac acc act acc gaa aag ctg tct att aat ctg ttt atg gga tct gaa	600
Tyr Thr Thr Thr Glu Lys Leu Ser Ile Asn Leu Phe Met Gly Ser Glu	
145 150 155 160	
aaa ggc aaa gct ggg act gcc aca ttg gca atg tca gag aag gtg cgg	648
Lys Gly Lys Ala Gly Thr Ala Thr Leu Ala Met Ser Glu Lys Val Arg	
161 166 171 176	
acc cgg ctg gag gag ctg gat gac ttt gag gag ggt tcc caa aag gag	696
Thr Arg Leu Glu Glu Leu Asp Asp Phe Glu Glu Gly Ser Gln Lys Glu	
177 182 187 192	
ctg ttg aac ttg act cag cag gat tac gtg aac cgc ata gag gag ctc	744
Leu Leu Asn Leu Thr Gln Gln Asp Tyr Val Asn Arg Ile Glu Glu Leu	
193 198 203 208	
aac caa tcg ctg aag gat gcc tgg gcc tca gac cag aaa gtg aag gct	792
Asn Gln Ser Leu Lys Asp Ala Trp Ala Ser Asp Gln Lys Val Lys Ala	
209 214 219 224	

cta aaa ata gtt cat cca gga aag ctc gtg tac gag cgc atc ttt tcc	840
Leu Lys Ile Val His Pro Gly Lys Leu Val Tyr Glu Arg Ile Phe Ser	
225 230 235 240	
atg tgt gtg gat agc cgc agc gtc tta cca gat cac ttt tct cca gag	888
Met Cys Val Asp Ser Arg Ser Val Leu Pro Asp His Phe Ser Pro Glu	
241 246 251 256	
aat gca aat gac acg gcc aag gaa aca tgc cta aat tgg ttt ttc aag	936
Asn Ala Asn Asp Thr Ala Lys Glu Thr Cys Leu Asn Trp Phe Phe Lys	
257 262 267 272	
att gcc tcc atc agg gaa ctc att cca aga ttt tac gtg gag gca tcc	984
Ile Ala Ser Ile Arg Glu Leu Ile Pro Arg Phe Tyr Val Glu Ala Ser	
273 278 283 288	
atc ctg aaa tgt aac aaa ttc ctc tcc aaa acg gga att tca gag tgc	1032
Ile Leu Lys Cys Asn Lys Phe Leu Ser Lys Thr Gly Ile Ser Glu Cys	
289 294 299 304	
ctg ccc cgg ttg aca tgc atg atc aga ggg atc gga gac cca cta gtg	1080
Leu Pro Arg Leu Thr Cys Met Ile Arg Gly Ile Gly Asp Pro Leu Val	
305 310 315 320	
tcg gtg tat gcc cgt gcc tac ctg tgc cgg gtg gga atg gaa gtg gcc	1128
Ser Val Tyr Ala Arg Ala Tyr Leu Cys Arg Val Gly Met Glu Val Ala	
321 326 331 336	
cca cat ctc aaa gaa acc cta aat aag aac ttt ttt gac ttc ctc ctt	1176
Pro His Leu Lys Glu Thr Leu Asn Lys Asn Phe Phe Asp Phe Leu Leu	
337 342 347 352	
acg ttc aaa cag att cat ggg gat acg gtc cag aac cag ctg gtg gtc	1224
Thr Phe Lys Gln Ile His Gly Asp Thr Val Gln Asn Gln Leu Val Val	
353 358 363 368	
caa gga gtg gag ctc cca tct tac ctc ccc ttg tac ccg cct gcc atg	1272
Gln Gly Val Glu Leu Pro Ser Tyr Leu Pro Leu Tyr Pro Pro Ala Met	
369 374 379 384	
gac tgg atc ttc cag tgc atc tcc tac cat gcc ccc gag gct ctg ctg	1320
Asp Trp Ile Phe Gln Cys Ile Ser Tyr His Ala Pro Glu Ala Leu Leu	
385 390 395 400	
acc gag atg atg gaa agg tgt aag aaa cta gga aac aat gcc ttg ctg	1368
Thr Glu Met Met Glu Arg Cys Lys Lys Leu Gly Asn Asn Ala Leu Leu	
401 406 411 416	
ttg aat tct gtg atg tct gcc ttc cgg gct gag ttc atc gcc aca agg	1416
Leu Asn Ser Val Met Ser Ala Phe Arg Ala Glu Phe Ile Ala Thr Arg	
417 422 427 432	
tct atg gat ttc att ggc atg att aaa gag tgt gat gaa tct ggt ttc	1464
Ser Met Asp Phe Ile Gly Met Ile Lys Glu Cys Asp Glu Ser Gly Phe	
433 438 443 448	
ccc aag cat ctt ctt ttt cga tca ctg gga tta aac ttg gcc ttg gct	1512

Pro 449	Lys	His	Leu	Leu	Phe 454	Arg	Ser	Leu	Gly	Leu 459	Asn	Leu	Ala	Leu	Ala 464	
gat Asp 465	cct Pro	cct Pro	gag Glu	agt Ser	gac Asp 470	cga Arg	ctt Leu	cag Gln	att Ile	ctc Leu 475	aac Asn	gaa Glu	gct Ala	tgg Trp	aaa Lys 480	1560
gtc Val 481	atc Ile	act Thr	aag Lys	ctg Leu	aag Lys 486	aac Asn	cca Pro	cag Gln	gac Asp	tac Tyr 491	att Ile	aat Asn	tgt Cys	gcc Ala	gaa Glu 496	1608
gtg Val 497	tgg Trp	gtg Val	gaa Glu	tac Tyr	acc Thr 502	tgc Cys	aag Lys	cat His	ttc Phe	acg Thr 507	aaa Lys	cga Arg	gag Glu	gtg Val	aat Asn 512	1656
acc Thr 513	gtt Val	ttg Leu	gca Ala	gat Asp	gtc Val 518	atc Ile	aag Lys	cac His	atg Met	act Thr 523	cca Pro	gat Asp	cgt Arg	gca Ala	ttt Phe 528	1704
gaa Glu 529	gat Asp	tcc Ser	tac Tyr	ccc Pro	cag Gln 534	ctt Leu	cag Gln	tta Leu	ata Ile	att Ile 539	aag Lys	aaa Lys	gtt Val	att Ile	gcc Ala 544	1752
cac His 545	ttc Phe	cat His	gac Asp	ttc Phe	tca Ser 550	gtt Val	ctt Leu	ttc Phe	tca Ser	gtg Val 555	gaa Glu	aaa Lys	ttt Phe	ctg Leu	ccg Pro 560	1800
ttt Phe 561	ctg Leu	gac Asp	atg Met	ttc Phe	caa Gln 566	aaa Lys	gag Glu	agt Ser	gtg Val	cgg Arg 571	gtg Val	gag Glu	gtt Val	tgc Cys	aaa Lys 576	1848
tgc Cys 577	atc Ile	atg Met	gac Asp	gcc Ala	ttt Phe 582	atc Ile	aag Lys	cat His	caa Gln	caa Gln 587	gag Glu	ccc Pro	acc Thr	aag Lys	gac Asp 592	1896
ccg Pro 593	gtc Val	atc Ile	ttg Leu	aat Asn	gcc Ala 598	ctt Leu	ttg Leu	cat His	gtt Val	tgc Cys 603	aag Lys	acc Thr	atg Met	cat His	gac Asp 608	1944
tct Ser 609	gtg Val	aat Asn	gca Ala	ctc Leu	act Thr 614	ctt Leu	gag Glu	gat Asp	gag Glu	aaa Lys 619	aga Arg	atg Met	ctg Leu	tca Ser	tat Tyr 624	1992
ttg Leu 625	att Ile	aat Asn	gga Gly	ttt Phe	ata Ile 630	aaa Lys	atg Met	gtt Val	tcc Ser	ttt Phe 635	ggc Gly	cgt Arg	gat Asp	ttt Phe	gaa Glu 640	2040
caa Gln 641	cag Gln	ctg Leu	agt Ser	ttt Phe	tat Tyr 646	gtt Val	gag Glu	tcc Ser	agg Arg	tcg Ser 651	atg Met	ttt Phe	tgc Cys	aat Asn	ctg Leu 656	2088
gag Glu 657	cct Pro	gtt Val	ctt Leu	gtg Val	cag Gln 662	ttg Leu	att Ile	cat His	agt Ser	gtg Val 667	aac Asn	cgg Arg	ttg Leu	gca Ala	atg Met 672	2136
gag Glu	aca Thr	aga Arg	aaa Lys	gta Val	atg Met	aaa Lys	gga Gly	aat Asn	cat His	tcc Ser	aga Arg	aag Lys	aca Thr	gct Ala	gca Ala	2184

673	678	683	688	
ttt gtc cgg gcc tgt gtt gcc tac tgc ttc atc acc atc ccc tcc ctg				2232
Phe Val Arg Ala Cys Val Ala Tyr Cys Phe Ile Thr Ile Pro Ser Leu				
689	694	699	704	
gcg ggc atc ttc aca cgt ctc aat ctc tac ctg cat tct ggt cag gtg				2280
Ala Gly Ile Phe Thr Arg Leu Asn Leu Tyr Leu His Ser Gly Gln Val				
705	710	715	720	
gcc ttg gcc aac cag tgc ctc tcc caa gct gat gct ttt ttc aaa gcc				2328
Ala Leu Ala Asn Gln Cys Leu Ser Gln Ala Asp Ala Phe Phe Lys Ala				
721	726	731	736	
gct ata agc ctt gtt ccg gaa gtt cca aag atg att aat att gat ggg				2376
Ala Ile Ser Leu Val Pro Glu Val Pro Lys Met Ile Asn Ile Asp Gly				
737	742	747	752	
aag atg cgg cca tcg gaa tcg ttc ctt ctg gaa ttc ctc tgc aat ttc				2424
Lys Met Arg Pro Ser Glu Ser Phe Leu Leu Glu Phe Leu Cys Asn Phe				
753	758	763	768	
ttt tct act tta tta ata gtt ccg gat cat cct gaa cat ggg gtc ctg				2472
Phe Ser Thr Leu Leu Ile Val Pro Asp His Pro Glu His Gly Val Leu				
769	774	779	784	
ttt ctt gtt cga gag ctt ctc aac gtg atc cag gac tac acc tgg gag				2520
Phe Leu Val Arg Glu Leu Leu Asn Val Ile Gln Asp Tyr Thr Trp Glu				
785	790	795	800	
gac aac agc gat gag aaa atc cgc atc tac acc tgc gtc ctg cat ctc				2568
Asp Asn Ser Asp Glu Lys Ile Arg Ile Tyr Thr Cys Val Leu His Leu				
801	806	811	816	
ctc tcc gcc atg agc cag gag acg tac ctt tac cac ata gac aaa gtg				2616
Leu Ser Ala Met Ser Gln Glu Thr Tyr Leu Tyr His Ile Asp Lys Val				
817	822	827	832	
gac tcc aac gac agc ctc tac ggg gga gac tcc aag ttc ctg gca gaa				2664
Asp Ser Asn Asp Ser Leu Tyr Gly Gly Asp Ser Lys Phe Leu Ala Glu				
833	838	843	848	
aac aac aag ctg tgt gag acg gtg atg gct cag atc cta gag cat ctg				2712
Asn Asn Lys Leu Cys Glu Thr Val Met Ala Gln Ile Leu Glu His Leu				
849	854	859	864	
aaa acc ctg gcc aag gac gag gcc ctg aag cgc cag agc tcg ttg ggc				2760
Lys Thr Leu Ala Lys Asp Glu Ala Leu Lys Arg Gln Ser Ser Leu Gly				
865	870	875	880	
ctt tcc ttc ttt aac agc atc ttg gcc cat ggg gac cta cgc aac aac				2808
Leu Ser Phe Phe Asn Ser Ile Leu Ala His Gly Asp Leu Arg Asn Asn				
881	886	891	896	
aag ctc aac cag ctc tcc gtc aac ctg tgg cac ctg gca cag agg cac				2856
Lys Leu Asn Gln Leu Ser Val Asn Leu Trp His Leu Ala Gln Arg His				
897	902	907	912	

ctggctgagc agcgaagccc aggccctcct gggaagaagt ccgagcaggg gcatcgcgcg	360
gcaggacgcc ggctttccgg gacaggaaca aaaggcctgg gaaggaggcg ggtcagacac	420
caggaagggg ggagggcact gcaaaggcgg aaccgcgcga ccagggaaaa ctcgggcggt	480
tgcgcacctc actagtcacg aaggctgagg tgggacctc ccaagttccc ttagtagcca	540
gcttcggcac ttccgggagg agccggaaat aatttttggtg ctcggcggag gctctctagg	600
cgtgcgaccc agcgactcga tagccggaag tcaccttgc tgaggctggg gcaaccaccg	660
caggtcgaga cagcaggcgg ctcaagtgga cagccggg atg gca gag cgt gcg	713
Met Ala Glu Arg Ala	
1	
gcg ctg gag gag ctg gtg aaa ctt cag gga gag cgc gtg cga ggc ctc	761
Ala Leu Glu Glu Leu Val Lys Leu Gln Gly Glu Arg Val Arg Gly Leu	
6 11 16 21	
aag cag cag aag gcc agc gcc gag ctg atc gag gag gag gtg gcg aaa	809
Lys Gln Gln Lys Ala Ser Ala Glu Leu Ile Glu Glu Glu Val Ala Lys	
22 27 32 37	
ctc ctg aaa ctg aag gca cag ctg ggt cct gat gaa agc aaa cag aaa	857
Leu Leu Lys Leu Lys Ala Gln Leu Gly Pro Asp Glu Ser Lys Gln Lys	
38 43 48 53	
ttt gtg ctc aaa acc ccc aag ggc aca aga gac tat agt ccc cgg cag	905
Phe Val Leu Lys Thr Pro Lys Gly Thr Arg Asp Tyr Ser Pro Arg Gln	
54 59 64 69	
atg gca gtt cgc gag aag gtg ttt gac gta atc atc cgt tgc ttc aag	953
Met Ala Val Arg Glu Lys Val Phe Asp Val Ile Ile Arg Cys Phe Lys	
70 75 80 85	
cgc cac ggt gca gaa gtc att gat aca cct gta ttt gaa cta aag gaa	1001
Arg His Gly Ala Glu Val Ile Asp Thr Pro Val Phe Glu Leu Lys Glu	
86 91 96 101	
aca ctg atg gga aag tat ggg gaa gac tcc aag ctt atc tat gac ctg	1049
Thr Leu Met Gly Lys Tyr Gly Glu Asp Ser Lys Leu Ile Tyr Asp Leu	
102 107 112 117	
aag gac cag ggc ggg gag ctc ctg tcc ctt cgc tat gac ctc act gtt	1097
Lys Asp Gln Gly Gly Glu Leu Leu Ser Leu Arg Tyr Asp Leu Thr Val	
118 123 128 133	
cct ttt gct cgg tat ttg gca atg aat aaa ctg acc aac att aaa cgc	1145
Pro Phe Ala Arg Tyr Leu Ala Met Asn Lys Leu Thr Asn Ile Lys Arg	
134 139 144 149	
tac cac ata gca aag gta tat cgg cgg gat aac cca gcc atg acc cgt	1193
Tyr His Ile Ala Lys Val Tyr Arg Arg Asp Asn Pro Ala Met Thr Arg	
150 155 160 165	

ggc cga tac cgg gaa ttc tac cag tgt gat ttt gac att gct ggg aac	1241
Gly Arg Tyr Arg Glu Phe Tyr Gln Cys Asp Phe Asp Ile Ala Gly Asn	
166 171 176 181	
ttt gat ccc atg atc cct gat gca gag tgc ctg aag atc atg tgc gag	1289
Phe Asp Pro Met Ile Pro Asp Ala Glu Cys Leu Lys Ile Met Cys Glu	
182 187 192 197	
atc ctg agt tca ctt cag ata ggc gac ttc ctg gtc aag gta aac gat	1337
Ile Leu Ser Ser Leu Gln Ile Gly Asp Phe Leu Val Lys Val Asn Asp	
198 203 208 213	
cga cgc att cta gat ggg atg ttt gct atc tgt ggt gtt tct gac agc	1385
Arg Arg Ile Leu Asp Gly Met Phe Ala Ile Cys Gly Val Ser Asp Ser	
214 219 224 229	
aag ttc cgt acc atc tgc tcc tca gta gac aag ctg gac aag gtg tcc	1433
Lys Phe Arg Thr Ile Cys Ser Ser Val Asp Lys Leu Asp Lys Val Ser	
230 235 240 245	
tgg gaa gag gtg aag aat gag atg gtg gga gag aag ggc ctt gca cct	1481
Trp Glu Glu Val Lys Asn Glu Met Val Gly Glu Lys Gly Leu Ala Pro	
246 251 256 261	
gag gtg gct gac cgc att ggg gac tat gtc cag caa cat ggt ggg gta	1529
Glu Val Ala Asp Arg Ile Gly Asp Tyr Val Gln Gln His Gly Gly Val	
262 267 272 277	
tcc ctg gtg gaa cag ctg ctc cag gat cct aaa cta tcc caa aac aag	1577
Ser Leu Val Glu Gln Leu Leu Gln Asp Pro Lys Leu Ser Gln Asn Lys	
278 283 288 293	
cag gcc ttg gag ggc ctg gga gac ctg aag ttg ctc ttt gag tac ctg	1625
Gln Ala Leu Glu Gly Leu Gly Asp Leu Lys Leu Leu Phe Glu Tyr Leu	
294 299 304 309	
acc cta ttt ggc att gat gac aaa atc tcc ttt gac ctg agc ctt gct	1673
Thr Leu Phe Gly Ile Asp Asp Lys Ile Ser Phe Asp Leu Ser Leu Ala	
310 315 320 325	
cga ggg ctg gat tac tac act ggg gtg atc tat gag gca gtg ctg cta	1721
Arg Gly Leu Asp Tyr Tyr Thr Gly Val Ile Tyr Glu Ala Val Leu Leu	
326 331 336 341	
cag acc cca gcc cag gca ggg gaa gag ccc ctg ggt gtg ggc agt gtg	1769
Gln Thr Pro Ala Gln Ala Gly Glu Glu Pro Leu Gly Val Gly Ser Val	
342 347 352 357	
gct gct gga gga cgc tat gat ggg cta gtg ggc atg ttc gac ccc aaa	1817
Ala Ala Gly Gly Arg Tyr Asp Gly Leu Val Gly Met Phe Asp Pro Lys	
358 363 368 373	
ggg cgc aag gtg cca tgt gtg ggg ctc agc att ggg gtg gag cgg att	1865
Gly Arg Lys Val Pro Cys Val Gly Leu Ser Ile Gly Val Glu Arg Ile	
374 379 384 389	
ttc tcc atc gtg gaa cag aga cta gag gct ttg gag gag aag ata cgg	1913

Phe Ser Ile Val Glu Gln Arg Leu Glu Ala Leu Glu Glu Lys Ile Arg	
390 395 400 405	
acc acg gag aca cag gtg ctt gtg gca tct gca cag aag aag ctg cta	1961
Thr Thr Glu Thr Gln Val Leu Val Ala Ser Ala Gln Lys Lys Leu Leu	
406 411 416 421	
gag gaa aga cta aag ctt gtc tca gaa ctg tgg gat gct ggg atc aag	2009
Glu Glu Arg Leu Lys Leu Val Ser Glu Leu Trp Asp Ala Gly Ile Lys	
422 427 432 437	
gct gag ctg ctg tac aag aag aac cca aag cta ctg aac cag tta cag	2057
Ala Glu Leu Leu Tyr Lys Lys Asn Pro Lys Leu Leu Asn Gln Leu Gln	
438 443 448 453	
tac tgt gag gag gca ggc atc cca ctg gtg gct atc atc ggc gag cag	2105
Tyr Cys Glu Glu Ala Gly Ile Pro Leu Val Ala Ile Ile Gly Glu Gln	
454 459 464 469	
gaa ctc aag gat ggg gtc atc aag ctc cgt tca gtg acg agc agg gaa	2153
Glu Leu Lys Asp Gly Val Ile Lys Leu Arg Ser Val Thr Ser Arg Glu	
470 475 480 485	
gag gtg gat gtc cga aga gaa gac ctt gtg gag gaa atc aaa agg aga	2201
Glu Val Asp Val Arg Arg Glu Asp Leu Val Glu Glu Ile Lys Arg Arg	
486 491 496 501	
aca ggc cag ccc ctc tgc atc tgc tga actga acaaactatc agaggaaagg	2253
Thr Gly Gln Pro Leu Cys Ile Cys *	
502 507	
aagtgggact ggcactatatt gaggttaaga caaactgcat atgtacttca attgctttgc	2313
actttttccgt ttcagcggga agacctgaag agtggtcaga acagagcctt tgatttttat	2373
tatgggttatt ttattgatta ttactggcaa aaacggccag gtacaacacc tttttcatac	2433
aaggcccagg aggcttagtc cagtctgtgc tcctgggcta caaggaccca gcctgagatg	2493
gtcccatctg cagggccccc caccagttgg agcagatgcc tccccaccac caattgccaa	2553
aggtccaata aaatgcctca accacggagt ctgcgtgtgt cagtgatgcc tagccccgcc	2613
ttccccagca gaccaatgta gggatggaaa agggagaaaa acagtaaact tgtgacctg	2673
aggttcttgt ctccagcgtc caccctgcgg cttgggagct cctcctcggg aggcagccac	2733
cgtacatacg caccgcgcac tttgcagctt tcacctgagc ggacgcgtgg gtgcacccgg	2793
gaattccgga ccggtacc	2811

<210> 3
 <211> 14899
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (467)..(14101)

<400> 3

```
cagcgggtgcg agctccaggc ccatgcactg aggaggcgga aacaagggga gccccagag      60
ctccatcaag cccctccaa aggctcccct acccggtcca cccccccac cccctccc      120
cgcctcctcc caattgtgca tttttgcagc cggaggcggc tccgagatgg ggctgtgagc      180
ttcgcccggg gagggggaaa gagcagcgag gagtgaagcg ggggggtggg gtgaagggtt      240
tggatttcgg ggcagggggc gcacccccgt cagcaggccc tccccaaggg gctcggaact      300
ctacctcttc acccagccc ctggtgcgct ttgccgaagg aaagaataag aacagagaag      360
gaggaggggg aaaggaggaa aagggggacc cccaactgg ggggggtgaa ggagagaagt      420
agcaggacca gaggggaagg ggctgctgct tgcacaaacc cacacc  atg ctg acc      475
                                     Met Leu Thr
                                     1

cgc cgc ttg ctc ctg ctg ctg ccc ctg ctc tca gct ctg gtc gcg gcg      523
Pro Pro Leu Leu Leu Leu Pro Leu Leu Ser Ala Leu Val Ala Ala
  4                               9                               14                               19

gct atc gac gcc cct aag act tgc agc ccc aag cag ttt gcc tgc aga      571
Ala Ile Asp Ala Pro Lys Thr Cys Ser Pro Lys Gln Phe Ala Cys Arg
 20                               25                               30                               35

gat caa ata acc tgt atc tca aag ggc tgg cgg tgc gac ggt gag agg      619
Asp Gln Ile Thr Cys Ile Ser Lys Gly Trp Arg Cys Asp Gly Glu Arg
 36                               41                               46                               51

gac tgc cca gac gga tct gac gag gcc cct gag att tgt cca cag agt      667
Asp Cys Pro Asp Gly Ser Asp Glu Ala Pro Glu Ile Cys Pro Gln Ser
 52                               57                               62                               67

aag gcc cag cga tgc cag cca aac gag cat aac tgc ctg ggt act gag      715
Lys Ala Gln Arg Cys Gln Pro Asn Glu His Asn Cys Leu Gly Thr Glu
 68                               73                               78                               83

ctg tgt gtt ccc atg tcc cgc ctc tgc aat ggg gtc cag gac tgc atg      763
Leu Cys Val Pro Met Ser Arg Leu Cys Asn Gly Val Gln Asp Cys Met
 84                               89                               94                               99

gac ggc tca gat gag ggg ccc cac tgc cga gag ctc caa ggc aac tgc      811
Asp Gly Ser Asp Glu Gly Pro His Cys Arg Glu Leu Gln Gly Asn Cys
100                               105                               110                               115

tct cgc ctg ggc tgc cag cac cat tgt gtc ccc aca ctc gat ggg ccc      859
Ser Arg Leu Gly Cys Gln His His Cys Val Pro Thr Leu Asp Gly Pro
116                               121                               126                               131
```


acc tgc tac tgc aac agc agc ttt cag ctt cag gca gat ggc aag acc	907
Thr Cys Tyr Cys Asn Ser Ser Phe Gln Leu Gln Ala Asp Gly Lys Thr	
132 137 142 147	
tgc aaa gat ttt gat gag tgc tca gtg tac ggc acc tgc agc cag cta	955
Cys Lys Asp Phe Asp Glu Cys Ser Val Tyr Gly Thr Cys Ser Gln Leu	
148 153 158 163	
tgc acc aac aca gac ggc tcc ttc ata tgt ggc tgt gtt gaa gga tac	1003
Cys Thr Asn Thr Asp Gly Ser Phe Ile Cys Gly Cys Val Glu Gly Tyr	
164 169 174 179	
ctc ctg cag ccg gat aac cgc tcc tgc aag gcc aag aac gag cca gta	1051
Leu Leu Gln Pro Asp Asn Arg Ser Cys Lys Ala Lys Asn Glu Pro Val	
180 185 190 195	
gac cgg ccc cct gtg ctg ttg ata gcc aac tcc cag aac atc ttg gcc	1099
Asp Arg Pro Pro Val Leu Leu Ile Ala Asn Ser Gln Asn Ile Leu Ala	
196 201 206 211	
acg tac ctg agt ggg gcc cag gtg tct acc atc aca cct acg agc acg	1147
Thr Tyr Leu Ser Gly Ala Gln Val Ser Thr Ile Thr Pro Thr Ser Thr	
212 217 222 227	
cgg cag acc aca gcc atg gac ttc agc tat gcc aac gag acc gta tgc	1195
Arg Gln Thr Thr Ala Met Asp Phe Ser Tyr Ala Asn Glu Thr Val Cys	
228 233 238 243	
tgg gtg cat gtt ggg gac agt gct gct cag acg cag ctc aag tgt gcc	1243
Trp Val His Val Gly Asp Ser Ala Ala Gln Thr Gln Leu Lys Cys Ala	
244 249 254 259	
cgc atg cct ggc cta aag ggc ttc gtg gat gag cac acc atc aac atc	1291
Arg Met Pro Gly Leu Lys Gly Phe Val Asp Glu His Thr Ile Asn Ile	
260 265 270 275	
tcc ctc agt ctg cac cac gtg gaa cag atg gcc atc gac tgg ctg aca	1339
Ser Leu Ser Leu His His Val Glu Gln Met Ala Ile Asp Trp Leu Thr	
276 281 286 291	
ggc aac ttc tac ttt gtg gat gac atc gat gat agg atc ttt gtc tgc	1387
Gly Asn Phe Tyr Phe Val Asp Asp Ile Asp Asp Arg Ile Phe Val Cys	
292 297 302 307	
aac aga aat ggg gac aca tgt gtc aca ttg cta gac ctg gaa ctc tac	1435
Asn Arg Asn Gly Asp Thr Cys Val Thr Leu Leu Asp Leu Glu Leu Tyr	
308 313 318 323	
aac ccc aag ggc att gcc ctg gac cct gcc atg ggg aag gtg ttt ttc	1483
Asn Pro Lys Gly Ile Ala Leu Asp Pro Ala Met Gly Lys Val Phe Phe	
324 329 334 339	
act gac tat ggg cag atc cca aag gtg gaa cgc tgt gac atg gat ggg	1531
Thr Asp Tyr Gly Gln Ile Pro Lys Val Glu Arg Cys Asp Met Asp Gly	
340 345 350 355	
cag aac cgc acc aag ctc gtc gac agc aag att gtg ttt cct cat ggc	1579

Gln 356	Asn	Arg	Thr	Lys	Leu 361	Val	Asp	Ser	Lys	Ile 366	Val	Phe	Pro	His	Gly 371	
atc Ile 372	acg Thr	ctg Leu	gac Asp	ctg Leu	gtc Val 377	agc Ser	cgc Arg	ott Leu	gtc Val	tac Tyr 382	tgg Trp	gca Ala	gat Asp	gcc Ala	tat Tyr 387	1627
ctg Leu 388	gac Asp	tat Tyr	att Ile	gaa Glu	gtg Val 393	gtg Val	gac Asp	tat Tyr	gag Glu	ggc Gly 398	aag Lys	ggc Gly	cgc Arg	cag Gln	acc Thr 403	1675
atc Ile 404	atc Ile	cag Gln	ggc Gly	atc Ile	ctg Leu 409	att Ile	gag Glu	cac His	ctg Leu	tac Tyr 414	ggc Gly	ctg Leu	act Thr	gtg Val	ttt Phe 419	1723
gag Glu 420	aat Asn	tat Tyr	ctc Leu	tat Tyr	gcc Ala 425	acc Thr	aac Asn	tgc Ser	gac Asp	aat Asn 430	gcc Ala	aat Asn	gcc Ala	cag Gln	cag Gln 435	1771
aag Lys 436	acg Thr	agt Ser	gtg Val	atc Ile	cgt Arg 441	gtg Val	aac Asn	cgc Arg	ttt Phe	aac Asn 446	agc Ser	acc Thr	gag Glu	tac Tyr	cag Gln 451	1819
gtt Val 452	gtc Val	acc Thr	cgg Arg	gtg Val	gac Asp 457	aag Lys	ggt Gly	ggt Gly	gcc Ala	ctc Leu 462	cac His	atc Ile	tac Tyr	cac His	cag Gln 467	1867
agg Arg 468	cgt Arg	cag Gln	ccc Pro	cga Arg	gtg Val 473	agg Arg	agc Ser	cat His	gcc Ala	tgt Cys 478	gaa Glu	aac Asn	gac Asp	cag Gln	tat Tyr 483	1915
ggg Gly 484	aag Lys	ccg Pro	ggt Gly	ggc Gly	tgc Cys 489	tct Ser	gac Asp	atc Ile	tgc Cys	ctg Leu 494	ctg Leu	gcc Ala	aac Asn	agc Ser	cac His 499	1963
aag Lys 500	gcg Ala	cgg Arg	acc Thr	tgc Cys	cgc Arg 505	tgc Cys	cgt Arg	tcc Ser	ggc Gly	ttc Phe 510	agc Ser	ctg Leu	ggc Gly	agt Ser	gac Asp 515	2011
ggg Gly 516	aag Lys	tca Ser	tgc Cys	aag Lys	aag Lys 521	ccg Pro	gag Glu	cat His	gag Glu	ctg Leu 526	ttc Phe	ctc Leu	gtg Val	tat Tyr	ggc Gly 531	2059
aag Lys 532	ggc Gly	cgg Arg	cca Pro	ggc Gly	atc Ile 537	atc Ile	cgg Arg	ggc Gly	atg Met	gat Asp 542	atg Met	ggg Gly	gcc Ala	aag Lys	gtc Val 547	2107
ccg Pro 548	gat Asp	gag Glu	cac His	atg Met	atc Ile 553	ccc Pro	att Ile	gaa Glu	aac Asn	ctc Leu 558	atg Met	aac Asn	ccc Pro	cga Arg	gcc Ala 563	2155
ctg Leu 564	gac Asp	ttc Phe	cac His	gct Ala	gag Glu 569	acc Thr	ggc Gly	ttc Phe	atc Ile	tac Tyr 574	ttt Phe	gcc Ala	gac Asp	acc Thr	acc Thr 579	2203
agc Ser	tac Tyr	ctc Leu	att Ile	ggc Gly	cgc Arg	cag Gln	aag Lys	att Ile	gat Asp	ggc Gly	act Thr	gag Glu	cgg Arg	gag Glu	acc Thr	2251

580	585	590	595	
atc ctg aag gac ggc	atc cac aat gtg gag	ggg gtg gcc gtg gac tgg	2299	
Ile Leu Lys Asp Gly	Ile His Asn Val Glu	Gly Val Ala Val Asp Trp		
596	601	606	611	
atg gga gac aat ctg	tac tgg acg gac gat	ggg ccc aaa aag aca atc	2347	
Met Gly Asp Asn Leu	Tyr Trp Thr Asp Asp	Gly Pro Lys Lys Thr Ile		
612	617	622	627	
agc gtg gcc agg ctg	gag aaa gct gct cag	acc cgc aag act tta atc	2395	
Ser Val Ala Arg Leu	Glu Lys Ala Ala Gln	Thr Arg Lys Thr Leu Ile		
628	633	638	643	
gag ggc aaa atg aca	cac ccc agg gct att	gtg gtg gat cca ctc aat	2443	
Glu Gly Lys Met Thr	His Pro Arg Ala Ile	Val Val Asp Pro Leu Asn		
644	649	654	659	
ggg tgg atg tac tgg	aca gac tgg gag gag	gac ccc aag gac agt cgg	2491	
Gly Trp Met Tyr Trp	Thr Asp Trp Glu Glu	Asp Pro Lys Asp Ser Arg		
660	665	670	675	
cgt ggg cgg ctg gag	agg gcg tgg atg gat	ggc tca cac cga gac atc	2539	
Arg Gly Arg Leu Glu	Arg Ala Trp Met Asp	Gly Ser His Arg Asp Ile		
676	681	686	691	
ttt gtc acc tcc aag	aca gtg ctt tgg ccc	aat ggg cta agc ctg gac	2587	
Phe Val Thr Ser Lys	Thr Val Leu Trp Pro	Asn Gly Leu Ser Leu Asp		
692	697	702	707	
atc ccg gct ggg cgc	ctc tac tgg gtg gat	gcc ttc tac gac cgc atc	2635	
Ile Pro Ala Gly Arg	Leu Tyr Trp Val Asp	Ala Phe Tyr Asp Arg Ile		
708	713	718	723	
gag acg ata ctg ctc	aat ggc aca gac cgg	aag att gtg tat gaa ggt	2683	
Glu Thr Ile Leu Leu	Asn Gly Thr Asp Arg	Lys Ile Val Tyr Glu Gly		
724	729	734	739	
cct gag ctg aac cac	gcc ttt ggc ctg tgt	cac cat ggc aac tac ctc	2731	
Pro Glu Leu Asn His	Ala Phe Gly Leu Cys	His His Gly Asn Tyr Leu		
740	745	750	755	
ttc tgg act gag tat	cgg agt ggc agt gtc	tac cgc ttg gaa cgg ggt	2779	
Phe Trp Thr Glu Tyr	Arg Ser Gly Ser Val	Tyr Arg Leu Glu Arg Gly		
756	761	766	771	
gta gga ggc gca ccc	ccc act gtg acc ctt	ctg cgc agt gag cgg ccc	2827	
Val Gly Gly Ala Pro	Pro Thr Val Thr Leu	Leu Arg Ser Glu Arg Pro		
772	777	782	787	
ccc atc ttt gag atc	cga atg tat gat gcc	cag cag cag caa gtt ggc	2875	
Pro Ile Phe Glu Ile	Arg Met Tyr Asp Ala	Gln Gln Gln Gln Val Gly		
788	793	798	803	
acc aac aaa tgc cgg	gtg aac aat ggc ggc	tgc agc agc ctg tgc ttg	2923	
Thr Asn Lys Cys Arg	Val Asn Asn Gly Gly	Cys Ser Ser Leu Cys Leu		
804	809	814	819	

gcc acc cct ggg agc cgc cag tgc gcc tgt gct gag gac cag gtg ttg	2971
Ala Thr Pro Gly Ser Arg Gln Cys Ala Cys Ala Glu Asp Gln Val Leu	
820 825 830 835	
gac gca gac ggc gtc act tgc ttg gcg aac cca tcc tac gtg cct cca	3019
Asp Ala Asp Gly Val Thr Cys Leu Ala Asn Pro Ser Tyr Val Pro Pro	
836 841 846 851	
ccc cag tgc cag cca ggc gag ttt gcc tgt gcc aac agc cgc tgc atc	3067
Pro Gln Cys Gln Pro Gly Glu Phe Ala Cys Ala Asn Ser Arg Cys Ile	
852 857 862 867	
cag gag cgc tgg aag tgt gac gga gac aac gat tgc ctg gac aac agt	3115
Gln Glu Arg Trp Lys Cys Asp Gly Asp Asn Asp Cys Leu Asp Asn Ser	
868 873 878 883	
gat gag gcc cca gcc ctc tgc cat cag cac acc tgc ccc tcg gac cga	3163
Asp Glu Ala Pro Ala Leu Cys His Gln His Thr Cys Pro Ser Asp Arg	
884 889 894 899	
ttc aag tgc gag aac aac cgg tgc atc ccc aac cgc tgg ctc tgc gac	3211
Phe Lys Cys Glu Asn Asn Arg Cys Ile Pro Asn Arg Trp Leu Cys Asp	
900 905 910 915	
ggg gac aat gac tgt ggg aac agt gaa gat gag tcc aat gcc act tgt	3259
Gly Asp Asn Asp Cys Gly Asn Ser Glu Asp Glu Ser Asn Ala Thr Cys	
916 921 926 931	
tca gcc cgc acc tgc ccc ccc aac cag ttc tcc tgt gcc agt ggc cgc	3307
Ser Ala Arg Thr Cys Pro Pro Asn Gln Phe Ser Cys Ala Ser Gly Arg	
932 937 942 947	
tgc atc ccc atc tcc tgg acg tgt gat ctg gat gac gac tgt ggg gac	3355
Cys Ile Pro Ile Ser Trp Thr Cys Asp Leu Asp Asp Asp Cys Gly Asp	
948 953 958 963	
cgc tct gat gag tct gct tcg tgt gcc tat ccc acc tgc ttc ccc ctg	3403
Arg Ser Asp Glu Ser Ala Ser Cys Ala Tyr Pro Thr Cys Phe Pro Leu	
964 969 974 979	
act cag ttt acc tgc aac aat ggc aga tgt atc aac atc aac tgg aga	3451
Thr Gln Phe Thr Cys Asn Asn Gly Arg Cys Ile Asn Ile Asn Trp Arg	
980 985 990 995	
tgc gac aat gac aat gac tgt ggg gac aac agt gac gaa gcc ggc tgc	3499
Cys Asp Asn Asp Asn Asp Cys Gly Asp Asn Ser Asp Glu Ala Gly Cys	
996 1001 1006 1011	
agc cac tcc tgt tct agc acc cag ttc aag tgc aac agc ggg cgt tgc	3547
Ser His Ser Cys Ser Ser Thr Gln Phe Lys Cys Asn Ser Gly Arg Cys	
1012 1017 1022 1027	
atc ccc gag cac tgg acc tgc gat ggg gac aat gac tgc gga gac tac	3595
Ile Pro Glu His Trp Thr Cys Asp Gly Asp Asn Asp Cys Gly Asp Tyr	
1028 1033 1038 1043	

agt gat gag aca cac gcc aac tgc acc aac cag gcc acg agg ccc cct	3643
Ser Asp Glu Thr His Ala Asn Cys Thr Asn Gln Ala Thr Arg Pro Pro	
1044 1049 1054 1059	
ggg ggc tgc cac act gat gag ttc cag tgc cgg ctg gat gga cta tgc	3691
Gly Gly Cys His Thr Asp Glu Phe Gln Cys Arg Leu Asp Gly Leu Cys	
1060 1065 1070 1075	
atc ccc ctg cgg tgg cgc tgc gat ggg gac act gac tgc atg gac tcc	3739
Ile Pro Leu Arg Trp Arg Cys Asp Gly Asp Thr Asp Cys Met Asp Ser	
1076 1081 1086 1091	
agc gat gag aag agc tgt gag gga gtg acc cac gtc tgc gat ccc agt	3787
Ser Asp Glu Lys Ser Cys Glu Gly Val Thr His Val Cys Asp Pro Ser	
1092 1097 1102 1107	
gtc aag ttt ggc tgc aag gac tca gct cgg tgc atc agc aaa gcg tgg	3835
Val Lys Phe Gly Cys Lys Asp Ser Ala Arg Cys Ile Ser Lys Ala Trp	
1108 1113 1118 1123	
gtg tgt gat ggc gac aat gac tgt gag gat aac tcg gac gag gag aac	3883
Val Cys Asp Gly Asp Asn Asp Cys Glu Asp Asn Ser Asp Glu Glu Asn	
1124 1129 1134 1139	
tgc gag tcc ctg gcc tgc agg cca ccc tcg cac cct tgt gcc aac aac	3931
Cys Glu Ser Leu Ala Cys Arg Pro Pro Ser His Pro Cys Ala Asn Asn	
1140 1145 1150 1155	
acc tca gtc tgc ctg ccc cct gac aag ctg tgt gat ggc aac gac gac	3979
Thr Ser Val Cys Leu Pro Pro Asp Lys Leu Cys Asp Gly Asn Asp Asp	
1156 1161 1166 1171	
tgt ggc gac ggc tca gat gag ggc gag ctc tgt gac cag tgc tct ctg	4027
Cys Gly Asp Gly Ser Asp Glu Gly Glu Leu Cys Asp Gln Cys Ser Leu	
1172 1177 1182 1187	
aat aac ggt ggc tgc agc cac aac tgc tca gtg gca cct ggc gaa ggc	4075
Asn Asn Gly Gly Cys Ser His Asn Cys Ser Val Ala Pro Gly Glu Gly	
1188 1193 1198 1203	
att gtg tgt tcc tgc cct ctg ggc atg gag ctg ggg ccc gac aac cac	4123
Ile Val Cys Ser Cys Pro Leu Gly Met Glu Leu Gly Pro Asp Asn His	
1204 1209 1214 1219	
acc tgc cag atc cag agc tac tgt gcc aag cat ctc aaa tgc agc caa	4171
Thr Cys Gln Ile Gln Ser Tyr Cys Ala Lys His Leu Lys Cys Ser Gln	
1220 1225 1230 1235	
aag tgc gac cag aac aag ttc agc gtg aag tgc tcc tgc tac gag ggc	4219
Lys Cys Asp Gln Asn Lys Phe Ser Val Lys Cys Ser Cys Tyr Glu Gly	
1236 1241 1246 1251	
tgg gtc ctg gaa cct gac ggc gag agc tgc cgc agc ctg gac ccc ttc	4267
Trp Val Leu Glu Pro Asp Gly Glu Ser Cys Arg Ser Leu Asp Pro Phe	
1252 1257 1262 1267	
aag ccg ttc atc att ttc tcc aac cgc cat gaa atc cgg cgc atc gat	4315

Lys 1268	Pro	Phe	Ile	Ile	Phe	Ser	Asn	Arg	His	Glu	Ile	Arg	Arg	Ile	Asp	
					1273					1278					1283	
ctt	cac	aaa	gga	gac	tac	agc	gtc	ctg	gtg	ccc	ggc	ctg	cgc	aac	acc	4363
Leu	His	Lys	Gly	Asp	Tyr	Ser	Val	Leu	Val	Pro	Gly	Leu	Arg	Asn	Thr	
1284					1289					1294					1299	
atc	gcc	ctg	gac	ttc	cac	ctc	agc	cag	agc	gcc	ctc	tac	tgg	acc	gac	4411
Ile	Ala	Leu	Asp	Phe	His	Leu	Ser	Gln	Ser	Ala	Leu	Tyr	Trp	Thr	Asp	
1300					1305					1310					1315	
gtg	gtg	gag	gac	aag	atc	tac	cgc	ggg	aag	ctg	ctg	gac	aac	gga	gcc	4459
Val	Val	Glu	Asp	Lys	Ile	Tyr	Arg	Gly	Lys	Leu	Leu	Asp	Asn	Gly	Ala	
1316					1321					1326					1331	
ctg	act	agt	ttc	gag	gtg	gtg	att	cag	tat	ggc	ctg	gcc	aca	ccc	gag	4507
Leu	Thr	Ser	Phe	Glu	Val	Val	Ile	Gln	Tyr	Gly	Leu	Ala	Thr	Pro	Glu	
1332					1337					1342					1347	
ggc	ctg	gct	gta	gac	tgg	att	gca	ggc	aac	atc	tac	tgg	gtg	gag	agt	4555
Gly	Leu	Ala	Val	Asp	Trp	Ile	Ala	Gly	Asn	Ile	Tyr	Trp	Val	Glu	Ser	
1348					1353					1358					1363	
aac	ctg	gat	cag	atc	gag	gtg	gcc	aag	ctg	gat	ggg	acc	ctc	cgg	acc	4603
Asn	Leu	Asp	Gln	Ile	Glu	Val	Ala	Lys	Leu	Asp	Gly	Thr	Leu	Arg	Thr	
1364					1369					1374					1379	
acc	ctg	ctg	gcc	ggc	gac	att	gag	cac	cca	agg	gca	atc	gca	ctg	gat	4651
Thr	Leu	Leu	Ala	Gly	Asp	Ile	Glu	His	Pro	Arg	Ala	Ile	Ala	Leu	Asp	
1380					1385					1390					1395	
ccc	cgg	gat	ggg	atc	ctg	ttt	tgg	aca	gac	tgg	gat	gcc	agc	ctg	ccc	4699
Pro	Arg	Asp	Gly	Ile	Leu	Phe	Trp	Thr	Asp	Trp	Asp	Ala	Ser	Leu	Pro	
1396					1401					1406					1411	
cgc	att	gag	gca	gcc	tcc	atg	agt	ggg	gct	ggg	cgc	cgc	acc	gtg	cac	4747
Arg	Ile	Glu	Ala	Ala	Ser	Met	Ser	Gly	Ala	Gly	Arg	Arg	Thr	Val	His	
1412					1417					1422					1427	
cgg	gag	acc	ggc	tct	ggg	ggc	tgg	ccc	aac	ggg	ctc	acc	gtg	gac	tac	4795
Arg	Glu	Thr	Gly	Ser	Gly	Gly	Trp	Pro	Asn	Gly	Leu	Thr	Val	Asp	Tyr	
1428					1433					1438					1443	
ctg	gag	aag	cgc	atc	ctt	tgg	att	gac	gcc	agg	tca	gat	gcc	att	tac	4843
Leu	Glu	Lys	Arg	Ile	Leu	Trp	Ile	Asp	Ala	Arg	Ser	Asp	Ala	Ile	Tyr	
1444					1449					1454					1459	
tca	gcc	cgt	tac	gac	ggc	tct	ggc	cac	atg	gag	gtg	ctt	cgg	gga	cac	4891
Ser	Ala	Arg	Tyr	Asp	Gly	Ser	Gly	His	Met	Glu	Val	Leu	Arg	Gly	His	
1460					1465					1470					1475	
gag	ttc	ctg	tcg	cac	ccg	ttt	gca	gtg	acg</							

1492	1497	1502	1507	
acc ggc cac aat gtc acc gtg gta cag agg acc aac acc cag ccc ttt				5035
Thr Gly His Asn Val Thr Val Val Gln Arg Thr Asn Thr Gln Pro Phe				
1508	1513	1518	1523	
gac ctg cag gtg tac cac ccc tcc cgc cag ccc atg gct ccc aat ccc				5083
Asp Leu Gln Val Tyr His Pro Ser Arg Gln Pro Met Ala Pro Asn Pro				
1524	1529	1534	1539	
tgt gag gcc aat ggg ggc cag ggc ccc tgc tcc cac ctg tgt ctc atc				5131
Cys Glu Ala Asn Gly Gly Gln Gly Pro Cys Ser His Leu Cys Leu Ile				
1540	1545	1550	1555	
aac tac aac cgg acc gtg tcc tgc gcc tgc ccc cac ctc atg aag ctc				5179
Asn Tyr Asn Arg Thr Val Ser Cys Ala Cys Pro His Leu Met Lys Leu				
1556	1561	1566	1571	
cac aag gac aac acc acc tgc tat gag ttt aag aag ttc ctg ctg tac				5227
His Lys Asp Asn Thr Thr Cys Tyr Glu Phe Lys Lys Phe Leu Leu Tyr				
1572	1577	1582	1587	
gca cgt cag atg gag atc cga ggt gtg gac ctg gat gct ccc tac tac				5275
Ala Arg Gln Met Glu Ile Arg Gly Val Asp Leu Asp Ala Pro Tyr Tyr				
1588	1593	1598	1603	
aac tac atc atc tcc ttc acg gtg ccc gac atc gac aac gtc aca gtg				5323
Asn Tyr Ile Ile Ser Phe Thr Val Pro Asp Ile Asp Asn Val Thr Val				
1604	1609	1614	1619	
cta gac tac gat gcc cgc gag cag cgt gtg tac tgg tct gac gtg cgg				5371
Leu Asp Tyr Asp Ala Arg Glu Gln Arg Val Tyr Trp Ser Asp Val Arg				
1620	1625	1630	1635	
aca cag gcc atc aag cgg gcc ttc atc aac ggc aca ggc gtg gag aca				5419
Thr Gln Ala Ile Lys Arg Ala Phe Ile Asn Gly Thr Gly Val Glu Thr				
1636	1641	1646	1651	
gtc gtc tct gca gac ttg cca aat gcc cac ggg ctg gct gtg gac tgg				5467
Val Val Ser Ala Asp Leu Pro Asn Ala His Gly Leu Ala Val Asp Trp				
1652	1657	1662	1667	
gtc tcc cga aac ctg ttc tgg aca agc tat gac acc aat aag aag cag				5515
Val Ser Arg Asn Leu Phe Trp Thr Ser Tyr Asp Thr Asn Lys Lys Gln				
1668	1673	1678	1683	
atc aat gtg gcc cgg ctg gat ggc tcc ttc aag aac gca gtg gtg cag				5563
Ile Asn Val Ala Arg Leu Asp Gly Ser Phe Lys Asn Ala Val Val Gln				
1684	1689	1694	1699	
ggc ctg gag cag ccc cat ggc ctt gtc gtc cac cct ctg cgt ggg aag				5611
Gly Leu Glu Gln Pro His Gly Leu Val Val His Pro Leu Arg Gly Lys				
1700	1705	1710	1715	
ctc tac tgg acc gat ggt gac aac atc agc atg gcc aac atg gat ggc				5659
Leu Tyr Trp Thr Asp Gly Asp Asn Ile Ser Met Ala Asn Met Asp Gly				
1716	1721	1726	1731	

agc aat cgc acc ctg ctc ttc agt ggc cag aag ggc ccc gtg ggc ctg	5707
Ser Asn Arg Thr Leu Leu Phe Ser Gly Gln Lys Gly Pro Val Gly Leu	
1732 1737 1742 1747	
gct att gac ttc cct gaa agc aaa ctc tac tgg atc agc tcc ggg aac	5755
Ala Ile Asp Phe Pro Glu Ser Lys Leu Tyr Trp Ile Ser Ser Gly Asn	
1748 1753 1758 1763	
cat acc atc aac cgc tgc aac ctg gat ggg agt ggg ctg gag gtc atc	5803
His Thr Ile Asn Arg Cys Asn Leu Asp Gly Ser Gly Leu Glu Val Ile	
1764 1769 1774 1779	
gat gcc atg cgg agc cag ctg ggc aag gcc acc gcc ctg gcc atc atg	5851
Asp Ala Met Arg Ser Gln Leu Gly Lys Ala Thr Ala Leu Ala Ile Met	
1780 1785 1790 1795	
ggg gac aag ctg tgg tgg gct gat cag gtg tgc gaa aag atg ggc aca	5899
Gly Asp Lys Leu Trp Trp Ala Asp Gln Val Ser Glu Lys Met Gly Thr	
1796 1801 1806 1811	
tgc agc aag gct gac ggc tgc ggc tcc gtg gtc ctt cgg aac agc acc	5947
Cys Ser Lys Ala Asp Gly Ser Gly Ser Val Val Leu Arg Asn Ser Thr	
1812 1817 1822 1827	
acc ctg gtg atg cac atg aag gtc tat gac gag agc atc cag ctg gac	5995
Thr Leu Val Met His Met Lys Val Tyr Asp Glu Ser Ile Gln Leu Asp	
1828 1833 1838 1843	
cat aag ggc acc aac ccc tgc agt gtc aac aac ggt gac tgc tcc cag	6043
His Lys Gly Thr Asn Pro Cys Ser Val Asn Asn Gly Asp Cys Ser Gln	
1844 1849 1854 1859	
ctc tgc ctg ccc acg tca gag acg acc cgc tcc tgc atg tgc aca gcc	6091
Leu Cys Leu Pro Thr Ser Glu Thr Thr Arg Ser Cys Met Cys Thr Ala	
1860 1865 1870 1875	
ggc tat agc ctc cgg agt ggc cag cag gcc tgc gag ggc gta ggt tcc	6139
Gly Tyr Ser Leu Arg Ser Gly Gln Gln Ala Cys Glu Gly Val Gly Ser	
1876 1881 1886 1891	
ttt ctc ctg tac tct gtg cat gag gga atc agg gga att ccc ctg gat	6187
Phe Leu Leu Tyr Ser Val His Glu Gly Ile Arg Gly Ile Pro Leu Asp	
1892 1897 1902 1907	
ccc aat gac aag tca gat gcc ctg gtc cca gtg tcc ggg acc tgc ctg	6235
Pro Asn Asp Lys Ser Asp Ala Leu Val Pro Val Ser Gly Thr Ser Leu	
1908 1913 1918 1923	
gct gtc ggc atc gac ttc cac gct gaa aat gac acc atc tac tgg gtg	6283
Ala Val Gly Ile Asp Phe His Ala Glu Asn Asp Thr Ile Tyr Trp Val	
1924 1929 1934 1939	
gac atg ggc ctg agc acg atc agc cgg gcc aag cgg gac cag acg tgg	6331
Asp Met Gly Leu Ser Thr Ile Ser Arg Ala Lys Arg Asp Gln Thr Trp	
1940 1945 1950 1955	

cgt gaa gac gtg gtg acc aat ggc att ggc cgt gtg gag ggc att gca Arg Glu Asp Val Val Thr Asn Gly Ile Gly Arg Val Glu Gly Ile Ala 1956 1961 1966 1971	6379
gtg gac tgg atc gca ggc aac atc tac tgg aca gac cag ggc ttt gat Val Asp Trp Ile Ala Gly Asn Ile Tyr Trp Thr Asp Gln Gly Phe Asp 1972 1977 1982 1987	6427
gtc atc gag gtc gcc cgg ctc aat ggc tcc ttc cgc tac gtg gtg atc Val Ile Glu Val Ala Arg Leu Asn Gly Ser Phe Arg Tyr Val Val Ile 1988 1993 1998 2003	6475
tcc cag ggt cta gac aag ccc cgg gcc atc acc gtc cac ccg gag aaa Ser Gln Gly Leu Asp Lys Pro Arg Ala Ile Thr Val His Pro Glu Lys 2004 2009 2014 2019	6523
ggg tac ttg ttc tgg act gag tgg ggt cag tat ccg cgt att gag cgg Gly Tyr Leu Phe Trp Thr Glu Trp Gly Gln Tyr Pro Arg Ile Glu Arg 2020 2025 2030 2035	6571
tct cgg cta gat ggc acg gag cgt gtg gtg ctg gtc aac gtc agc atc Ser Arg Leu Asp Gly Thr Glu Arg Val Val Leu Val Asn Val Ser Ile 2036 2041 2046 2051	6619
agc tgg ccc aac ggc atc tca gtg gac tac cag gat ggg aag ctg tac Ser Trp Pro Asn Gly Ile Ser Val Asp Tyr Gln Asp Gly Lys Leu Tyr 2052 2057 2062 2067	6667
tgg tgc gat gca cgg aca gac aag att gaa cgg atc gac ctg gag aca Trp Cys Asp Ala Arg Thr Asp Lys Ile Glu Arg Ile Asp Leu Glu Thr 2068 2073 2078 2083	6715
ggt gag aac cgc gag gtg gtt ctg tcc agc aac aac atg gac atg ttt Gly Glu Asn Arg Glu Val Val Leu Ser Ser Asn Asn Met Asp Met Phe 2084 2089 2094 2099	6763
tca gtg tct gtg ttt gag gat ttc atc tac tgg agt gac agg act cat Ser Val Ser Val Phe Glu Asp Phe Ile Tyr Trp Ser Asp Arg Thr His 2100 2105 2110 2115	6811
gcc aac ggc tct atc aag cgc ggg agc aaa gac aat gcc aca gac tcc Ala Asn Gly Ser Ile Lys Arg Gly Ser Lys Asp Asn Ala Thr Asp Ser 2116 2121 2126 2131	6859
gtg ccc ctg cga acc ggc atc ggc gtc cag ctt aaa gac atc aaa gtc Val Pro Leu Arg Thr Gly Ile Gly Val Gln Leu Lys Asp Ile Lys Val 2132 2137 2142 2147	6907
ttc aac cgg gac cgg cag aaa ggc acc aac gtg tgc gcg gtg gcc aat Phe Asn Arg Asp Arg Gln Lys Gly Thr Asn Val Cys Ala Val Ala Asn 2148 2153 2158 2163	6955
ggc ggg tgc cag cag ctg tgc ctg tac cgg ggc cgt ggg cag cgg gcc Gly Gly Cys Gln Gln Leu Cys Leu Tyr Arg Gly Arg Gly Gln Arg Ala 2164 2169 2174 2179	7003
tgc gcc tgt gcc cac ggg atg ctg gct gaa gac gga gca tcg tgc cgc	7051

Cys Ala Cys Ala His Gly Met Leu Ala Glu Asp Gly Ala Ser Cys Arg	
2180	2185 2190 2195
gag tat gcc ggc tac ctg ctc tac tca gag cgc acc att ctc aag agt	7099
Glu Tyr Ala Gly Tyr Leu Leu Tyr Ser Glu Arg Thr Ile Leu Lys Ser	
2196	2201 2206 2211
atc cac ctg tgc gat gag cgc aac ctc aat gcg ccc gtg cag ccc ttc	7147
Ile His Leu Ser Asp Glu Arg Asn Leu Asn Ala Pro Val Gln Pro Phe	
2212	2217 2222 2227
gag gac cct gag cac atg aag aac gtc atc gcc ctg gcc ttt gac tac	7195
Glu Asp Pro Glu His Met Lys Asn Val Ile Ala Leu Ala Phe Asp Tyr	
2228	2233 2238 2243
cgg gca ggc acc tct ccg ggc acc ccc aat cgc atc ttc ttc agc gac	7243
Arg Ala Gly Thr Ser Pro Gly Thr Pro Asn Arg Ile Phe Phe Ser Asp	
2244	2249 2254 2259
atc cac ttt ggg aac atc caa cag atc aac gac gat ggc tcc agg agg	7291
Ile His Phe Gly Asn Ile Gln Gln Ile Asn Asp Asp Gly Ser Arg Arg	
2260	2265 2270 2275
atc acc att gtg gaa aac gtg ggc tcc gtg gaa ggc ctg gcc tat cac	7339
Ile Thr Ile Val Glu Asn Val Gly Ser Val Glu Gly Leu Ala Tyr His	
2276	2281 2286 2291
cgt ggc tgg gac act ctc tat tgg aca agc tac acg aca tcc acc atc	7387
Arg Gly Trp Asp Thr Leu Tyr Trp Thr Ser Tyr Thr Thr Ser Thr Ile	
2292	2297 2302 2307
acg cgc cac aca gtg gac cag acc cgc cca ggg gcc ttc gag cgt gag	7435
Thr Arg His Thr Val Asp Gln Thr Arg Pro Gly Ala Phe Glu Arg Glu	
2308	2313 2318 2323
acc gtc atc act atg tct gga gat gac cac cca cgg gcc ttc gtt ttg	7483
Thr Val Ile Thr Met Ser Gly Asp Asp His Pro Arg Ala Phe Val Leu	
2324	2329 2334 2339
gac gag tgc cag aac ctc atg ttc tgg acc aac tgg aat gag cag cat	7531
Asp Glu Cys Gln Asn Leu Met Phe Trp Thr Asn Trp Asn Glu Gln His	
2340	2345 2350 2355
ccc agc atc atg cgg gcg gcg ctc tgc gga gcc aat gtc ctg acc ctt	7579
Pro Ser Ile Met Arg Ala Ala Leu Ser Gly Ala Asn Val Leu Thr Leu	
2356	2361 2366 2371
atc gag aag gac atc cgt acc ccc aat ggc ctg gcc atc gac cac cgt	7627
Ile Glu Lys Asp Ile Arg Thr Pro Asn Gly Leu Ala Ile Asp His Arg	
2372	2377 2382 2387
gcc gag aag ctc tac ttc tct gac gcc acc ctg gac aag atc gag cgg	7675
Ala Glu Lys Leu Tyr Phe Ser Asp Ala Thr Leu Asp Lys Ile Glu Arg	
2388	2393 2398 2403
tgc gag tat gac ggc tcc cac cgc tat gtg atc cta aag tca gag cct	7723
Cys Glu Tyr Asp Gly Ser His Arg Tyr Val Ile Leu Lys Ser Glu Pro	

2404	2409	2414	2419	
gtc cac ccc ttc ggg ctg gcc gtg tat ggg gag cac att ttc tgg act				7771
Val His Pro Phe Gly Leu Ala Val Tyr Gly Glu His Ile Phe Trp Thr				
2420	2425	2430	2435	
gac tgg gtg cgg cgg gca gtg cag cgg gcc aac aag cac gtg ggc agc				7819
Asp Trp Val Arg Arg Ala Val Gln Arg Ala Asn Lys His Val Gly Ser				
2436	2441	2446	2451	
aac atg aag ctg ctg cgc gtg gac atc ccc cag cag ccc atg ggc atc				7867
Asn Met Lys Leu Leu Arg Val Asp Ile Pro Gln Gln Pro Met Gly Ile				
2452	2457	2462	2467	
atc gcc gtg gcc aac gac acc aac agc tgt gaa ctc tct cca tgc cga				7915
Ile Ala Val Ala Asn Asp Thr Asn Ser Cys Glu Leu Ser Pro Cys Arg				
2468	2473	2478	2483	
atc aac aac ggt ggc tgc cag gac ctg tgt ctg ctc act cac cag ggc				7963
Ile Asn Asn Gly Gly Cys Gln Asp Leu Cys Leu Leu Thr His Gln Gly				
2484	2489	2494	2499	
cat gtc aac tgc tca tgc cga ggg ggc cga atc ctc cag gat gac ctc				8011
His Val Asn Cys Ser Cys Arg Gly Gly Arg Ile Leu Gln Asp Asp Leu				
2500	2505	2510	2515	
acc tgc cga gcg gtg aat tcc tct tgc cga gca caa gat gag ttt gag				8059
Thr Cys Arg Ala Val Asn Ser Ser Cys Arg Ala Gln Asp Glu Phe Glu				
2516	2521	2526	2531	
tgt gcc aat ggc gag tgc atc aac ttc agc ctg acc tgc gac ggc gtc				8107
Cys Ala Asn Gly Glu Cys Ile Asn Phe Ser Leu Thr Cys Asp Gly Val				
2532	2537	2542	2547	
ccc cac tgc aag gac aag tcc gat gag aag cca tcc tac tgc aac tcc				8155
Pro His Cys Lys Asp Lys Ser Asp Glu Lys Pro Ser Tyr Cys Asn Ser				
2548	2553	2558	2563	
cgc cgc tgc aag aag act ttc cgg cag tgc agc aat ggg cgc tgt gtg				8203
Arg Arg Cys Lys Lys Thr Phe Arg Gln Cys Ser Asn Gly Arg Cys Val				
2564	2569	2574	2579	
tcc aac atg ctg tgg tgc aac ggg gcc gac gac tgt ggg gat ggc tct				8251
Ser Asn Met Leu Trp Cys Asn Gly Ala Asp Asp Cys Gly Asp Gly Ser				
2580	2585	2590	2595	
gac gag atc cct tgc aac aag aca gcc tgt ggt gtg ggc gag ttc cgc				8299
Asp Glu Ile Pro Cys Asn Lys Thr Ala Cys Gly Val Gly Glu Phe Arg				
2596	2601	2606	2611	
tgc cgg gac ggg acc tgc atc ggg aac tcc agc cgc tgc aac cag ttt				8347
Cys Arg Asp Gly Thr Cys Ile Gly Asn Ser Ser Arg Cys Asn Gln Phe				
2612	2617	2622	2627	
gtg gat tgt gag gac gcc tca gat gag atg aac tgc agt gcc acc gac				8395
Val Asp Cys Glu Asp Ala Ser Asp Glu Met Asn Cys Ser Ala Thr Asp				
2628	2633	2638	2643	

tgc agc agc tac ttc cgc ctg ggc gtg aag ggc gtg ctc ttc cag ccc Cys Ser Ser Tyr Phe Arg Leu Gly Val Lys Gly Val Leu Phe Gln Pro 2644 2649 2654 2659	8443
tgc gag cgg acc tca ctc tgc tac gca ccc agc tgg gtg tgt gat ggc Cys Glu Arg Thr Ser Leu Cys Tyr Ala Pro Ser Trp Val Cys Asp Gly 2660 2665 2670 2675	8491
gcc aat gac tgt ggg gac tac agt gat gag cgc gac tgc cca ggt gtg Ala Asn Asp Cys Gly Asp Tyr Ser Asp Glu Arg Asp Cys Pro Gly Val 2676 2681 2686 2691	8539
aaa cgc ccc aga tgc cct ctg aat tac ttc gcc tgc cct agt ggg cgc Lys Arg Pro Arg Cys Pro Leu Asn Tyr Phe Ala Cys Pro Ser Gly Arg 2692 2697 2702 2707	8587
tgc atc ccc atg agc tgg acg tgt gac aaa gag gat gac tgt gaa cat Cys Ile Pro Met Ser Trp Thr Cys Asp Lys Glu Asp Asp Cys Glu His 2708 2713 2718 2723	8635
ggc gag gac gag acc cac tgc aac aag ttc tgc tca gag gcc cag ttt Gly Glu Asp Glu Thr His Cys Asn Lys Phe Cys Ser Glu Ala Gln Phe 2724 2729 2734 2739	8683
gag tgc cag aac cat cgc tgc atc tcc aag cag tgg ctg tgt gac ggc Glu Cys Gln Asn His Arg Cys Ile Ser Lys Gln Trp Leu Cys Asp Gly 2740 2745 2750 2755	8731
agc gat gac tgt ggg gat ggc tca gac gag gct gct cac tgt gaa ggc Ser Asp Asp Cys Gly Asp Gly Ser Asp Glu Ala Ala His Cys Glu Gly 2756 2761 2766 2771	8779
aag acg tgc ggc ccc tcc tcc ttc tcc tgc cct ggc acc cac gtg tgc Lys Thr Cys Gly Pro Ser Ser Phe Ser Cys Pro Gly Thr His Val Cys 2772 2777 2782 2787	8827
gtc ccc gag cgc tgg ctc tgt gac ggt gac aaa gac tgt gct gat ggt Val Pro Glu Arg Trp Leu Cys Asp Gly Asp Lys Asp Cys Ala Asp Gly 2788 2793 2798 2803	8875
gca gac gag agc atc gca gct ggt tgc ttg tac aac agc act tgt gac Ala Asp Glu Ser Ile Ala Ala Gly Cys Leu Tyr Asn Ser Thr Cys Asp 2804 2809 2814 2819	8923
gac cgt gag ttc atg tgc cag aac cgc cag tgc atc ccc aag cac ttc Asp Arg Glu Phe Met Cys Gln Asn Arg Gln Cys Ile Pro Lys His Phe 2820 2825 2830 2835	8971
gtg tgt gac cac gac cgt gac tgt gca gat ggc tct gat gag tcc ccc Val Cys Asp His Asp Arg Asp Cys Ala Asp Gly Ser Asp Glu Ser Pro 2836 2841 2846 2851	9019
gag tgt gag tac ccg acc tgc ggc ccc agt gag ttc cgc tgt gcc aat Glu Cys Glu Tyr Pro Thr Cys Gly Pro Ser Glu Phe Arg Cys Ala Asn 2852 2857 2862 2867	9067

ggg cgc tgt ctg agc tcc cgc cag tgg gag tgt gat ggc gag aat gac Gly Arg Cys Leu Ser Ser Arg Gln Trp Glu Cys Asp Gly Glu Asn Asp 2868 2873 2878 2883	9115
tgc cac gac cag agt gac gag gct ccc aag aac cca cac tgc acc agc Cys His Asp Gln Ser Asp Glu Ala Pro Lys Asn Pro His Cys Thr Ser 2884 2889 2894 2899	9163
cca gag cac aag tgc aat gcc tcg tca cag ttc ctg tgc agc agt ggg Pro Glu His Lys Cys Asn Ala Ser Ser Gln Phe Leu Cys Ser Ser Gly 2900 2905 2910 2915	9211
cgc tgt gtg gct gag gca ctg ctc tgc aac ggc cag gat gac tgt ggc Arg Cys Val Ala Glu Ala Leu Leu Cys Asn Gly Gln Asp Asp Cys Gly 2916 2921 2926 2931	9259
gac agc tcg gac gag cgt ggc tgc cac atc aat gag tgt ctc agc cgc Asp Ser Ser Asp Glu Arg Gly Cys His Ile Asn Glu Cys Leu Ser Arg 2932 2937 2942 2947	9307
aag ctc agt ggc tgc agc cag gac tgt gag gac ctc aag atc ggc ttc Lys Leu Ser Gly Cys Ser Gln Asp Cys Glu Asp Leu Lys Ile Gly Phe 2948 2953 2958 2963	9355
aag tgc cgc tgt cgc cct ggc ttc cgg ctg aag gac gac ggc cgg acg Lys Cys Arg Cys Arg Pro Gly Phe Arg Leu Lys Asp Asp Gly Arg Thr 2964 2969 2974 2979	9403
tgt gct gat gtg gac gag tgc agc acc acc ttc ccc tgc agc cag cgc Cys Ala Asp Val Asp Glu Cys Ser Thr Thr Phe Pro Cys Ser Gln Arg 2980 2985 2990 2995	9451
tgc atc aac acc cat ggc agc tat aag tgt ctg tgt gtg gag ggc tat Cys Ile Asn Thr His Gly Ser Tyr Lys Cys Leu Cys Val Glu Gly Tyr 2996 3001 3006 3011	9499
gca ccc cgc ggc ggc gac ccc cac agc tgc aag gct gtg act gac gag Ala Pro Arg Gly Gly Asp Pro His Ser Cys Lys Ala Val Thr Asp Glu 3012 3017 3022 3027	9547
gaa ccg ttt ctg atc ttc gcc aac cgg tac tac ctg cgc aag ctc aac Glu Pro Phe Leu Ile Phe Ala Asn Arg Tyr Tyr Leu Arg Lys Leu Asn 3028 3033 3038 3043	9595
ctg gac ggg tcc aac tac acg tta ctt aag cag ggc ctg aac aac gcc Leu Asp Gly Ser Asn Tyr Thr Leu Leu Lys Gln Gly Leu Asn Asn Ala 3044 3049 3054 3059	9643
gtt gcc ttg gat ttt gac tac cga gag cag atg atc tac tgg aca gat Val Ala Leu Asp Phe Asp Tyr Arg Glu Gln Met Ile Tyr Trp Thr Asp 3060 3065 3070 3075	9691
gtg acc acc cag ggc agc atg atc cga agg atg cac ctt aac ggg agc Val Thr Thr Gln Gly Ser Met Ile Arg Arg Met His Leu Asn Gly Ser 3076 3081 3086 3091	9739
aat gtg cag gtc cta cac cgt aca ggc ctc agc aac ccc gat ggg ctg	9787

Asn Val Gln Val Leu His Arg Thr Gly Leu Ser Asn Pro Asp Gly Leu	
3092 3097 3102 3107	
gct gtg gac tgg gtg ggt ggc aac ctg tac tgg tgc gac aaa ggc cgg	9835
Ala Val Asp Trp Val Gly Gly Asn Leu Tyr Trp Cys Asp Lys Gly Arg	
3108 3113 3118 3123	
gac acc atc gag gtg tcc aag ctc aat ggg gcc tat cgg acg gtg ctg	9883
Asp Thr Ile Glu Val Ser Lys Leu Asn Gly Ala Tyr Arg Thr Val Leu	
3124 3129 3134 3139	
gtc agc tct ggc ctc cgt gag ccc agg gct ctg gtg gtg gat gtg cag	9931
Val Ser Ser Gly Leu Arg Glu Pro Arg Ala Leu Val Val Asp Val Gln	
3140 3145 3150 3155	
aat ggg tac ctg tac tgg aca gac tgg ggt gac cat tca ctg atc ggc	9979
Asn Gly Tyr Leu Tyr Trp Thr Asp Trp Gly Asp His Ser Leu Ile Gly	
3156 3161 3166 3171	
cgc atc ggc atg gat ggg tcc agc cgc agc gtc atc gtg gac acc aag	10027
Arg Ile Gly Met Asp Gly Ser Ser Arg Ser Val Ile Val Asp Thr Lys	
3172 3177 3182 3187	
atc aca tgg ccc aat ggc ctg acg ctg gac tat gtc act gag cgc atc	10075
Ile Thr Trp Pro Asn Gly Leu Thr Leu Asp Tyr Val Thr Glu Arg Ile	
3188 3193 3198 3203	
tac tgg gcc gac gcc cgc gag gac tac att gaa ttt gcc agc ctg gat	10123
Tyr Trp Ala Asp Ala Arg Glu Asp Tyr Ile Glu Phe Ala Ser Leu Asp	
3204 3209 3214 3219	
ggc tcc aat cgc cac gtt gtg ctg agc cag gac atc ccg cac atc ttt	10171
Gly Ser Asn Arg His Val Val Leu Ser Gln Asp Ile Pro His Ile Phe	
3220 3225 3230 3235	
gca ctg acc ctg ttt gag gac tac gtc tac tgg acc gac tgg gaa aca	10219
Ala Leu Thr Leu Phe Glu Asp Tyr Val Tyr Trp Thr Asp Trp Glu Thr	
3236 3241 3246 3251	
aag tcc att aac cga gcc cac aag acc aca ggc acc aac aaa acg ctc	10267
Lys Ser Ile Asn Arg Ala His Lys Thr Thr Gly Thr Asn Lys Thr Leu	
3252 3257 3262 3267	
ctc atc agc acg ctg cac cgg ccc atg gac ctg cat gtc ttc cat gcc	10315
Leu Ile Ser Thr Leu His Arg Pro Met Asp Leu His Val Phe His Ala	
3268 3273 3278 3283	
ctg cgc cag cca gac gtg ccc aat cac ccc tgc aag gtc aac aat ggt	10363
Leu Arg Gln Pro Asp Val Pro Asn His Pro Cys Lys Val Asn Asn Gly	
3284 3289 3294 3299	
ggc tgc agc aac ctg tgc ctg ctg tcc ccc ggg gga ggg cac aaa tgt	10411
Gly Cys Ser Asn Leu Cys Leu Leu Ser Pro Gly Gly Gly His Lys Cys	
3300 3305 3310 3315	
gcc tgc ccc acc aac ttc tac ctg ggc agc gat ggg cgc acc tgt gtg	10459
Ala Cys Pro Thr Asn Phe Tyr Leu Gly Ser Asp Gly Arg Thr Cys Val	

3316	3321	3326	3331	
tcc aac tgc acg gct agc cag ttt gta tgc aag aac gac aag tgc atc				10507
Ser Asn Cys Thr Ala Ser Gln Phe Val Cys Lys Asn Asp Lys Cys Ile				
3332	3337	3342	3347	
ccc ttc tgg tgg aag tgt gac acc gag gac gac tgc ggg gac cac tca				10555
Pro Phe Trp Trp Lys Cys Asp Thr Glu Asp Asp Cys Gly Asp His Ser				
3348	3353	3358	3363	
gac gag ccc ccg gac tgc cct gag ttc aag tgc cgg ccc gga cag ttc				10603
Asp Glu Pro Pro Asp Cys Pro Glu Phe Lys Cys Arg Pro Gly Gln Phe				
3364	3369	3374	3379	
cag tgc tcc aca ggt atc tgc aca aac cct gcc ttc atc tgc gat ggc				10651
Gln Cys Ser Thr Gly Ile Cys Thr Asn Pro Ala Phe Ile Cys Asp Gly				
3380	3385	3390	3395	
gac aat gac tgc cag gac aac agt gac gag gcc aac tgt gac atc cac				10699
Asp Asn Asp Cys Gln Asp Asn Ser Asp Glu Ala Asn Cys Asp Ile His				
3396	3401	3406	3411	
gtc tgc ttg ccc agt cag ttc aaa tgc acc aac acc aac cgc tgt att				10747
Val Cys Leu Pro Ser Gln Phe Lys Cys Thr Asn Thr Asn Arg Cys Ile				
3412	3417	3422	3427	
ccc ggc atc ttc cgc tgc aat ggg cag gac aac tgc gga gat ggg gag				10795
Pro Gly Ile Phe Arg Cys Asn Gly Gln Asp Asn Cys Gly Asp Gly Glu				
3428	3433	3438	3443	
gat gag agg gac tgc ccc gag gtg acc tgc gcc ccc aac cag ttc cag				10843
Asp Glu Arg Asp Cys Pro Glu Val Thr Cys Ala Pro Asn Gln Phe Gln				
3444	3449	3454	3459	
tgc tcc att acc aaa cgg tgc atc ccc cgg gtc tgg gtc tgc gac cgg				10891
Cys Ser Ile Thr Lys Arg Cys Ile Pro Arg Val Trp Val Cys Asp Arg				
3460	3465	3470	3475	
gac aat gac tgt gtg gat ggc agt gat gag ccc gcc aac tgc acc cag				10939
Asp Asn Asp Cys Val Asp Gly Ser Asp Glu Pro Ala Asn Cys Thr Gln				
3476	3481	3486	3491	
atg acc tgt ggt gtg gac gag ttc cgc tgc aag gat tcg ggc cgc tgc				10987
Met Thr Cys Gly Val Asp Glu Phe Arg Cys Lys Asp Ser Gly Arg Cys				
3492	3497	3502	3507	
atc cca gcg cgt tgg aag tgt gac gga gag gat gac tgt ggg gat ggc				11035
Ile Pro Ala Arg Trp Lys Cys Asp Gly Glu Asp Asp Cys Gly Asp Gly				
3508	3513	3518	3523	
tcg gat gag ccc aag gaa gag tgt gat gaa cgc acc tgt gag cca tac				11083
Ser Asp Glu Pro Lys Glu Glu Cys Asp Glu Arg Thr Cys Glu Pro Tyr				
3524	3529	3534	3539	
cag ttc cgc tgc aag aac aac cgc tgc gtg ccc ggc cgc tgg cag tgc				11131
Gln Phe Arg Cys Lys Asn Asn Arg Cys Val Pro Gly Arg Trp Gln Cys				
3540	3545	3550	3555	

gac tac gac aac gat tgc ggt gac aac tcc gat gaa gag agc tgc acc Asp Tyr Asp Asn Asp Cys Gly Asp Asn Ser Asp Glu Glu Ser Cys Thr 3556 3561 3566 3571	11179
cct cgg ccc tgc tcc gag agt gag ttc tcc tgt gcc aac ggc cgc tgc Pro Arg Pro Cys Ser Glu Ser Glu Phe Ser Cys Ala Asn Gly Arg Cys 3572 3577 3582 3587	11227
atc gcg ggg cgc tgg aaa tgc gat gga gac cac gac tgc gcg gac ggc Ile Ala Gly Arg Trp Lys Cys Asp Gly Asp His Asp Cys Ala Asp Gly 3588 3593 3598 3603	11275
tgc gac gag aaa gac tgc acc ccc cgc tgt gac atg gac cag ttc cag Ser Asp Glu Lys Asp Cys Thr Pro Arg Cys Asp Met Asp Gln Phe Gln 3604 3609 3614 3619	11323
tgc aag agc ggc cac tgc atc ccc ctg cgc tgg cgc tgt gac gca gac Cys Lys Ser Gly His Cys Ile Pro Leu Arg Trp Arg Cys Asp Ala Asp 3620 3625 3630 3635	11371
gcc gac tgc atg gac ggc agc gac gag gag gcc tgc ggc act ggc gtg Ala Asp Cys Met Asp Gly Ser Asp Glu Glu Ala Cys Gly Thr Gly Val 3636 3641 3646 3651	11419
cgg acc tgc ccc ctg gac gag ttc cag tgc aac aac acc ttg tgc aag Arg Thr Cys Pro Leu Asp Glu Phe Gln Cys Asn Asn Thr Leu Cys Lys 3652 3657 3662 3667	11467
ccg ctg gcc tgg aag tgc gat ggc gag gat gac tgt ggg gac aac tca Pro Leu Ala Trp Lys Cys Asp Gly Glu Asp Asp Cys Gly Asp Asn Ser 3668 3673 3678 3683	11515
gat gag aac ccc gag gag tgt gcc cgg ttc gtg tgc cct ccc aac cgg Asp Glu Asn Pro Glu Glu Cys Ala Arg Phe Val Cys Pro Pro Asn Arg 3684 3689 3694 3699	11563
ccc ttc cgt tgc aag aat gac cgc gtc tgt ctg tgg atc ggg cgc caa Pro Phe Arg Cys Lys Asn Asp Arg Val Cys Leu Trp Ile Gly Arg Gln 3700 3705 3710 3715	11611
tgc gat ggc acg gac aac tgt ggg gat ggg act gat gaa gag gac tgt Cys Asp Gly Thr Asp Asn Cys Gly Asp Gly Thr Asp Glu Glu Asp Cys 3716 3721 3726 3731	11659
gag ccc ccc aca gcc cac acc acc cac tgc aaa gac aag aag gag ttt Glu Pro Pro Thr Ala His Thr Thr His Cys Lys Asp Lys Lys Glu Phe 3732 3737 3742 3747	11707
ctg tgc cgg aac cag cgc tgc ctc tcc tcc tcc ctg cgc tgc aac atg Leu Cys Arg Asn Gln Arg Cys Leu Ser Ser Ser Leu Arg Cys Asn Met 3748 3753 3758 3763	11755
ttc gat gac tgc ggg gac ggc tct gac gag gag gac tgc agc atc gac Phe Asp Asp Cys Gly Asp Gly Ser Asp Glu Glu Asp Cys Ser Ile Asp 3764 3769 3774 3779	11803

ccc aag ctg acc agc tgc gcc acc aat gcc agc atc tgt ggg gac gag	11851
Pro Lys Leu Thr Ser Cys Ala Thr Asn Ala Ser Ile Cys Gly Asp Glu	
3780 3785 3790 3795	
gca cgc tgc gtg cgc acc gag aaa gcg gcc tac tgt gcc tgc cgc tcg	11899
Ala Arg Cys Val Arg Thr Glu Lys Ala Ala Tyr Cys Ala Cys Arg Ser	
3796 3801 3806 3811	
ggc ttc cac acc gtg ccc ggc cag ccc gga tgc caa gac atc aac gag	11947
Gly Phe His Thr Val Pro Gly Gln Pro Gly Cys Gln Asp Ile Asn Glu	
3812 3817 3822 3827	
tgc ctg cgc ttc ggc acc tgc tcc cag ctc tgc aac aac acc aag ggc	11995
Cys Leu Arg Phe Gly Thr Cys Ser Gln Leu Cys Asn Asn Thr Lys Gly	
3828 3833 3838 3843	
ggc cac ctc tgc agc tgc gct cgg aac ttc atg aag acg cac aac acc	12043
Gly His Leu Cys Ser Cys Ala Arg Asn Phe Met Lys Thr His Asn Thr	
3844 3849 3854 3859	
tgc aag gcc gaa ggc tct gag tac cag gtc ctg tac atc gct gat gag	12091
Cys Lys Ala Glu Gly Ser Glu Tyr Gln Val Leu Tyr Ile Ala Asp Asp	
3860 3865 3870 3875	
aat gag atc cgc agc ctg ttc ccc ggc cac ccc cat tcg gct tac gag	12139
Asn Glu Ile Arg Ser Leu Phe Pro Gly His Pro His Ser Ala Tyr Glu	
3876 3881 3886 3891	
cag gca ttc cag ggt gac gag agt gtc cgc att gat gct atg gat gtc	12187
Gln Ala Phe Gln Gly Asp Glu Ser Val Arg Ile Asp Ala Met Asp Val	
3892 3897 3902 3907	
cat gtc aag gct ggc cgt gtc tat tgg acc aac tgg cac acg ggc acc	12235
His Val Lys Ala Gly Arg Val Tyr Trp Thr Asn Trp His Thr Gly Thr	
3908 3913 3918 3923	
atc tcc tac cgc agc ctg cca cct gct gcg cct cct acc act tcc aac	12283
Ile Ser Tyr Arg Ser Leu Pro Pro Ala Ala Pro Pro Thr Thr Ser Asn	
3924 3929 3934 3939	
cgc cac cgg cga cag att gac cgg ggt gtc acc cac ctc aac att tca	12331
Arg His Arg Arg Gln Ile Asp Arg Gly Val Thr His Leu Asn Ile Ser	
3940 3945 3950 3955	
ggg ctg aag atg ccc aga ggc atc gcc atc gac tgg gtg gcc gga aac	12379
Gly Leu Lys Met Pro Arg Gly Ile Ala Ile Asp Trp Val Ala Gly Asn	
3956 3961 3966 3971	
gtg tac tgg acc gac tcg ggc cga gat gtg att gag gtg gcg cag atg	12427
Val Tyr Trp Thr Asp Ser Gly Arg Asp Val Ile Glu Val Ala Gln Met	
3972 3977 3982 3987	
aag ggc gag aac cgc aag acg ctc atc tcg ggc atg att gac gag ccc	12475
Lys Gly Glu Asn Arg Lys Thr Leu Ile Ser Gly Met Ile Asp Glu Pro	
3988 3993 3998 4003	
cac gcc att gtg gtg gac cca ctg agg ggg acc atg tac tgg tca gac	12523

His Ala Ile Val Val Asp Pro Leu Arg Gly Thr Met Tyr Trp Ser Asp	
4004	4009 4014 4019
tgg ggc aac cac ccc aag att gag acg gca gcg atg gat ggg acg ctt	12571
Trp Gly Asn His Pro Lys Ile Glu Thr Ala Ala Met Asp Gly Thr Leu	
4020	4025 4030 4035
cgg gag aca ctg gtg cag gac aac att cag tgg ccc aca ggc ctg gcc	12619
Arg Glu Thr Leu Val Gln Asp Asn Ile Gln Trp Pro Thr Gly Leu Ala	
4036	4041 4046 4051
gtg gat tat cac aat gag cgg ctg tac tgg gca gac gcc aag ctt tca	12667
Val Asp Tyr His Asn Glu Arg Leu Tyr Trp Ala Asp Ala Lys Leu Ser	
4052	4057 4062 4067
gtc atc ggc agc atc cgg ctc aat ggc acg gac ccc att gtg gct gct	12715
Val Ile Gly Ser Ile Arg Leu Asn Gly Thr Asp Pro Ile Val Ala Ala	
4068	4073 4078 4083
gac agc aaa cga ggc cta agt cac ccc ttc agc atc gac gtc ttt gag	12763
Asp Ser Lys Arg Gly Leu Ser His Pro Phe Ser Ile Asp Val Phe Glu	
4084	4089 4094 4099
gat tac atc tat ggt gtc acc tac atc aat aat cgt gtc ttc aag atc	12811
Asp Tyr Ile Tyr Gly Val Thr Tyr Ile Asn Asn Arg Val Phe Lys Ile	
4100	4105 4110 4115
cat aag ttt ggc cac agc ccc ttg gtc aac ctg aca ggg ggc ctg agc	12859
His Lys Phe Gly His Ser Pro Leu Val Asn Leu Thr Gly Gly Leu Ser	
4116	4121 4126 4131
cac gcc tct gac gtg gtc ctt tac cat cag cac aag cag ccc gaa gtg	12907
His Ala Ser Asp Val Val Leu Tyr His Gln His Lys Gln Pro Glu Val	
4132	4137 4142 4147
acc aac cca tgt gac cgc aag aaa tgc gag tgg ctc tgc ctg ctg agc	12955
Thr Asn Pro Cys Asp Arg Lys Lys Cys Glu Trp Leu Cys Leu Leu Ser	
4148	4153 4158 4163
ccc agt ggg cct gtc tgc acc tgt ccc aat ggg aag cgg ctg gac aac	13003
Pro Ser Gly Pro Val Cys Thr Cys Pro Asn Gly Lys Arg Leu Asp Asn	
4164	4169 4174 4179
ggc aca tgc gtg cct gtg ccc tct cca acg ccc ccc cca gat gct ccc	13051
Gly Thr Cys Val Pro Val Pro Ser Pro Thr Pro Pro Pro Asp Ala Pro	
4180	4185 4190 4195
cgg cct gga acc tgt aac ctg cag tgc ttc aac ggt ggc agc tgt ttc	13099
Arg Pro Gly Thr Cys Asn Leu Gln Cys Phe Asn Gly Gly Ser Cys Phe	
4196	4201 4206 4211
ctc aat gca cgg agg cag ccc aag tgc cgc tgc caa ccc cgc tac acg	13147
Leu Asn Ala Arg Arg Gln Pro Lys Cys Arg Cys Gln Pro Arg Tyr Thr	
4212	4217 4222 4227
ggt gac aag tgt gaa ctg gac cag tgc tgg gag cac tgt cgc aat ggg	13195
Gly Asp Lys Cys Glu Leu Asp Gln Cys Trp Glu His Cys Arg Asn Gly	

4228	4233	4238	4243	
ggc acc tgt gct gcc tcc ccc tct ggc atg ccc acg tgc cgg tgc ccc				13243
Gly Thr Cys Ala Ala Ser Pro Ser Gly Met Pro Thr Cys Arg Cys Pro				
4244	4249	4254	4259	
acg ggc ttc acg ggc ccc aaa tgc acc cag cag gtg tgt gcg ggc tac				13291
Thr Gly Phe Thr Gly Pro Lys Cys Thr Gln Gln Val Cys Ala Gly Tyr				
4260	4265	4270	4275	
tgt gcc aac aac agc acc tgc act gtc aac cag ggc aac cag ccc cag				13339
Cys Ala Asn Asn Ser Thr Cys Thr Val Asn Gln Gly Asn Gln Pro Gln				
4276	4281	4286	4291	
tgc cga tgc cta ccc ggc ttc ctg ggc gac cgc tgc cag tac cgg cag				13387
Cys Arg Cys Leu Pro Gly Phe Leu Gly Asp Arg Cys Gln Tyr Arg Gln				
4292	4297	4302	4307	
tgc tct ggc tac tgt gag aac ttt ggc aca tgc cag atg gct gct gat				13435
Cys Ser Gly Tyr Cys Glu Asn Phe Gly Thr Cys Gln Met Ala Ala Asp				
4308	4313	4318	4323	
ggc tcc cga caa tgc cgc tgc act gcc tac ttt gag gga tcg agg tgt				13483
Gly Ser Arg Gln Cys Arg Cys Thr Ala Tyr Phe Glu Gly Ser Arg Cys				
4324	4329	4334	4339	
gag gtg aac aag tgc agc cgc tgt ctc gaa ggg gcc tgt gtg gtc aac				13531
Glu Val Asn Lys Cys Ser Arg Cys Leu Glu Gly Ala Cys Val Val Asn				
4340	4345	4350	4355	
aag cag agt ggg gat gtc acc tgc aac tgc acg gat ggc cgg gtg gcc				13579
Lys Gln Ser Gly Asp Val Thr Cys Asn Cys Thr Asp Gly Arg Val Ala				
4356	4361	4366	4371	
ccc agc tgt ctg acc tgc gtc ggc cac tgc agc aat ggc ggc tcc tgt				13627
Pro Ser Cys Leu Thr Cys Val Gly His Cys Ser Asn Gly Gly Ser Cys				
4372	4377	4382	4387	
acc atg aac agc aaa atg atg cct gag tgc cag tgc cca ccc cac atg				13675
Thr Met Asn Ser Lys Met Met Pro Glu Cys Gln Cys Pro Pro His Met				
4388	4393	4398	4403	
aca ggg ccc cgg tgt gag gag cac gtc ttc agc cag cag cag cca gga				13723
Thr Gly Pro Arg Cys Glu Glu His Val Phe Ser Gln Gln Gln Pro Gly				
4404	4409	4414	4419	
cat ata gcc tcc atc cta atc cct ctg ctg ttg ctg ctg ctg ctg gtt				13771
His Ile Ala Ser Ile Leu Ile Pro Leu Leu Leu Leu Leu Leu Val				
4420	4425	4430	4435	
ctg gtg gcc gga gtg gta ttc tgg tat aag cgg cga gtc caa ggg gct				13819
Leu Val Ala Gly Val Val Phe Trp Tyr Lys Arg Arg Val Gln Gly Ala				
4436	4441	4446	4451	
aag ggc ttc cag cac caa cgg atg acc aac ggg gcc atg aac gtg gag				13867
Lys Gly Phe Gln His Gln Arg Met Thr Asn Gly Ala Met Asn Val Glu				
4452	4457	4462	4467	

```

att gga aac ccc acc tac aag atg tac gaa ggc gga gag cct gat gat 13915
Ile Gly Asn Pro Thr Tyr Lys Met Tyr Glu Gly Gly Glu Pro Asp Asp
4468          4473          4478          4483

gtg gga ggc cta ctg gac gct gac ttt gcc ctg gac cct gac aag ccc 13963
Val Gly Gly Leu Leu Asp Ala Asp Phe Ala Leu Asp Pro Asp Lys Pro
4484          4489          4494          4499

acc aac ttc acc aac ccc gtg tat gcc aca ctc tac atg ggg ggc cat 14011
Thr Asn Phe Thr Asn Pro Val Tyr Ala Thr Leu Tyr Met Gly Gly His
4500          4505          4510          4515

ggc agt cgc cac tcc ctg gcc agc acg gac gag aag cga gaa ctc ctg 14059
Gly Ser Arg His Ser Leu Ala Ser Thr Asp Glu Lys Arg Glu Leu Leu
4516          4521          4526          4531

ggc cgg ggc cct gag gac gag ata ggg gac ccc ttg gca tag ggccctg 14108
Gly Arg Gly Pro Glu Asp Glu Ile Gly Asp Pro Leu Ala *
4532          4537          4542

ccccgtcgga ctgccccag aaagcctcct gccccctgcc ggtgaagtcc ttcagtgagc 14168
ccctccccag ccagcccttc cctggccccg ccgatgtat aaatgtaaaa atgaaggaat 14228
tacattttat atgtgagcga gcaagccggc aagcgagcac agtattat ttccatcccc 14288
tccctgcctg ctcttgga ccccatgct gccttcaggg agacaggcag ggagggcctg 14348
gggctgcacc tctaccctc ccaccagaac gcacccact gggagagctg gtggtgcagc 14408
cttccccctc ctgtataaga cactttgcca aggtctctcc ctctcgcccc atccctgctt 14468
gcccgtccc acagcttctt gagggcta at tctgggaagg gagagttctt tgctgcccc 14528
gtctggaaga cgtggctctg ggtgaggtag gcgggaaagg atggagtgtt ttagttcttg 14588
ggggaggcca ccccaaacc cagccccaac tccaggggca cctatgagat ggccatgctc 14648
aacccccctc ccagacaggc cctccctgtc tccagggccc ccaccgaggt tcccagggct 14708
ggagacttcc tctggtaaac attcctccag cctccccctc cctggggacg ccaaggaggt 14768
gggccacacc caggaaggga aagcgggcag ccccgttttg gggacgtgaa cgttttaata 14828
atttttgctg aattccttta caactaaata acacagatat tgttataaat aaaattgtaa 14888
aaaaaaaaa a 14899

```

<210> 4
 <211> 1538
 <212> DNA
 <213> Homo sapiens

[illegible]

31

173	178	183	188	
atc tat cag ctt gac act gca tcc att agt ggc acc atc aca aat gaa				806
Ile Tyr Gln Leu Asp Thr Ala Ser Ile Ser Gly Thr Ile Thr Asn Glu				
189	194	199	204	
aag aga att tcc tct gtt aaa ttt ctt tca gag tct gtc ctt gca gtg				854
Lys Arg Ile Ser Ser Val Lys Phe Leu Ser Glu Ser Val Leu Ala Val				
205	210	215	220	
gct gga gat gaa gaa gtt ata agg ttt ttt gac tgt gat tca cta gtg				902
Ala Gly Asp Glu Glu Val Ile Arg Phe Phe Asp Cys Asp Ser Leu Val				
221	226	231	236	
tgc ctc tgc gaa ttt aaa gct cat gaa aac agg gta aag gac atg ttc				950
Cys Leu Cys Glu Phe Lys Ala His Glu Asn Arg Val Lys Asp Met Phe				
237	242	247	252	
agt ttt gaa att cca gag cat cat gtt att gtt tca gca tcg agt gat				998
Ser Phe Glu Ile Pro Glu His His Val Ile Val Ser Ala Ser Ser Asp				
253	258	263	268	
ggc ttc atc aaa atg tgg aag ctt aag cag gat aag aaa gtt ccc cca				1046
Gly Phe Ile Lys Met Trp Lys Leu Lys Gln Asp Lys Lys Val Pro Pro				
269	274	279	284	
tct tta ctc tgt gaa ata aac act aat gcc agg ctg acg tgt ctt gga				1094
Ser Leu Leu Cys Glu Ile Asn Thr Asn Ala Arg Leu Thr Cys Leu Gly				
285	290	295	300	
gtg tgg cta gac aaa gtg gca gac atg aaa gaa agc ctt cct cca gct				1142
Val Trp Leu Asp Lys Val Ala Asp Met Lys Glu Ser Leu Pro Pro Ala				
301	306	311	316	
gca gag cct tct cct gta agt aaa gaa cag tcc aaa att ggc aaa aag				1190
Ala Glu Pro Ser Pro Val Ser Lys Glu Gln Ser Lys Ile Gly Lys Lys				
317	322	327	332	
gag cct ggt gac aca gtg cac aaa gaa gaa aag cgg tca aaa cct aac				1238
Glu Pro Gly Asp Thr Val His Lys Glu Glu Lys Arg Ser Lys Pro Asn				
333	338	343	348	
aca aag aaa cgc ggt tta aca ggt gac agt aag aaa gca aca aaa gaa				1286
Thr Lys Lys Arg Gly Leu Thr Gly Asp Ser Lys Lys Ala Thr Lys Glu				
349	354	359	364	
agt ggc ctg ata tca acc aag aag agg aaa atg gta gaa atg ttg gaa				1334
Ser Gly Leu Ile Ser Thr Lys Lys Arg Lys Met Val Glu Met Leu Glu				
365	370	375	380	
aag aag agg aaa aag aag aaa ata aaa cca atg cag tga atcacagatg				1383
Lys Lys Arg Lys Lys Lys Lys Ile Lys Pro Met Gln *				
381	386	391		
tctcctgaaa gaactctttt agatgaaatc attctactca aatgtacott aatttttttt				1443
ttttccctga gtaaaagcaa gaaatttctt ccttttgaaa aaatatatat attaaaaaac				1503

cactttttaga tggttttttt taaaaaaaaa aaaaa

1538

<210> 5
<211> 1588
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (466)..(1266)

<400> 5
tagcatgatg tatataacta tctattcgat gatgaagata cccacacaaa cccaaaaaaaa 60
gagatctctc gaggatccga attcgcggcc gcgctgcacgt gtaggccagg ggggtggcgg 120
tgccgtgtca tggaggctca gtctctgagc agccattgaa ggggaaggaa ctgcgggtgt 180
gtgtgtgtat gtgtgtgtgt atgtgtgtgc gcgctgcgct gcgtgtgtgt gcgcgcgcta 240
gtgtgtggac aaggaggtgg gggcagctga gttagagtcc caactcttgg actccatttg 300
ctattctctt ctttctcccc cacacctatc tggtggtggt agtgggcgtt tatatttgcg 360
ttccttttca ttcatttcta aatctcttaa aaattttggg ttgggggtat tggggaaggc 420
aggaaagggg aaaggagagt agtagctgaa gagcaagagg aggac atg gag atg 474
Met Glu Met
1
aag aag aag att aac ctg gag tta agg aac aga tcc ccg gag gag gtg 522
Lys Lys Lys Ile Asn Leu Glu Leu Arg Asn Arg Ser Pro Glu Glu Val
4 9 14 19
aca gag tta gtc ctt gat aat tgc ctg tgt gtc aat ggg gaa att gaa 570
Thr Glu Leu Val Leu Asp Asn Cys Leu Cys Val Asn Gly Glu Ile Glu
20 25 30 35
ggc ctg aat gat act ttc aaa gaa cta gaa ttt ctg agt atg gct aat 618
Gly Leu Asn Asp Thr Phe Lys Glu Leu Glu Phe Leu Ser Met Ala Asn
36 41 46 51
gtg gaa cta agt tgc ctg gcc cgg ctt ccc agc tta aat aaa ctt cga 666
Val Glu Leu Ser Ser Leu Ala Arg Leu Pro Ser Leu Asn Lys Leu Arg
52 57 62 67
aaa ttg gag ctt agt gat aat ata att tct gga ggc ttg gaa gtc ctg 714
Lys Leu Glu Leu Ser Asp Asn Ile Ile Ser Gly Gly Leu Glu Val Leu
68 73 78 83
gca gag aaa tgt cca aat ctt acc tac ctc aat ctg agt gga aac aaa 762
Ala Glu Lys Cys Pro Asn Leu Thr Tyr Leu Asn Leu Ser Gly Asn Lys
84 89 94 99

ata aaa gat ctc agt aca gta gaa gct ctg caa aat ctt aaa aat ttg	810
Ile Lys Asp Leu Ser Thr Val Glu Ala Leu Gln Asn Leu Lys Asn Leu	
100 105 110 115	
aaa agt ctt gac ctg ttt aac tgt gag atc aca aac ctg gaa gat tat	858
Lys Ser Leu Asp Leu Phe Asn Cys Glu Ile Thr Asn Leu Glu Asp Tyr	
116 121 126 131	
aga gaa agt att ttt gaa cta ctg cag caa atc aca tac tta gat gga	906
Arg Glu Ser Ile Phe Glu Leu Leu Gln Gln Ile Thr Tyr Leu Asp Gly	
132 137 142 147	
ttt gat cag gag gat aat gaa gcg ccg gac tct gaa gag gag gat gat	954
Phe Asp Gln Glu Asp Asn Glu Ala Pro Asp Ser Glu Glu Glu Asp Asp	
148 153 158 163	
gag gat gga gat gaa gat gat gaa gag gaa gag gaa aat gaa gct ggt	1002
Glu Asp Gly Asp Glu Asp Asp Glu Glu Glu Glu Glu Asn Glu Ala Gly	
164 169 174 179	
cca ccg gaa gga tat gag gaa gag gag gag gaa gag gag gat gag gat	1050
Pro Pro Glu Gly Tyr Glu Glu Glu Glu Glu Glu Glu Glu Asp Glu Asp	
180 185 190 195	
gag gat gaa gat gaa gat gaa gca ggt tca gag ttg gga gag gga gaa	1098
Glu Asp Glu Asp Glu Asp Glu Ala Gly Ser Glu Leu Gly Glu Gly Glu	
196 201 206 211	
gag gaa gtg ggc ctc tca tac tta atg aaa gaa gaa att cag gat gaa	1146
Glu Glu Val Gly Leu Ser Tyr Leu Met Lys Glu Glu Ile Gln Asp Glu	
212 217 222 227	
gaa gat gat gat gac tat gtt gaa gaa ggg gaa gaa gag gaa gaa gag	1194
Glu Asp Asp Asp Asp Tyr Val Glu Glu Gly Glu Glu Glu Glu Glu Glu	
228 233 238 243	
gaa gaa gga ggt ctt cga ggg gag aag agg aaa cga gat gct gaa gac	1242
Glu Glu Gly Gly Leu Arg Gly Glu Lys Arg Lys Arg Asp Ala Glu Asp	
244 249 254 259	
gat gga gag gaa gaa gat gac tag atcattctaa gaccagattc tctaattgttt	1296
Asp Gly Glu Glu Glu Asp Asp *	
260 265	
ctgggtgtgc aatagagtga tcacatcttt gtttcttcat gtacgatagc tatccctaca	1356
gaagataatg tgtaactttt tataggaaaa gtgtggtttt actatttttg ccttatcatt	1416
ccaaataaga actagtctgt taatgatcat attgtatgta gagaaaaatt ttcattgact	1476
cccattgtgg aattccctag caatttattt agacttaatt ttttaaattc aagcttactg	1536
tattagtcatt ttttagccca taattaaaac atgatcactt ttaaaaaaaaa aa	1588

<210> 6
 <211> 1033
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (53)..(766)

<400> 6

```

gtaccggtcc ggaattcccg ggtcgacgat ttcgtgtgcc cgggacgaag cc      atg      55
                                   Met
                                   1

gcc ctg gag gcg gcg gga ggg ccg ccg gag gaa acg ctg tca ctg tgg      103
Ala Leu Glu Ala Ala Gly Gly Pro Pro Glu Glu Thr Leu Ser Leu Trp
   2                               7                               12                               17

aaa cgg gag caa gct cgg ctg aag gcc cac gtc gta gac cgg gac acc      151
Lys Arg Glu Gln Ala Arg Leu Lys Ala His Val Val Asp Arg Asp Thr
  18                               23                               28                               33

gag gcg tgg cag cga gac ccc gcc ttc tcg ggt ctg cag agg gtc ggg      199
Glu Ala Trp Gln Arg Asp Pro Ala Phe Ser Gly Leu Gln Arg Val Gly
  34                               39                               44                               49

ggc gtt gac gtg tcc ttc gtg aaa ggg gac agt gtc cgc gct tgt gct      247
Gly Val Asp Val Ser Phe Val Lys Gly Asp Ser Val Arg Ala Cys Ala
  50                               55                               60                               65

tcc ctg gtg gtg ctc agc ttc cct gag ctc gag gtc ctt ctt gtg gat      295
Ser Leu Val Val Leu Ser Phe Pro Glu Leu Glu Val Leu Leu Val Asp
  66                               71                               76                               81

gga aac ggg gta ctc cac cac cga ggc ttt ggg gtg gcc tgc cac ctt      343
Gly Asn Gly Val Leu His His Arg Gly Phe Gly Val Ala Cys His Leu
  82                               87                               92                               97

ggc gtc ctt aca gac ctg ccg tgt gtt ggg gtg gcc aag aaa ctt ctg      391
Gly Val Leu Thr Asp Leu Pro Cys Val Gly Val Ala Lys Lys Leu Leu
  98                               103                               108                               113

cag gtg gat ggg ctg gag aac aac gcc ctg cac aag gag aag atc cga      439
Gln Val Asp Gly Leu Glu Asn Asn Ala Leu His Lys Glu Lys Ile Arg
 114                               119                               124                               129

ctc ctg cag act cga gga gac tca ttc cct ctg ctg gga gac tct ggg      487
Leu Leu Gln Thr Arg Gly Asp Ser Phe Pro Leu Leu Gly Asp Ser Gly
 130                               135                               140                               145

act gtc ctg gga atg gcc ctg agg agc cac gac cgc agc acc agg ccc      535
Thr Val Leu Gly Met Ala Leu Arg Ser His Asp Arg Ser Thr Arg Pro
 146                               151                               156                               161

ctc tac atc tcc gtg ggc cac agg atg agc ctg gag gcc gct gtg cgc      583
Leu Tyr Ile Ser Val Gly His Arg Met Ser Leu Glu Ala Ala Val Arg

```


ggc gtt gac gtg tcc ttc gtg aaa ggg gac agt gtc cgc gct tgt gct	247
Gly Val Asp Val Ser Phe Val Lys Gly Asp Ser Val Arg Ala Cys Ala	
50 55 60 65	
tcc ctg gtg gtg ctc agc ttc cct gag ctc gag gtg gtg tat gag gag	295
Ser Leu Val Val Leu Ser Phe Pro Glu Leu Glu Val Val Tyr Glu Glu	
66 71 76 81	
agc cgc atg gtc agc ctc aca gcc ccc tac gtg tcg ggc ttc ctg gcc	343
Ser Arg Met Val Ser Leu Thr Ala Pro Tyr Val Ser Gly Phe Leu Ala	
82 87 92 97	
ttc cga gag gtg ccc ttc ttg ctg gag ctg gtg caa cag ctg cgg gag	391
Phe Arg Glu Val Pro Phe Leu Leu Glu Leu Val Gln Gln Leu Arg Glu	
98 103 108 113	
aag gag ccg ggc ctc atg ccc cag gtc ctt ctt gtg gat gga aac ggg	439
Lys Glu Pro Gly Leu Met Pro Gln Val Leu Leu Val Asp Gly Asn Gly	
114 119 124 129	
gta ctc cac cac cga ggc ttt ggg gtg gcc tgc cac ctt ggc gtc ctt	487
Val Leu His His Arg Gly Phe Gly Val Ala Cys His Leu Gly Val Leu	
130 135 140 145	
aca gac ctg ccg tgt gtt ggg gtg gcc aag aaa ctt ctg cag gtg gat	535
Thr Asp Leu Pro Cys Val Gly Val Ala Lys Lys Leu Leu Gln Val Asp	
146 151 156 161	
ggg ctg gag aac aac gcc ctg cac aag gag aag atc cga ctc ctg cag	583
Gly Leu Glu Asn Asn Ala Leu His Lys Glu Lys Ile Arg Leu Leu Gln	
162 167 172 177	
act cga gga gac tca ttc cct ctg ctg gga gac tct ggg act gtc ctg	631
Thr Arg Gly Asp Ser Phe Pro Leu Leu Gly Asp Ser Gly Thr Val Leu	
178 183 188 193	
gga atg gcc ctg agg agc cac gac cgc agc acc agg ccc ctc tac atc	679
Gly Met Ala Leu Arg Ser His Asp Arg Ser Thr Arg Pro Leu Tyr Ile	
194 199 204 209	
tcc gtg ggc cac agg atg agc ctg gag gcc gct gtg cgc ctg act tgc	727
Ser Val Gly His Arg Met Ser Leu Glu Ala Ala Val Arg Leu Thr Cys	
210 215 220 225	
tgc tgc tgc agg ttc cgg atc cca gag ccc gtg cgc cag gct gac atc	775
Cys Cys Cys Arg Phe Arg Ile Pro Glu Pro Val Arg Gln Ala Asp Ile	
226 231 236 241	
tgc tcc cga gag cac atc cgc aag tcg ctg gga ctc ccc ggg cca ccc	823
Cys Ser Arg Glu His Ile Arg Lys Ser Leu Gly Leu Pro Gly Pro Pro	
242 247 252 257	
aca ccg agg agc ccg aag gcg cag agg cca gtg gca tgc ccc aaa gga	871
Thr Pro Arg Ser Pro Lys Ala Gln Arg Pro Val Ala Cys Pro Lys Gly	
258 263 268 273	
gac tcc gga gag tcc tca gca ctt tgt tga a cgtggtggtg agagcacacg	922

Asp Ser Gly Glu Ser Ser Ala Leu Cys *

274

279

tcctcgtctc attcctgata gaacgcggtg gtgagagcac acgtcctcgt ctcgttcgtg 982
acagaacgcg gtggtgagag cacacgtcgt cgtttcgate ctgatcgaac gcggtggtga 1042
gagcgcacgt cctcgtctcg ttccctgaacg aacgcggtgg tgagagccca cgtcgtggtc 1102
tcgatcctga ttgaactagg agacgaaatc gtcgacagcg aagtcgaccc ggggaattccg 1162
ggcccg 1168

<210> 8

<211> 4076

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (243) .. (3329)

<400> 8

aagctggcac gcctgcaggt accggtccgg aattccccgg tcgacgattt cgtgtccccg 60
cagtgtcgag gcgcggggccc tggcaggtcc tttctcgagg cagggggcac ggtagcacag 120
ggagcttctc tttgtgggcg ggcgcgaggc ccgctagggg gttatactgg ggaacgtgcc 180
tgcgcggtgct tggatagttc atttaaagcc cccatccctg caaggtggtg ctttctacca 240
at atg aat ctt ttc aac ctg gac cgt ttt ggc ttt gag aaa agg aat 287
Met Asn Leu Phe Asn Leu Asp Arg Phe Gly Phe Glu Lys Arg Asn
1 5 10
aag att gag gaa gcg ccc gaa gca acc cct caa cct tcc cag cct ggc 335
Lys Ile Glu Glu Ala Pro Glu Ala Thr Pro Gln Pro Ser Gln Pro Gly
16 21 26 31
cct tct tca cca att tct ctt agt gct gaa gag gag aat gct gaa ggg 383
Pro Ser Ser Pro Ile Ser Leu Ser Ala Glu Glu Asn Ala Glu Gly
32 37 42 47
gaa gtt agc agg gca aac act cct gat tca gat ata act gaa aaa aca 431
Glu Val Ser Arg Ala Asn Thr Pro Asp Ser Asp Ile Thr Glu Lys Thr
48 53 58 63
gaa gat tct agt gtt cca gaa act cca gat aat gaa aga aaa gca agt 479
Glu Asp Ser Ser Val Pro Glu Thr Pro Asp Asn Glu Arg Lys Ala Ser
64 69 74 79
ata tca tat ttc aaa aat caa aga gga ata cag tat att gat ttg tct 527
Ile Ser Tyr Phe Lys Asn Gln Arg Gly Ile Gln Tyr Ile Asp Leu Ser
80 85 90 95

tct gat agt gaa gat gtc gtt tcc cca aat tgc tcc aat aca gtt caa	575
Ser Asp Ser Glu Asp Val Val Ser Pro Asn Cys Ser Asn Thr Val Gln	
96 101 106 111	
gag aaa aca ttc aac aaa gat aca gtg att ata gtt tct gag cca tct	623
Glu Lys Thr Phe Asn Lys Asp Thr Val Ile Ile Val Ser Glu Pro Ser	
112 117 122 127	
gaa gat gaa gag tcc caa ggc ctt cct acc atg gca cgt aga aat gat	671
Glu Asp Glu Glu Ser Gln Gly Leu Pro Thr Met Ala Arg Arg Asn Asp	
128 133 138 143	
gat att tca gaa ctg gaa gac ctt tcg gaa ttg gaa gac ctt aaa gat	719
Asp Ile Ser Glu Leu Glu Asp Leu Ser Glu Leu Glu Asp Leu Lys Asp	
144 149 154 159	
gct aaa ctt cag act ttg aag gaa ctt ttt cca caa aga agt gac aat	767
Ala Lys Leu Gln Thr Leu Lys Glu Leu Phe Pro Gln Arg Ser Asp Asn	
160 165 170 175	
gat tta ctt aag ttg att gaa tca aca agc act atg gat gga gca att	815
Asp Leu Leu Lys Leu Ile Glu Ser Thr Ser Thr Met Asp Gly Ala Ile	
176 181 186 191	
gct gct gcc ttg ctg atg ttt ggt gat gca ggt ggt ggg ccc agg aaa	863
Ala Ala Ala Leu Leu Met Phe Gly Asp Ala Gly Gly Gly Pro Arg Lys	
192 197 202 207	
aga aaa tta tct tct tct tca gag cca tat gag gaa gat gaa ttt aat	911
Arg Lys Leu Ser Ser Ser Ser Glu Pro Tyr Glu Glu Asp Glu Phe Asn	
208 213 218 223	
gat gat caa tct ata aaa aag aca aga ctg gat cat gga gag gaa tca	959
Asp Asp Gln Ser Ile Lys Lys Thr Arg Leu Asp His Gly Glu Glu Ser	
224 229 234 239	
aat gag tct gca gaa tct agc agt aat tgg gaa aag cag gaa agt att	1007
Asn Glu Ser Ala Glu Ser Ser Ser Asn Trp Glu Lys Gln Glu Ser Ile	
240 245 250 255	
gta ctg aaa ttg caa aag gaa ttt ccc aat ttt gat aaa cag gaa ctt	1055
Val Leu Lys Leu Gln Lys Glu Phe Pro Asn Phe Asp Lys Gln Glu Leu	
256 261 266 271	
aga gaa gta ctc aag gaa cat gaa tgg atg tac aca gaa gct tta gaa	1103
Arg Glu Val Leu Lys Glu His Glu Trp Met Tyr Thr Glu Ala Leu Glu	
272 277 282 287	
tct cta aaa gtg ttt gca gaa gac caa gat atg caa tat gca tca caa	1151
Ser Leu Lys Val Phe Ala Glu Asp Gln Asp Met Gln Tyr Ala Ser Gln	
288 293 298 303	
agt gag gtt cca aat gga aaa gaa gtt tct tca aga agt caa aat tac	1199
Ser Glu Val Pro Asn Gly Lys Glu Val Ser Ser Arg Ser Gln Asn Tyr	
304 309 314 319	

cct Pro 320	aaa Lys 320	aat Asn 320	gca Ala 320	act Thr 320	aaa Lys 325	aca Thr 325	aaa Lys 325	cta Leu 325	aaa Lys 325	cag Gln 330	aaa Lys 330	ttt Phe 330	tca Ser 330	atg Met 330	aaa Lys 335	1247
gca Ala 336	caa Gln 336	aat Asn 336	ggc Gly 336	ttt Phe 341	aac Asn 341	aaa Lys 341	aaa Lys 341	aaa Lys 341	aaa Lys 346	aaa Lys 346	aat Asn 346	gtt Val 346	ttt Phe 346	aat Asn 351	cca Pro 351	1295
aag Lys 352	aga Arg 352	gtt Val 352	gtt Val 352	gaa Glu 357	gac Asp 357	tct Ser 357	gaa Glu 357	tat Tyr 357	gat Asp 362	tca Ser 362	ggg Gly 362	tct Ser 362	gat Asp 362	gtc Val 367	ggg Gly 367	1343
agt Ser 368	tca Ser 368	cta Leu 368	gat Asp 368	gag Glu 373	gac Asp 373	tat Tyr 373	agt Ser 373	agt Ser 373	ggg Gly 378	gaa Glu 378	gaa Glu 378	gtg Val 378	atg Met 378	gag Glu 383	gat Asp 383	1391
ggc Gly 384	tat Tyr 384	aaa Lys 384	ggg Gly 384	aaa Lys 389	att Ile 389	ctt Leu 389	cac His 389	ttc Phe 389	ctt Leu 394	caa Gln 394	gat Asp 394	gct Ala 394	tca Ser 394	att Ile 399	ggg Gly 399	1439
gaa Glu 400	ctt Leu 400	act Thr 400	ttg Leu 400	att Ile 405	cct Pro 405	cag Gln 405	tgt Cys 405	tct Ser 405	cag Gln 410	aaa Lys 410	aag Lys 410	gct Ala 410	cag Gln 410	aag Lys 415	ata Ile 415	1487
aca Thr 416	gaa Glu 416	ctc Leu 416	cgg Arg 416	ccc Pro 421	ttt Phe 421	aat Asn 421	agt Ser 421	tgg Trp 421	gag Glu 426	gct Ala 426	ctg Leu 426	ttc Phe 426	aca Thr 426	aag Lys 431	atg Met 431	1535
tcc Ser 432	aaa Lys 432	act Thr 432	aat Asn 432	ggc Gly 437	tta Leu 437	tca Ser 437	gaa Glu 437	gat Asp 437	ttg Leu 442	ata Ile 442	tgg Trp 442	cac His 442	tgt Cys 442	aaa Lys 447	aca Thr 447	1583
ctg Leu 448	atc Ile 448	caa Gln 448	gaa Glu 448	aga Arg 453	gat Asp 453	gta Val 453	gtt Val 453	ata Ile 453	agg Arg 458	ctt Leu 458	atg Met 458	aac Asn 458	aaa Lys 458	tgt Cys 463	gaa Glu 463	1631
gac Asp 464	att Ile 464	tca Ser 464	aat Asn 464	aaa Lys 469	ttg Leu 469	acc Thr 469	aaa Lys 469	caa Gln 469	gtt Val 474	acc Thr 474	atg Met 474	ctt Leu 474	act Thr 474	gga Gly 479	aat Asn 479	1679
gga Gly 480	ggg Gly 480	gga Gly 480	tgg Trp 480	aac Asn 485	ata Ile 485	gaa Glu 485	caa Gln 485	cct Pro 485	tcc Ser 490	att Ile 490	cta Leu 490	aac Asn 490	caa Gln 490	agt Ser 495	ttg Leu 495	1727
tca Ser 496	ctc Leu 496	aag Lys 496	ccc Pro 496	tat Tyr 501	cag Gln 501	aag Lys 501	gtt Val 501	ggg Gly 501	ttg Leu 506	aat Asn 506	tgg Trp 506	ctg Leu 506	gca Ala 506	ttg Leu 511	gta Val 511	1775
cat His 512	aaa Lys 512	cat His 512	gga Gly 512	ctt Leu 517	aat Asn 517	ggc Gly 517	att Ile 517	ttg Leu 517	gca Ala 522	gat Asp 522	gaa Glu 522	atg Met 522	ggc Gly 522	cta Leu 527	gga Gly 527	1823
aaa Lys 528	act Thr 528	att Ile 528	caa Gln 528	gcc Ala 533	att Ile 533	gca Ala 533	ttt Phe 533	ctg Leu 533	gca Ala 538	tac Tyr 538	ctc Leu 538	tat Tyr 538	cag Gln 538	gag Glu 543	ggg Gly 543	1871
aat 320	aat 320	ggg 320	cct 320	cat 320	ttg 320	atc 320	gtt 320	gtt 320	cca 320	gct 320	tca 320	act 320	ata 320	gat 320	aac 320	1919

Asn 544	Asn	Gly	Pro	His	Leu 549	Ile	Val	Val	Pro	Ala 554	Ser	Thr	Ile	Asp	Asn 559	
tgg tta agg gaa gtt aat tta tgg tgc cct act ttg aag gtc ctc tgt																1967
Trp 560	Leu	Arg	Glu	Val	Asn 565	Leu	Trp	Cys	Pro	Thr 570	Leu	Lys	Val	Leu	Cys 575	
tac tat ggt tct caa gaa gaa cgt aaa caa att aga ttt aac att cat																2015
Tyr 576	Tyr	Gly	Ser	Gln	Glu 581	Glu	Arg	Lys	Gln	Ile 586	Arg	Phe	Asn	Ile	His 591	
agt aga tat gaa gat tac aat gta att gtg acc aca tat aac tgt gcg																2063
Ser 592	Arg	Tyr	Glu	Asp	Tyr 597	Asn	Val	Ile	Val	Thr 602	Thr	Tyr	Asn	Cys	Ala 607	
atc agc agt tct gat gat cgt agt ctg ttt cga cgg ctg aaa ctt aat																2111
Ile 608	Ser	Ser	Ser	Asp	Asp 613	Arg	Ser	Leu	Phe	Arg 618	Arg	Leu	Lys	Leu	Asn 623	
tac gca att ttt gat gag ggc cat atg ctg aag aat atg ggc tcc att																2159
Tyr 624	Ala	Ile	Phe	Asp	Glu 629	Gly	His	Met	Leu	Lys 634	Asn	Met	Gly	Ser	Ile 639	
cgc tac cag cac ctt atg aca att aat gca aat aac cgt ttg ctg ctc																2207
Arg 640	Tyr	Gln	His	Leu	Met 645	Thr	Ile	Asn	Ala	Asn 650	Asn	Arg	Leu	Leu	Leu 655	
aca ggc aca cct gta cag aac aat ctg tta gaa ctc atg tcg ctg ttg																2255
Thr 656	Gly	Thr	Pro	Val	Gln 661	Asn	Asn	Leu	Leu	Glu 666	Leu	Met	Ser	Leu	Leu 671	
aat ttt gtt atg cca cac atg ttt agt agt agc acc agt gaa ata cga																2303
Asn 672	Phe	Val	Met	Pro	His 677	Met	Phe	Ser	Ser	Ser 682	Thr	Ser	Glu	Ile	Arg 687	
aga atg ttt tcc tct aag aca aaa tca gca gat gag caa agc ata tat																2351
Arg 688	Met	Phe	Ser	Ser	Lys 693	Thr	Lys	Ser	Ala	Asp 698	Glu	Gln	Ser	Ile	Tyr 703	
gaa aag gag aga ata gca cat gca aaa caa att ata aag cca ttt att																2399
Glu 704	Lys	Glu	Arg	Ile	Ala 709	His	Ala	Lys	Gln	Ile 714	Ile	Lys	Pro	Phe	Ile 719	
ctc aga aga gta aaa gaa gag gtt ctc aag cag tta ccc ccc aag aaa																2447
Leu 720	Arg	Arg	Val	Lys	Glu 725	Glu	Val	Leu	Lys	Gln 730	Leu	Pro	Pro	Lys	Lys 735	
gat cga att gag ttg tgt gca atg tcg gag aag cag gag caa ctc tat																2495
Asp 736	Arg	Ile	Glu	Leu	Cys 741	Ala	Met	Ser	Glu	Lys 746	Gln	Glu	Gln	Leu	Tyr 751	
ttg ggt ctt ttc aac aga ttg aaa aaa tct atc aat aac ttg gtc aca																2543
Leu 752	Gly	Leu	Phe	Asn	Arg 757	Leu	Lys	Lys	Ser	Ile 762	Asn	Asn	Leu	Val	Thr 767	
gaa aaa aac aca gaa atg tgc aat gtc atg atg cag ttg agg aaa atg																2591
Glu	Lys	Asn	Thr	Glu	Met	Cys	Asn	Val	Met	Met	Gln	Leu	Arg	Lys	Met	

768		773		778		783	
gcc aat cat cct tta tta cat cgc caa tat tac aca gct gaa aaa ctc	2639						
Ala Asn His Pro Leu Leu His Arg Gln Tyr Tyr Thr Ala Glu Lys Leu							
784		789		794		799	
aag gaa atg tct cag ctt atg cta aag gaa cct aca cat tgt gag gct	2687						
Lys Glu Met Ser Gln Leu Met Leu Lys Glu Pro Thr His Cys Glu Ala							
800		805		810		815	
aac cct gac ctg atc ttt gaa gat atg gaa gtt atg aca gac ttc gaa	2735						
Asn Pro Asp Leu Ile Phe Glu Asp Met Glu Val Met Thr Asp Phe Glu							
816		821		826		831	
cta cat gta ctt tgt aaa cag tac cga cac att aat aac ttt cag tta	2783						
Leu His Val Leu Cys Lys Gln Tyr Arg His Ile Asn Asn Phe Gln Leu							
832		837		842		847	
gac atg gac ttg att tta gat tct gga aaa ttt cga gtt tta gga tgc	2831						
Asp Met Asp Leu Ile Leu Asp Ser Gly Lys Phe Arg Val Leu Gly Cys							
848		853		858		863	
atc ttg tct gaa ttg aaa cag aag ggt gat aga gtt gtg tta ttt agc	2879						
Ile Leu Ser Glu Leu Lys Gln Lys Gly Asp Arg Val Val Leu Phe Ser							
864		869		874		879	
caa ttt acc atg atg ctg gat atc tta gag gtt cta tta aaa cat cat	2927						
Gln Phe Thr Met Met Leu Asp Ile Leu Glu Val Leu Leu Lys His His							
880		885		890		895	
cag cat agg tac ctc aga tta gat gga aag act cag att tct gaa agg	2975						
Gln His Arg Tyr Leu Arg Leu Asp Gly Lys Thr Gln Ile Ser Glu Arg							
896		901		906		911	
att cat cta att gat gag ttt aat acc gat atg gat atc ttt gtg ttt	3023						
Ile His Leu Ile Asp Glu Phe Asn Thr Asp Met Asp Ile Phe Val Phe							
912		917		922		927	
ctg cta tca aca aaa gct ggt gga tta gga ata aat ctg act tca gca	3071						
Leu Leu Ser Thr Lys Ala Gly Gly Leu Gly Ile Asn Leu Thr Ser Ala							
928		933		938		943	
aat gtt gtt ata ctt cac gat att gac tgt aat cct tat aat gac aaa	3119						
Asn Val Val Ile Leu His Asp Ile Asp Cys Asn Pro Tyr Asn Asp Lys							
944		949		954		959	
caa gca gaa gat aga tgc cat aga gta ggc cag act aaa gaa gta cta	3167						
Gln Ala Glu Asp Arg Cys His Arg Val Gly Gln Thr Lys Glu Val Leu							
960		965		970		975	
gtt ata aaa cta ata agc caa ggg acg att gaa gaa tcc atg cta aaa	3215						
Val Ile Lys Leu Ile Ser Gln Gly Thr Ile Glu Glu Ser Met Leu Lys							
976		981		986		991	
att aac caa cag aaa ttg aaa cta gaa cag gat atg act aca gta gat	3263						
Ile Asn Gln Gln Lys Leu Lys Leu Glu Gln Asp Met Thr Thr Val Asp							
992		997		1002		1007	

gaa ggt gat gaa ggg agt atg cca gca gat ata gcc aca tta cta aaa 3311
 Glu Gly Asp Glu Gly Ser Met Pro Ala Asp Ile Ala Thr Leu Leu Lys
 1008 1013 1018 1023

aca tca atg ggc ctg tga aataag aactgtgaac tctcaattga tgaggaaata 3365
 Thr Ser Met Gly Leu *
 1024 1029

tcaacttggg gcactcaagg acatttacat tatgatgacc atgggggttta tgaacattta 3425

taacttttta taatttccat attacatttc tcatagtatg gacaactttt tgccactaac 3485

tgaattctcc aaatactcac acgtgaaatt tcaaaaaaga agccacaaat atgtagttct 3545

gaagatgttg aataatcatt ttacaaagca gttttctgaa tggggattag ttggtgattg 3605

tttgtaacaa atatgctaata gcttttagaaa tgtcagtatt tttgtaatta tttctacctc 3665

caaatatata tatattgtct ttcactggat aatgtgtgta gattttttaca tgtgccttat 3725

ttgacaatgc ttatgtcttg tttttgcttg tctcatttga agttcttttt tattatgtta 3785

aagaatgcag ctgtatagat tatatagctt tcattttatt gctatttgaa gcagatgttc 3845

accaatgtca gcaagaactc aacctgaatt taaagggtggc attccatata ctaacatccc 3905

ccaggtcctc tcaagtactt ctgctgaaac aaatttatct ggctaggcac taagttgttt 3965

tccagtgaat agtaactaaa gaagccccta ccttgctcca tggattaagc ccttccgttc 4025

attttccaac tggcctaattg gggcctatta ctcttgctaa tctgtgcat c 4076

<210> 9
 <211> 912
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (9) .. (908)

<400> 9
 ccactcgc atg cag cta ccg ctc cgg aat tcc cgg gtc gac ggt ttc gtc 50
 Met Gln Leu Pro Leu Arg Asn Ser Arg Val Asp Gly Phe Val
 1 5 10

tcg aac ttg gtc ggg gcg cgg atc ccg aga ggg aaa gtc ata aca acc 98
 Ser Asn Leu Val Gly Ala Arg Ile Pro Arg Gly Lys Val Ile Thr Thr
 15 20 25 30

gca cga ggg agt tcg act ggc gaa ctg gaa ggc cac gcc tcc tcc cgc 146
 Ala Arg Gly Ser Ser Thr Gly Glu Leu Glu Gly His Ala Ser Ser Arg
 31 36 41 46

ctg ccc cct cag ccc tgt ggc tgg ggg cag agc tca gac tta tta tct	194
Leu Pro Pro Gln Pro Cys Gly Trp Gly Gln Ser Ser Asp Leu Leu Ser	
47 52 57 62	
agg ata gat ttg gat gaa cta atg aaa aaa gat gaa ccg cct ctt gat	242
Arg Ile Asp Leu Asp Glu Leu Met Lys Lys Asp Glu Pro Pro Leu Asp	
63 68 73 78	
ttt cct gat acc ctg gaa gga ttt gaa tat gct ttt aat gaa aag gga	290
Phe Pro Asp Thr Leu Glu Gly Phe Glu Tyr Ala Phe Asn Glu Lys Gly	
79 84 89 94	
cag tta aga cac ata aaa act ggg gaa cca ttt gtt ttt aac tac cgg	338
Gln Leu Arg His Ile Lys Thr Gly Glu Pro Phe Val Phe Asn Tyr Arg	
95 100 105 110	
gaa gat tta cac aga tgg aac cag aaa aga tac gag gct cta gga gag	386
Glu Asp Leu His Arg Trp Asn Gln Lys Arg Tyr Glu Ala Leu Gly Glu	
111 116 121 126	
atc atc acg aag tat gta tat gag ctc ctg gaa aag gat tgt aat ttg	434
Ile Ile Thr Lys Tyr Val Tyr Glu Leu Leu Glu Lys Asp Cys Asn Leu	
127 132 137 142	
aaa aaa gta tct att cca gta gat gcc act gag agt gaa cca aag agt	482
Lys Lys Val Ser Ile Pro Val Asp Ala Thr Glu Ser Glu Pro Lys Ser	
143 148 153 158	
ttt atc ttt atg agt gag gat gct ttg aca aat cca cag aaa ctg atg	530
Phe Ile Phe Met Ser Glu Asp Ala Leu Thr Asn Pro Gln Lys Leu Met	
159 164 169 174	
gtt tta att cat ggt agt ggt gtt gtc agg gca ggg cag tgg gct aga	578
Val Leu Ile His Gly Ser Gly Val Val Arg Ala Gly Gln Trp Ala Arg	
175 180 185 190	
aga ctt att ata aat gaa gat ctg gac agt ggc aca cag ata ccg ttt	626
Arg Leu Ile Ile Asn Glu Asp Leu Asp Ser Gly Thr Gln Ile Pro Phe	
191 196 201 206	
att aaa aga gct gtg gct gaa gga tat gga gta ata gta cta aat ccc	674
Ile Lys Arg Ala Val Ala Glu Gly Tyr Gly Val Ile Val Leu Asn Pro	
207 212 217 222	
aat gaa aac tat att gaa gta gaa aag ccg aag ata cac gta cag tca	722
Asn Glu Asn Tyr Ile Glu Val Glu Lys Pro Lys Ile His Val Gln Ser	
223 228 233 238	
tca tct gat agt tca gat gaa cca gca gaa aaa ccg gaa aga aaa gat	770
Ser Ser Asp Ser Ser Asp Glu Pro Ala Glu Lys Arg Glu Arg Lys Asp	
239 244 249 254	
aaa gtt tct aaa gaa aca aag aag cga cgt gat ttc tat gag aag tat	818
Lys Val Ser Lys Glu Thr Lys Lys Arg Arg Asp Phe Tyr Glu Lys Tyr	
255 260 265 270	

cgt aac aac aaa aaa aaa aaa aaa aca cag aag ggg ggc cag gta 866
 Arg Asn Asn Lys Lys Lys Lys Lys Lys Thr Gln Lys Gly Gly Gln Val
 271 276 281 286

caa caa tac aac ctg ata atg agt cat aat aca att cac tag acca 912
 Gln Gln Tyr Asn Leu Ile Met Ser His Asn Thr Ile His *
 287 292 297

<210> 10
 <211> 3835
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (14)..(3175)

<400> 10
 gagagaagat aga atg gct ctt gac aat tta ttg gca aac cta ccc ccg 49
 Met Ala Leu Asp Asn Leu Leu Ala Asn Leu Pro Pro
 1 5 10

gcc aag cca gga aaa agt agc agt tta gaa atg act ccc tac aat aca 97
 Ala Lys Pro Gly Lys Ser Ser Ser Leu Glu Met Thr Pro Tyr Asn Thr
 13 18 23 28

cct cag cta tct cca gca acc act cca gca aat aaa aag aat cga tta 145
 Pro Gln Leu Ser Pro Ala Thr Thr Pro Ala Asn Lys Lys Asn Arg Leu
 29 34 39 44

cct ata gca act cgg agc aga agc cgc acc aat atg cta atg gac cta 193
 Pro Ile Ala Thr Arg Ser Arg Ser Arg Thr Asn Met Leu Met Asp Leu
 45 50 55 60

cat atg gac cat gaa gga tca tct caa gaa acc atc cag gag gtg caa 241
 His Met Asp His Glu Gly Ser Ser Gln Glu Thr Ile Gln Glu Val Gln
 61 66 71 76

cca gaa gag gtg ttg gtc att tcc tta ggt aca ggt ccc cag ctt act 289
 Pro Glu Glu Val Leu Val Ile Ser Leu Gly Thr Gly Pro Gln Leu Thr
 77 82 87 92

cca ggg atg atg tca gaa aat gag gtc cta aac atg cag ctt tcg gat 337
 Pro Gly Met Met Ser Glu Asn Glu Val Leu Asn Met Gln Leu Ser Asp
 93 98 103 108

gga gga caa gga gat gtc cct gtt gat gaa aac aaa ctc cat ggt aaa 385
 Gly Gly Gln Gly Asp Val Pro Val Asp Glu Asn Lys Leu His Gly Lys
 109 114 119 124

cct gat aaa acc ttg cgc ttt tcc ctc tgc agt gat aat ctg gaa gga 433
 Pro Asp Lys Thr Leu Arg Phe Ser Leu Cys Ser Asp Asn Leu Glu Gly
 125 130 135 140

ata tct gaa ggt cct tca aat cgc tcc aat tca gtg tcc tcc cta gac	481
Ile Ser Glu Gly Pro Ser Asn Arg Ser Asn Ser Val Ser Ser Leu Asp	
141 146 151 156	
cta gaa gga gag tct gtg tca gaa ctt gga gca gga cct tct ggc agt	529
Leu Glu Gly Glu Ser Val Ser Glu Leu Gly Ala Gly Pro Ser Gly Ser	
157 162 167 172	
aat gga gtt gaa gct cta cag ctg tta gaa cat gag caa gct aca aca	577
Asn Gly Val Glu Ala Leu Gln Leu Leu Glu His Glu Gln Ala Thr Thr	
173 178 183 188	
cag gat aac ctt gat gat aag cta agg aag ttt gaa att cgt gac atg	625
Gln Asp Asn Leu Asp Asp Lys Leu Arg Lys Phe Glu Ile Arg Asp Met	
189 194 199 204	
atg gga tta aca gat gat agg gac ata tca gaa aca gtg agt gag acc	673
Met Gly Leu Thr Asp Asp Arg Asp Ile Ser Glu Thr Val Ser Glu Thr	
205 210 215 220	
tgg agt aca gac gtc ttg gga agt gac ttt gac cct aat att gat gaa	721
Trp Ser Thr Asp Val Leu Gly Ser Asp Phe Asp Pro Asn Ile Asp Glu	
221 226 231 236	
gat cgc ttg caa gaa att gca ggt gct gca gca gag aac atg tta ggc	769
Asp Arg Leu Gln Glu Ile Ala Gly Ala Ala Ala Glu Asn Met Leu Gly	
237 242 247 252	
agt ttg ctg tgc ctc cca ggt tca ggg tca gtg ctt ctt gac ccc tgc	817
Ser Leu Leu Cys Leu Pro Gly Ser Gly Ser Val Leu Leu Asp Pro Cys	
253 258 263 268	
act ggt tct acc ata tca gag aca aca agt gaa gct tgg agt gta gag	865
Thr Gly Ser Thr Ile Ser Glu Thr Thr Ser Glu Ala Trp Ser Val Glu	
269 274 279 284	
gta ttg cca agt gac tca gag gcc cca gac cta aag cag gag gag cgt	913
Val Leu Pro Ser Asp Ser Glu Ala Pro Asp Leu Lys Gln Glu Glu Arg	
285 290 295 300	
ctg caa gaa ctg gag agc tgt tct gga ctg ggt agc aca tct gat gat	961
Leu Gln Glu Leu Glu Ser Cys Ser Gly Leu Gly Ser Thr Ser Asp Asp	
301 306 311 316	
acg gat gtc agg gag gtc agt tcc cgc ccc agc aca cca ggc ctc agt	1009
Thr Asp Val Arg Glu Val Ser Ser Arg Pro Ser Thr Pro Gly Leu Ser	
317 322 327 332	
gtt gtg tcc ggc ata agt gca acc tct gag gat att ccc aat aag att	1057
Val Val Ser Gly Ile Ser Ala Thr Ser Glu Asp Ile Pro Asn Lys Ile	
333 338 343 348	
gaa gac ctg aga tct gag tgc agc tct gat ttt ggg ggt aaa gat tct	1105
Glu Asp Leu Arg Ser Glu Cys Ser Ser Asp Phe Gly Gly Lys Asp Ser	
349 354 359 364	

gtc act agt cca gac atg gat gaa ata act cac gat ttt ctt tat ata Val Thr Ser Pro Asp Met Asp Glu Ile Thr His Asp Phe Leu Tyr Ile 365 370 375 380	1153
ctt cag cca aaa caa cat ttt caa cac att gaa gca gaa gca gac atg Leu Gln Pro Lys Gln His Phe Gln His Ile Glu Ala Glu Ala Asp Met 381 386 391 396	1201
aga atc cag ctg tct tct agt gcc cac cag ctg acc tct cct cct tct Arg Ile Gln Leu Ser Ser Ser Ala His Gln Leu Thr Ser Pro Pro Ser 397 402 407 412	1249
cag tca gag tct ctg ctg gcc atg ttt gat cca ctg tct tca cat gaa Gln Ser Glu Ser Leu Leu Ala Met Phe Asp Pro Leu Ser Ser His Glu 413 418 423 428	1297
ggg gct tct gct gtg gta agg cca aag gtt cac tat gct agg cca tcg Gly Ala Ser Ala Val Val Arg Pro Lys Val His Tyr Ala Arg Pro Ser 429 434 439 444	1345
cat cca cca cca gat ccc cca atc ctg gaa gga gct gtg gga gga aat His Pro Pro Pro Asp Pro Pro Ile Leu Glu Gly Ala Val Gly Gly Asn 445 450 455 460	1393
gag gcc agg ttg cca aac ttt ggt tcc cat gtt tta act cca gct gaa Glu Ala Arg Leu Pro Asn Phe Gly Ser His Val Leu Thr Pro Ala Glu 461 466 471 476	1441
atg gag gca ttc aag caa agg cat tct tac cct gag aga cta gtt cga Met Glu Ala Phe Lys Gln Arg His Ser Tyr Pro Glu Arg Leu Val Arg 477 482 487 492	1489
agc agg agc tct gat ata gta tct tct gtc cgg aga ccc atg agt gac Ser Arg Ser Ser Asp Ile Val Ser Ser Val Arg Arg Pro Met Ser Asp 493 498 503 508	1537
ccc agc tgg aac cgg cgt cca gga aat gaa gag cga gaa ctc cct cca Pro Ser Trp Asn Arg Arg Pro Gly Asn Glu Glu Arg Glu Leu Pro Pro 509 514 519 524	1585
gct gca gcc att ggt gct act tct ttg gtg gct gca cct cat tca tca Ala Ala Ala Ile Gly Ala Thr Ser Leu Val Ala Ala Pro His Ser Ser 525 530 535 540	1633
tct tca tcc ccg agt aag gac tcc tca aga gga gag act gaa gaa cgc Ser Ser Ser Pro Ser Lys Asp Ser Ser Arg Gly Glu Thr Glu Glu Arg 541 546 551 556	1681
aaa gat agc gat gat gag aaa tca gac agg aac aga cct tgg tgg aga Lys Asp Ser Asp Asp Glu Lys Ser Asp Arg Asn Arg Pro Trp Trp Arg 557 562 567 572	1729
aaa cgt ttt gtt tca gcc atg cct aaa gct cct ata cca ttt aga aag Lys Arg Phe Val Ser Ala Met Pro Lys Ala Pro Ile Pro Phe Arg Lys 573 578 583 588	1777
aaa gaa aaa caa gaa aaa gac aaa gat gat ctg ggg cct gac aga ttc	1825

Lys Glu Lys Gln Glu Lys Asp Lys Asp Asp Leu Gly Pro Asp Arg Phe 589 594 599 604	
tca aca ctc aca gat gat ccc agc cct aga ctc agt gca caa gct cag Ser Thr Leu Thr Asp Asp Pro Ser Pro Arg Leu Ser Ala Gln Ala Gln 605 610 615 620	1873
gtg gct gag gat att ctg gac aaa tac agg aat gcc att aaa cgg acc Val Ala Glu Asp Ile Leu Asp Lys Tyr Arg Asn Ala Ile Lys Arg Thr 621 626 631 636	1921
agc ccc agt gat gga gca atg gca aac tat gaa agt aca gag gtt atg Ser Pro Ser Asp Gly Ala Met Ala Asn Tyr Glu Ser Thr Glu Val Met 637 642 647 652	1969
ggc gat ggt gaa agt gca cat gat tct ccc cgt gac gaa gca ctg cag Gly Asp Gly Glu Ser Ala His Asp Ser Pro Arg Asp Glu Ala Leu Gln 653 658 663 668	2017
aac atc tcg gct gat gat ctc cca gac tct gca agc caa gca gcc cac Asn Ile Ser Ala Asp Asp Leu Pro Asp Ser Ala Ser Gln Ala Ala His 669 674 679 684	2065
cgc cag gat tca gct ttc tct tac aga gat gca aaa aag aaa ctg agg Pro Gln Asp Ser Ala Phe Ser Tyr Arg Asp Ala Lys Lys Lys Leu Arg 685 690 695 700	2113
ctt gct ctt tgc tct gcg gac tct gtt gcc ttc cca gtg ctg acc cat Leu Ala Leu Cys Ser Ala Asp Ser Val Ala Phe Pro Val Leu Thr His 701 706 711 716	2161
tca aca agg aat ggt tta cca gac cac aca gac cca gaa gac aat gaa Ser Thr Arg Asn Gly Leu Pro Asp His Thr Asp Pro Glu Asp Asn Glu 717 722 727 732	2209
att gta tgc ttc tta aaa gtt caa ata gct gaa gca att aat tta caa Ile Val Cys Phe Leu Lys Val Gln Ile Ala Glu Ala Ile Asn Leu Gln 733 738 743 748	2257
gat aag aat cta atg gct caa ctt caa gaa aca atg cgc tgt gtg tgc Asp Lys Asn Leu Met Ala Gln Leu Gln Glu Thr Met Arg Cys Val Cys 749 754 759 764	2305
cgt ttt gat aat agg act tgt agg aaa ctg ctg gct tcg att gct gag Arg Phe Asp Asn Arg Thr Cys Arg Lys Leu Leu Ala Ser Ile Ala Glu 765 770 775 780	2353
gac tac aga aaa aga gcc cca tat att gct tat ctc act cgt tgt cga Asp Tyr Arg Lys Arg Ala Pro Tyr Ile Ala Tyr Leu Thr Arg Cys Arg 781 786 791 796	2401
caa gga cta cag acc aca cag gct cac ctg gaa agg cta ttg caa aga Gln Gly Leu Gln Thr Thr Gln Ala His Leu Glu Arg Leu Leu Gln Arg 797 802 807 812	2449
gtt ttg cgg gac aaa gaa gtg gcc aat cga tac ttt acc act gtc tgt Val Leu Arg Asp Lys Glu Val Ala Asn Arg Tyr Phe Thr Thr Val Cys 813 818 823 828	2497

aag tga ccaagaccaa ggcccaccaa ggcagcagac tgttaatcag acaaacagat 3225
 Lys *
 1053

ctctgagaag gtgcatcagc tgctttgaag gctgaagatt gttttgtatg atactgcaca 3285
 gcatcaggca ttttaaagca gatctttact aaacagggtta atgagctaac aagcagggtc 3345
 tctcgtcttt gggctctttc ctttctgagt tgcataattct attttcttgt cccaagtag 3405
 agactagtac tacaaaaagg gaccacattt ttcaagtatt tctaagtata aaaaacaaaa 3465
 caaaaatctc ttaggaaatg tctagacctc cattcttgga ttccctttct ttccttttat 3525
 tttaaaaaag aacagtaccc ctcttttaag atgctgtctt acattaatga gcatctaatt 3585
 gaaagaaggt atgagttgca ctgaggatta gaatagtggg gcgttagtgg cattatctat 3645
 aaatacactc acctaaattg aaagctaaga aggaaatgta aatataatat atatttatat 3705
 ttgatgtaat atggacatct gcagattcta ataaacaagg actattgctg atagtaggct 3765
 gtgacatact gtcttgtgaa atggtttcct tgacaaaatt taagctgagc ttaaaagcaa 3825
 aaaaaaaaaa 3835

<210> 11
 <211> 3754
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (14) .. (3094)

<400> 11
 gagagaagat aga atg gct ctt gac aat tta ttg gca aac cta ccc ccg 49
 Met Ala Leu Asp Asn Leu Leu Ala Asn Leu Pro Pro
 1 5 10
 gcc aag cca gga aaa agt agc agt tta gaa atg act ccc tac aat aca 97
 Ala Lys Pro Gly Lys Ser Ser Ser Leu Glu Met Thr Pro Tyr Asn Thr
 13 18 23 28
 cct cag cta tct cca gca acc act cca gca aat aaa aag aat cga tta 145
 Pro Gln Leu Ser Pro Ala Thr Thr Pro Ala Asn Lys Lys Asn Arg Leu
 29 34 39 44
 cct ata gca act cgg agc aga agc cgc acc aat atg cta atg gac cta 193
 Pro Ile Ala Thr Arg Ser Arg Ser Arg Thr Asn Met Leu Met Asp Leu
 45 50 55 60
 cat atg gac cat gaa gga tca tct caa gaa acc atc cag gag gtg caa 241

His	Met	Asp	His	Glu	Gly	Ser	Ser	Gln	Glu	Thr	Ile	Gln	Glu	Val	Gln	
61					66					71					76	
cca	gaa	gag	gtg	ttg	gtc	att	tcc	tta	ggg	aca	ggg	ccc	cag	ctt	act	289
Pro	Glu	Glu	Val	Leu	Val	Ile	Ser	Leu	Gly	Thr	Gly	Pro	Gln	Leu	Thr	
77					82					87					92	
cca	ggg	atg	atg	tca	gaa	aat	gag	gtc	cta	aac	atg	cag	ctt	tcg	gat	337
Pro	Gly	Met	Met	Ser	Glu	Asn	Glu	Val	Leu	Asn	Met	Gln	Leu	Ser	Asp	
93					98					103					108	
gga	gga	caa	gga	gat	gtc	cct	gtt	gat	gaa	aac	aaa	ctc	cat	ggg	aaa	385
Gly	Gly	Gln	Gly	Asp	Val	Pro	Val	Asp	Glu	Asn	Lys	Leu	His	Gly	Lys	
109					114					119					124	
cct	gat	aaa	acc	ttg	cgc	ttt	tcc	ctc	tgc	agt	gat	aat	ctg	gaa	gga	433
Pro	Asp	Lys	Thr	Leu	Arg	Phe	Ser	Leu	Cys	Ser	Asp	Asn	Leu	Glu	Gly	
125					130					135					140	
ata	tct	gaa	ggg	cct	tca	aat	cgc	tcc	aat	tca	gtg	tcc	tcc	cta	gac	481
Ile	Ser	Glu	Gly	Pro	Ser	Asn	Arg	Ser	Asn	Ser	Val	Ser	Ser	Leu	Asp	
141					146					151					156	
cta	gaa	gga	gag	tct	gtg	tca	gaa	ctt	gga	gca	gga	cct	tct	ggc	agt	529
Leu	Glu	Gly	Glu	Ser	Val	Ser	Glu	Leu	Gly	Ala	Gly	Pro	Ser	Gly	Ser	
157					162					167					172	
aat	gga	gtt	gaa	gct	cta	cag	ctg	tta	gaa	cat	gag	caa	gct	aca	aca	577
Asn	Gly	Val	Glu	Ala	Leu	Gln	Leu	Leu	Glu	His	Glu	Gln	Ala	Thr	Thr	
173					178					183					188	
cag	gat	aac	ctt	gat	gat	aag	cta	agg	aag	ttt	gaa	att	cgt	gac	atg	625
Gln	Asp	Asn	Leu	Asp	Asp	Lys	Leu	Arg	Lys	Phe	Glu	Ile	Arg	Asp	Met	
189					194					199					204	
atg	gga	tta	aca	gat	gat	agg	gac	ata	tca	gaa	aca	gtg	agt	gag	acc	673
Met	Gly	Leu	Thr	Asp	Asp	Arg	Asp	Ile	Ser	Glu	Thr	Val	Ser	Glu	Thr	
205					210					215					220	
tgg	agt	aca	gac	gtc	ttg	gga	agt	gac	ttt	gac	cct	aat	att	gat	gaa	721
Trp	Ser	Thr	Asp	Val	Leu	Gly	Ser	Asp	Phe	Asp	Pro	Asn	Ile	Asp	Glu	
221					226					231					236	
gat	cgc	ttg	caa	gaa	att	gca	ggg	gct	gca	gca	gag	aac	atg	tta	ggc	769
Asp	Arg	Leu	Gln	Glu	Ile	Ala	Gly	Ala	Ala	Ala	Glu	Asn	Met	Leu	Gly	
237					242					247					252	
agt	ttg	ctg	tgc	ctc	cca	ggg	tca	ggg	tca	gtg	ctt	ctt	gac	ccc	tgc	817
Ser	Leu	Leu	Cys	Leu	Pro	Gly	Ser	Gly	Ser	Val	Leu	Leu	Asp	Pro	Cys	
253					258					263					268	
act	ggg	tct	acc	ata	tca	gag	aca	aca	agt	gaa	gct	tgg	agt	gta	gag	865
Thr	Gly	Ser	Thr	Ile	Ser	Glu	Thr	Thr	Ser	Glu	Ala	Trp	Ser	Val	Glu	
269					274					279					284	
gta	ttg	cca	agt	gac	tca	gag	gcc	cca	gac	cta	aag	cag	gag	gag	cgt	913
Val	Leu	Pro	Ser	Asp	Ser	Glu	Ala	Pro	Asp	Leu	Lys	Gln	Glu	Glu	Arg	

285		290		295		300	
ctg caa gaa ctg gag agc tgt tct gga ctg ggt agc aca tct gat gat	961						
Leu Gln Glu Leu Glu Ser Cys Ser Gly Leu Gly Ser Thr Ser Asp Asp							
301		306		311		316	
acg gat gtc agg gag gtc agt tcc cgc ccc agc aca cca ggc ctc agt	1009						
Thr Asp Val Arg Glu Val Ser Ser Arg Pro Ser Thr Pro Gly Leu Ser							
317		322		327		332	
gtt gtg tcc ggc ata agt gca acc tct gag gat att ccc aat aag att	1057						
Val Val Ser Gly Ile Ser Ala Thr Ser Glu Asp Ile Pro Asn Lys Ile							
333		338		343		348	
gaa gac ctg aga tct gag tgc agc tct gat ttt ggg ggt aaa gat tct	1105						
Glu Asp Leu Arg Ser Glu Cys Ser Ser Asp Phe Gly Gly Lys Asp Ser							
349		354		359		364	
gtc act agt cca gac atg gat gaa ata act cac ggt gcc cac cag ctg	1153						
Val Thr Ser Pro Asp Met Asp Glu Ile Thr His Gly Ala His Gln Leu							
365		370		375		380	
acc tct cct cct tct cag tca gag tct ctg ctg gcc atg ttt gat cca	1201						
Thr Ser Pro Pro Ser Gln Ser Glu Ser Leu Leu Ala Met Phe Asp Pro							
381		386		391		396	
ctg tct tca cat gaa ggg gct tct gct gtg gta agg cca aag gtt cac	1249						
Leu Ser Ser His Glu Gly Ala Ser Ala Val Val Arg Pro Lys Val His							
397		402		407		412	
tat gct agg cca tgc cat cca cca cca gat ccc cca atc ctg gaa gga	1297						
Tyr Ala Arg Pro Ser His Pro Pro Pro Asp Pro Pro Ile Leu Glu Gly							
413		418		423		428	
gct gtg gga gga aat gag gcc agg ttg cca aac ttt ggt tcc cat gtt	1345						
Ala Val Gly Gly Asn Glu Ala Arg Leu Pro Asn Phe Gly Ser His Val							
429		434		439		444	
tta act cca gct gaa atg gag gca ttc aag caa agg cat tct tac cct	1393						
Leu Thr Pro Ala Glu Met Glu Ala Phe Lys Gln Arg His Ser Tyr Pro							
445		450		455		460	
gag aga cta gtt cga agc agg agc tct gat ata gta tct tct gtc cgg	1441						
Glu Arg Leu Val Arg Ser Arg Ser Ser Asp Ile Val Ser Ser Val Arg							
461		466		471		476	
aga ccc atg agt gac ccc agc tgg aac cgg cgt cca gga aat gaa gag	1489						
Arg Pro Met Ser Asp Pro Ser Trp Asn Arg Arg Pro Gly Asn Glu Glu							
477		482		487		492	
cga gaa ctc cct cca gct gca gcc att ggt gct act tct ttg gtg gct	1537						
Arg Glu Leu Pro Pro Ala Ala Ala Ile Gly Ala Thr Ser Leu Val Ala							
493		498		503		508	
gca cct cat tca tca tct tca tcc ccg agt aag gac tcc tca aga gga	1585						
Ala Pro His Ser Ser Ser Ser Ser Pro Ser Lys Asp Ser Ser Arg Gly							
509		514		519		524	

gag Glu 525	act Thr	gaa Glu	gaa Glu	cgc Arg	aaa Lys 530	gat Asp	agc Ser	gat Asp	gat Asp	gag Glu 535	aaa Lys	tca Ser	gac Asp	agg Arg	aac Asn 540	1633
aga Arg 541	cct Pro	tgg Trp	tgg Trp	aga Arg	aaa Lys 546	cgt Arg	ttt Phe	gtt Val	tca Ser	gcc Ala 551	atg Met	cct Pro	aaa Lys	gct Ala	cct Pro 556	1681
ata Ile 557	cca Pro	ttt Phe	aga Arg	aag Lys	aaa Lys 562	gaa Glu	aaa Lys	caa Gln	gaa Glu	aaa Lys 567	gac Asp	aaa Lys	gat Asp	gat Asp	ctg Leu 572	1729
ggg Gly 573	cct Pro	gac Asp	aga Arg	ttc Phe	tca Ser 578	aca Thr	ctc Leu	aca Thr	gat Asp	gat Asp 583	ccc Pro	agc Ser	cct Pro	aga Arg	ctc Leu 588	1777
agt Ser 589	gca Ala	caa Gln	gct Ala	cag Gln	gtg Val 594	gct Ala	gag Glu	gat Asp	att Ile	ctg Leu 599	gac Asp	aaa Lys	tac Tyr	agg Arg	aat Asn 604	1825
gcc Ala 605	att Ile	aaa Lys	cgg Arg	acc Thr	agc Ser 610	ccc Pro	agt Ser	gat Asp	gga Gly	gca Ala 615	atg Met	gca Ala	aac Asn	tat Tyr	gaa Glu 620	1873
agt Ser 621	aca Thr	gag Glu	gtt Val	atg Met	ggc Gly 626	gat Asp	ggc Gly	gaa Glu	agt Ser	gca Ala 631	cat His	gat Asp	tct Ser	ccc Pro	cgt Arg 636	1921
gac Asp 637	gaa Glu	gca Ala	ctg Leu	cag Gln	aac Asn 642	atc Ile	tcg Ser	gct Ala	gat Asp	gat Asp 647	ctc Leu	cca Pro	gac Asp	tct Ser	gca Ala 652	1969
agc Ser 653	caa Gln	gca Ala	gcc Ala	cac His	ccg Pro 658	cag Gln	gat Asp	tca Ser	gct Ala	ttc Phe 663	tct Ser	tac Tyr	aga Arg	gat Asp	gca Ala 668	2017
aaa Lys 669	aag Lys	aaa Lys	ctg Leu	agg Arg	ctt Leu 674	gct Ala	ctt Leu	tgc Cys	tct Ser	gcg Ala 679	gac Asp	tct Ser	gtt Val	gcc Ala	ttc Phe 684	2065
cca Pro 685	gtg Val	ctg Leu	acc Thr	cat His	tca Ser 690	aca Thr	agg Arg	aat Asn	ggc Gly	tta Leu 695	cca Pro	gac Asp	cac His	aca Thr	gac Asp 700	2113
cca Pro 701	gaa Glu	gac Asp	aat Asn	gaa Glu	att Ile 706	gta Val	tgc Cys	ttc Phe	tta Leu	aaa Lys 711	gtt Val	caa Gln	ata Ile	gct Ala	gaa Glu 716	2161
gca Ala 717	att Ile	aat Asn	tta Leu	caa Gln	gat Asp 722	aag Lys	aat Asn	cta Leu	atg Met	gct Ala 727	caa Gln	ctt Leu	caa Gln	gaa Glu	aca Thr 732	2209
atg Met 733	cgc Arg	tgt Cys	gtg Val	tgc Cys	cgt Arg 738	ttt Phe	gat Asp	aat Asn	agg Arg	act Thr 743	tgt Cys	agg Arg	aaa Lys	ctg Leu	ctg Leu 748	2257

gct tcg att gct gag gac tac aga aaa aga gcc cca tat att gct tat Ala Ser Ile Ala Glu Asp Tyr Arg Lys Arg Ala Pro Tyr Ile Ala Tyr 749 754 759 764	2305
ctc act cgt tgt cga caa gga cta cag acc aca cag gct cac ctg gaa Leu Thr Arg Cys Arg Gln Gly Leu Gln Thr Thr Gln Ala His Leu Glu 765 770 775 780	2353
agg cta ttg caa aga gtt ttg cgg gac aaa gaa gtg gcc aat cga tac Arg Leu Leu Gln Arg Val Leu Arg Asp Lys Glu Val Ala Asn Arg Tyr 781 786 791 796	2401
ttt acc act gtc tgt gtg aga tta ctg ctt gag agc aaa gaa aag aag Phe Thr Thr Val Cys Val Arg Leu Leu Leu Glu Ser Lys Glu Lys Lys 797 802 807 812	2449
atc agg gaa ttc att caa gac ttt cag aaa ctc acc gca gct gac gat Ile Arg Glu Phe Ile Gln Asp Phe Gln Lys Leu Thr Ala Ala Asp Asp 813 818 823 828	2497
aaa act gct cag gta gaa gat ttt ctg cag ttt ctt tat ggt gca atg Lys Thr Ala Gln Val Glu Asp Phe Leu Gln Phe Leu Tyr Gly Ala Met 829 834 839 844	2545
gcc cag gat gtc ata tgg caa aac gcg agt gaa gaa cag ctt caa gat Ala Gln Asp Val Ile Trp Gln Asn Ala Ser Glu Glu Gln Leu Gln Asp 845 850 855 860	2593
gca cag ctg gcc att gag cga agc gtg atg aac cgg att ttc aag ctc Ala Gln Leu Ala Ile Glu Arg Ser Val Met Asn Arg Ile Phe Lys Leu 861 866 871 876	2641
gcc ttc tac cct aat caa gat ggg gac ata ctt cgc gac cag gtt ctt Ala Phe Tyr Pro Asn Gln Asp Gly Asp Ile Leu Arg Asp Gln Val Leu 877 882 887 892	2689
cat gaa cat atc cag aga ttg tct aaa gta gtg act gca aat cac aga His Glu His Ile Gln Arg Leu Ser Lys Val Val Thr Ala Asn His Arg 893 898 903 908	2737
gct ctt cag ata cca gag gtt tat ctt cga gaa gca cca tgg cca tct Ala Leu Gln Ile Pro Glu Val Tyr Leu Arg Glu Ala Pro Trp Pro Ser 909 914 919 924	2785
gca caa tca gaa atc agg aca ata agt gct tat aaa acc ccc cgg gac Ala Gln Ser Glu Ile Arg Thr Ile Ser Ala Tyr Lys Thr Pro Arg Asp 925 930 935 940	2833
aaa gtg cag tgc atc ctg aga atg tgc tct acg att atg aac ctc ctg Lys Val Gln Cys Ile Leu Arg Met Cys Ser Thr Ile Met Asn Leu Leu 941 946 951 956	2881
agc ctg gcc aat gag gac tct gtc cct gga gcg gat gac ttt gtt cct Ser Leu Ala Asn Glu Asp Ser Val Pro Gly Ala Asp Asp Phe Val Pro 957 962 967 972	2929
gtg ttg gtg ttt gtg ttg ata aag gca aat cca ccc tgt ttg ctg tct	2977

```

Val Leu Val Phe Val Leu Ile Lys Ala Asn Pro Pro Cys Leu Leu Ser
973                      978                      983                      988

act gtg cag tat atc agt agc ttt tat gct agc tgt ctg tct gga gag      3025
Thr Val Gln Tyr Ile Ser Ser Phe Tyr Ala Ser Cys Leu Ser Gly Glu
989                      994                      999                      1004

gag tcc tat tgg tgg atg cag ttc aca gca gca gta gaa ttc att aaa      3073
Glu Ser Tyr Trp Trp Met Gln Phe Thr Ala Ala Val Glu Phe Ile Lys
1005                      1010                      1015                      1020

acc atc gat gac cga aag tga cc aagaccaagg cccaccaagg cagcagactg      3126
Thr Ile Asp Asp Arg Lys *
1021                      1026

ttaatcagac aaacagatct ctgagaaggt gcatcagctg ctttgaaggc tgaagattgt      3186

tttgtatgat actgcacagc atcaggcatt ttaaagcaga tctttactaa acagggttaat      3246

gagctaacaa gcaggttctc tcgtctttgg gctctttcct ttctgagttg catattctat      3306

tttcttgtcc ccaagtagag actagtacta caaaaaggga ccacattttt caagtatttc      3366

taagtataaa aaacaaaaca aaaatctctt aggaaatgtc tagacctcca ttcttggatt      3426

ccctttcttt ccttttattt taaaaaagaa cagtaccctt cttttaagat gctgtcttac      3486

attaatgagc atctaattgga aagaaggat gagttgcact gaggattaga atagtgggtgc      3546

gttagtggca ttatctataa atacactcac ctaaattgaa agctaagaag gaaatgtaaa      3606

tataatatat atttatatat gatgtaatat ggacatctgc agattctaata aaacaaggac      3666

tattgctgat agtaggctgt gacatactgt cttgtgaaat ggtttccttg acaaaaattta      3726

agctgagctt aaaagcaaaa aaaaaaaa                                     3754

```

```

<210> 12
<211> 3754
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (14)..(3094)

```

```

<400> 12
gagagaagat aga      atg gct ctt gac aat tta ttg gca aac cta ccc ccg      49
                      Met Ala Leu Asp Asn Leu Leu Ala Asn Leu Pro Pro
                      1                      5                      10

gcc aag cca gga aaa agt agc agt tta gaa atg act ccc tac aat aca      97
Ala Lys Pro Gly Lys Ser Ser Ser Leu Glu Met Thr Pro Tyr Asn Thr
13                      18                      23                      28

```

cct cag cta tct cca gca acc act cca gca aat aaa aag aat cga tta	145
Pro Gln Leu Ser Pro Ala Thr Thr Pro Ala Asn Lys Lys Asn Arg Leu	
29 34 39 44	
cct ata gca act cgg agc aga agc cgc acc aat atg cta atg gac cta	193
Pro Ile Ala Thr Arg Ser Arg Ser Arg Thr Asn Met Leu Met Asp Leu	
45 50 55 60	
cat atg gac cat gaa gga tca tct caa gaa acc atc cag gag gtg caa	241
His Met Asp His Glu Gly Ser Ser Gln Glu Thr Ile Gln Glu Val Gln	
61 66 71 76	
cca gaa gag gtg ttg gtc att tcc tta ggt aca ggt ccc cag ctt act	289
Pro Glu Glu Val Leu Val Ile Ser Leu Gly Thr Gly Pro Gln Leu Thr	
77 82 87 92	
cca ggg atg atg tca gaa aat gag gtc cta aac atg cag ctt tcg gat	337
Pro Gly Met Met Ser Glu Asn Glu Val Leu Asn Met Gln Leu Ser Asp	
93 98 103 108	
gga gga caa gga gat gtc cct gtt gat gaa aac aaa ctc cat ggt aaa	385
Gly Gly Gln Gly Asp Val Pro Val Asp Glu Asn Lys Leu His Gly Lys	
109 114 119 124	
cct gat aaa acc ttg cgc ttt tcc ctc tgc agt gat aat ctg gaa gga	433
Pro Asp Lys Thr Leu Arg Phe Ser Leu Cys Ser Asp Asn Leu Glu Gly	
125 130 135 140	
ata tct gaa ggt cct tca aat cgc tcc aat tca gtg tcc tcc cta gac	481
Ile Ser Glu Gly Pro Ser Asn Arg Ser Asn Ser Val Ser Ser Leu Asp	
141 146 151 156	
cta gaa gga gag tct gtg tca gaa ctt gga gca gga cct tct ggc agt	529
Leu Glu Gly Glu Ser Val Ser Glu Leu Gly Ala Gly Pro Ser Gly Ser	
157 162 167 172	
aat gga gtt gaa gct cta cag ctg tta gaa cat gag caa gct aca aca	577
Asn Gly Val Glu Ala Leu Gln Leu Leu Glu His Glu Gln Ala Thr Thr	
173 178 183 188	
cag gat aac ctt gat gat aag cta agg aag ttt gaa att cgt gac atg	625
Gln Asp Asn Leu Asp Asp Lys Leu Arg Lys Phe Glu Ile Arg Asp Met	
189 194 199 204	
atg gga tta aca gat gat agg gac ata tca gaa aca gtg agt gag acc	673
Met Gly Leu Thr Asp Asp Arg Asp Ile Ser Glu Thr Val Ser Glu Thr	
205 210 215 220	
tgg agt aca gac gtc ttg gga agt gac ttt gac cct aat att gat gaa	721
Trp Ser Thr Asp Val Leu Gly Ser Asp Phe Asp Pro Asn Ile Asp Glu	
221 226 231 236	
gat cgc ttg caa gaa att gca ggt gct gca gca gag aac atg tta ggc	769
Asp Arg Leu Gln Glu Ile Ala Gly Ala Ala Ala Glu Asn Met Leu Gly	
237 242 247 252	

agt Ser 253	ttg Leu	ctg Leu	tgc Cys	ctc Leu	cca Pro 258	ggg Gly	tca Ser	ggg Gly	tca Ser	gtg Val 263	ctt Leu	ctt Leu	gac Asp	ccc Pro	tgc Cys 268	817
act Thr 269	ggg Gly	tct Ser	acc Thr	ata Ile	tca Ser 274	gag Glu	aca Thr	aca Thr	agt Ser	gaa Glu 279	gct Ala	tgg Trp	agt Ser	gta Val	gag Glu 284	865
gta Val 285	ttg Leu	cca Pro	agt Ser	gac Asp	tca Ser 290	gag Glu	gcc Ala	cca Pro	gac Asp	cta Leu 295	aag Lys	cag Gln	gag Glu	gag Glu	cgt Arg 300	913
ctg Leu 301	caa Gln	gaa Glu	ctg Leu	gag Glu	agc Ser 306	tgt Cys	tct Ser	gga Gly	ctg Leu	ggg Gly 311	agc Ser	aca Thr	tct Ser	gat Asp	gat Asp 316	961
acg Thr 317	gat Asp	gtc Val	agg Arg	gag Glu	gtc Val 322	agt Ser	tcc Ser	cgc Arg	ccc Pro	agc Ser 327	aca Thr	cca Pro	ggc Gly	ctc Leu	agt Ser 332	1009
gtt Val 333	gtg Val	tcc Ser	ggc Gly	ata Ile	agt Ser 338	gca Ala	acc Thr	tct Ser	gag Glu	gat Asp 343	att Ile	ccc Pro	aat Asn	aag Lys	att Ile 348	1057
gaa Glu 349	gac Asp	ctg Leu	aga Arg	tct Ser	gag Glu 354	tgc Cys	agc Ser	tct Ser	gat Asp	ttt Phe 359	ggg Gly	ggg Gly	aaa Lys	gat Asp	tct Ser 364	1105
gtc Val 365	act Thr	agt Ser	cca Pro	gac Asp	atg Met 370	gat Asp	gaa Glu	ata Ile	act Thr	cac His 375	gat Asp	ttt Phe	ctt Leu	tat Tyr	ata Ile 380	1153
ctt Leu 381	cag Gln	cca Pro	aaa Lys	caa Gln	cat His 386	ttt Phe	caa Gln	cac His	att Ile	gaa Glu 391	gca Ala	gaa Glu	gca Ala	gac Asp	atg Met 396	1201
aga Arg 397	atc Ile	cag Gln	ctg Leu	tct Ser	tct Ser 402	agt Ser	gcc Ala	cac His	cag Gln	ctg Leu 407	acc Thr	tct Ser	cct Pro	cct Pro	tct Ser 412	1249
cag Gln 413	tca Ser	gag Glu	tct Ser	ctg Leu	ctg Leu 418	gcc Ala	atg Met	ttt Phe	gat Asp	cca Pro 423	ctg Leu	tct Ser	tca Ser	cat His	gaa Glu 428	1297
ggg Gly 429	gct Ala	tct Ser	gct Ala	gtg Val	gta Val 434	agg Arg	cca Pro	aag Lys	gtt Val	cac His 439	tat Tyr	gct Ala	agg Arg	cca Pro	tgc Ser 444	1345
cat His 445	cca Pro	cca Pro	cca Pro	gat Asp	ccc Pro 450	cca Pro	atc Ile	ctg Leu	gaa Glu	gga Gly 455	gct Ala	gtg Val	gga Gly	gga Gly	aat Asn 460	1393
gag Glu 461	gcc Ala	agg Arg	ttg Leu	cca Pro	aac Asn 466	ttt Phe	ggg Gly	tcc Ser	cat His	gtt Val 471	tta Leu	act Thr	cca Pro	gct Ala	gaa Glu 476	1441
atg	gag	gca	ttc	aag	caa	agg	cat	tct	tac	cct	gag	aga	cta	gtt	cga	1489

Met	Glu	Ala	Phe	Lys	Gln	Arg	His	Ser	Tyr	Pro	Glu	Arg	Leu	Val	Arg	
477					482					487					492	
agc	agg	agc	tct	gat	ata	gta	tct	tct	gtc	cgg	aga	ccc	atg	agt	gac	1537
Ser	Arg	Ser	Ser	Asp	Ile	Val	Ser	Ser	Val	Arg	Arg	Pro	Met	Ser	Asp	
493					498					503					508	
ccc	agc	tgg	aac	cgg	cgt	cca	gga	aat	gaa	gag	cga	gaa	ctc	cct	cca	1585
Pro	Ser	Trp	Asn	Arg	Arg	Pro	Gly	Asn	Glu	Glu	Arg	Glu	Leu	Pro	Pro	
509					514					519					524	
gct	gca	gcc	att	ggc	gct	act	tct	ttg	gtg	gct	gca	cct	cat	tca	tca	1633
Ala	Ala	Ala	Ile	Gly	Ala	Thr	Ser	Leu	Val	Ala	Ala	Pro	His	Ser	Ser	
525					530					535					540	
tct	tca	tcc	ccg	agt	aag	gac	tcc	tca	aga	gga	gag	act	gaa	gaa	cgc	1681
Ser	Ser	Ser	Pro	Ser	Lys	Asp	Ser	Ser	Arg	Gly	Glu	Thr	Glu	Glu	Arg	
541					546					551					556	
aaa	gat	agc	gat	gat	gag	aaa	tca	gac	agg	aac	aga	cct	tgg	tgg	aga	1729
Lys	Asp	Ser	Asp	Asp	Glu	Lys	Ser	Asp	Arg	Asn	Arg	Pro	Trp	Trp	Arg	
557					562					567					572	
aaa	cgt	ttt	gtt	tca	gcc	atg	cct	aaa	gat	gat	ccc	agc	cct	aga	ctc	1777
Lys	Arg	Phe	Val	Ser	Ala	Met	Pro	Lys	Asp	Asp	Pro	Ser	Pro	Arg	Leu	
573					578					583					588	
agt	gca	caa	gct	cag	gtg	gct	gag	gat	att	ctg	gac	aaa	tac	agg	aat	1825
Ser	Ala	Gln	Ala	Gln	Val	Ala	Glu	Asp	Ile	Leu	Asp	Lys	Tyr	Arg	Asn	
589					594					599					604	
gcc	att	aaa	cgg	acc	agc	ccc	agt	gat	gga	gca	atg	gca	aac	tat	gaa	1873
Ala	Ile	Lys	Arg	Thr	Ser	Pro	Ser	Asp	Gly	Ala	Met	Ala	Asn	Tyr	Glu	
605					610					615					620	
agt	aca	gag	gtt	atg	ggc	gat	ggc	gaa	agt	gca	cat	gat	tct	ccc	cgt	1921
Ser	Thr	Glu	Val	Met	Gly	Asp	Gly	Glu	Ser	Ala	His	Asp	Ser	Pro	Arg	
621					626					631					636	
gac	gaa	gca	ctg	cag	aac	atc	tcg	gct	gat	gat	ctc	cca	gac	tct	gca	1969
Asp	Glu	Ala	Leu	Gln	Asn	Ile	Ser	Ala	Asp	Asp	Leu	Pro	Asp	Ser	Ala	
637					642					647					652	
agc	caa	gca	gcc	cac	ccg	cag	gat	tca	gct	ttc	tct	tac	aga	gat	gca	2017
Ser	Gln	Ala	Ala	His	Pro	Gln	Asp	Ser	Ala	Phe	Ser	Tyr	Arg	Asp	Ala	
653					658					663					668	
aaa	aag	aaa	ctg	agg	ctt	gct	ctt	tgc	tct	gcg	gac	tct	gtt	gcc	ttc	2065
Lys	Lys	Lys	Leu	Arg	Leu	Ala	Leu	Cys	Ser	Ala	Asp	Ser	Val	Ala	Phe	
669					674					679					684	
cca	gtg	ctg	acc	cat	tca	aca	agg	aat	ggc	tta	cca	gac	cac	aca	gac	2113
Pro	Val	Leu	Thr	His	Ser	Thr	Arg	Asn	Gly	Leu	Pro	Asp	His	Thr	Asp	
685					690					695					700	
cca	gaa	gac	aat	gaa	att	gta	tgc	ttc	tta	aaa	gtt	caa	ata	gct	gaa	2161
Pro	Glu	Asp	Asn	Glu	Ile	Val	Cys	Phe	Leu	Lys	Val	Gln	Ile	Ala	Glu	

701	706	711	716	
gca att aat tta caa gat aag aat cta atg gct caa ctt caa gaa aca				2209
Ala Ile Asn Leu Gln Asp Lys Asn Leu Met Ala Gln Leu Gln Glu Thr				
717	722	727	732	
atg cgc tgt gtg tgc cgt ttt gat aat agg act tgt agg aaa ctg ctg				2257
Met Arg Cys Val Cys Arg Phe Asp Asn Arg Thr Cys Arg Lys Leu Leu				
733	738	743	748	
gct tcg att gct gag gac tac aga aaa aga gcc cca tat att gct tat				2305
Ala Ser Ile Ala Glu Asp Tyr Arg Lys Arg Ala Pro Tyr Ile Ala Tyr				
749	754	759	764	
ctc act cgt tgt cga caa gga cta cag acc aca cag gct cac ctg gaa				2353
Leu Thr Arg Cys Arg Gln Gly Leu Gln Thr Thr Gln Ala His Leu Glu				
765	770	775	780	
agg cta ttg caa aga gtt ttg cgg gac aaa gaa gtg gcc aat cga tac				2401
Arg Leu Leu Gln Arg Val Leu Arg Asp Lys Glu Val Ala Asn Arg Tyr				
781	786	791	796	
ttt acc act gtc tgt gtg aga tta ctg ctt gag agc aaa gaa aag aag				2449
Phe Thr Thr Val Cys Val Arg Leu Leu Leu Glu Ser Lys Glu Lys Lys				
797	802	807	812	
atc agg gaa ttc att caa gac ttt cag aaa ctc acc gca gct gac gat				2497
Ile Arg Glu Phe Ile Gln Asp Phe Gln Lys Leu Thr Ala Ala Asp Asp				
813	818	823	828	
aaa act gct cag gta gaa gat ttt ctg cag ttt ctt tat ggt gca atg				2545
Lys Thr Ala Gln Val Glu Asp Phe Leu Gln Phe Leu Tyr Gly Ala Met				
829	834	839	844	
gcc cag gat gtc ata tgg caa aac gcg agt gaa gaa cag ctt caa gat				2593
Ala Gln Asp Val Ile Trp Gln Asn Ala Ser Glu Glu Gln Leu Gln Asp				
845	850	855	860	
gca cag ctg gcc att gag cga agc gtg atg aac cgg att ttc aag ctc				2641
Ala Gln Leu Ala Ile Glu Arg Ser Val Met Asn Arg Ile Phe Lys Leu				
861	866	871	876	
gcc ttc tac cct aat caa gat ggg gac ata ctt cgc gac cag gtt ctt				2689
Ala Phe Tyr Pro Asn Gln Asp Gly Asp Ile Leu Arg Asp Gln Val Leu				
877	882	887	892	
cat gaa cat atc cag aga ttg tct aaa gta gtg act gca aat cac aga				2737
His Glu His Ile Gln Arg Leu Ser Lys Val Val Thr Ala Asn His Arg				
893	898	903	908	
gct ctt cag ata cca gag gtt tat ctt cga gaa gca cca tgg cca tct				2785
Ala Leu Gln Ile Pro Glu Val Tyr Leu Arg Glu Ala Pro Trp Pro Ser				
909	914	919	924	
gca caa tca gaa atc agg aca ata agt gct tat aaa acc ccc cgg gac				2833
Ala Gln Ser Glu Ile Arg Thr Ile Ser Ala Tyr Lys Thr Pro Arg Asp				
925	930	935	940	

<222> (1)..(2058)

<400> 13

atg gaa aca ctg gag tct gaa ttg acc tgt cca atc tgc cta gag ttg	48
Met Glu Thr Leu Glu Ser Glu Leu Thr Cys Pro Ile Cys Leu Glu Leu	
1 5 10	
ttt gaa gac ccc ctt ctg ctc cct tgt gct cac agc ctc tgc ttc agc	96
Phe Glu Asp Pro Leu Leu Leu Pro Cys Ala His Ser Leu Cys Phe Ser	
17 22 27 32	
tgt gcc cat cgc att ttg gta tca agc tgc agc tct ggt gaa tcc att	144
Cys Ala His Arg Ile Leu Val Ser Ser Cys Ser Ser Gly Glu Ser Ile	
33 38 43 48	
gaa ccc att act gct ttc cag tgt cct acc tgc agg tat gtt atc tcg	192
Glu Pro Ile Thr Ala Phe Gln Cys Pro Thr Cys Arg Tyr Val Ile Ser	
49 54 59 64	
ctg aac cac cgg ggc ctg gat ggc ctc aag agg aat gtg act ctg cag	240
Leu Asn His Arg Gly Leu Asp Gly Leu Lys Arg Asn Val Thr Leu Gln	
65 70 75 80	
aac att att gat cgc ttc cag aag gct tca gtc agt ggg ccc aat tcc	288
Asn Ile Ile Asp Arg Phe Gln Lys Ala Ser Val Ser Gly Pro Asn Ser	
81 86 91 96	
cct agt gag agc cgc cgg gaa agg act tac agg ccc acc act gcc atg	336
Pro Ser Glu Ser Arg Arg Glu Arg Thr Tyr Arg Pro Thr Thr Ala Met	
97 102 107 112	
tct agc gag cga att gct tgc caa ttc tgt gag cag gac ccg cca agg	384
Ser Ser Glu Arg Ile Ala Cys Gln Phe Cys Glu Gln Asp Pro Pro Arg	
113 118 123 128	
gat gca gta aaa aca tgc atc acc tgt gag gtc tcc tac tgt gac cgt	432
Asp Ala Val Lys Thr Cys Ile Thr Cys Glu Val Ser Tyr Cys Asp Arg	
129 134 139 144	
tgc ctg cgg gcc acg cac ccc aac aag aaa cct ttc acc agc cac cgc	480
Cys Leu Arg Ala Thr His Pro Asn Lys Lys Pro Phe Thr Ser His Arg	
145 150 155 160	
ctg gtg gaa cca gtg cca gac aca cat ctt cga ggg atc acc tgc ctg	528
Leu Val Glu Pro Val Pro Asp Thr His Leu Arg Gly Ile Thr Cys Leu	
161 166 171 176	
gac cat gag aat gag aaa gtg aac atg tac tgt gta tct gat gac caa	576
Asp His Glu Asn Glu Lys Val Asn Met Tyr Cys Val Ser Asp Asp Gln	
177 182 187 192	
ttg atc tgt gcc tta tgc aaa ctg gtg ggt cgt cac cga gac cat cag	624
Leu Ile Cys Ala Leu Cys Lys Leu Val Gly Arg His Arg Asp His Gln	
193 198 203 208	
gtc gca tcc ctg aat gat cga ttt gag aaa ctc aag caa act ctg gag	672
Val Ala Ser Leu Asn Asp Arg Phe Glu Lys Leu Lys Gln Thr Leu Glu	

209	214	219	224	
atg aac ctc acc aac ctg gtt aag cgc aac agc gaa cta gaa aat caa				720
Met Asn Leu Thr Asn Leu Val Lys Arg Asn Ser Glu Leu Glu Asn Gln				
225	230	235	240	
atg gcc aaa cta ata cag atc tgc cag cag gtt gag gtg aat act gct				768
Met Ala Lys Leu Ile Gln Ile Cys Gln Gln Val Glu Val Asn Thr Ala				
241	246	251	256	
atg cat gag gca aaa ctt atg gaa gaa tgt gac gag ttg gta gag atc				816
Met His Glu Ala Lys Leu Met Glu Glu Cys Asp Glu Leu Val Glu Ile				
257	262	267	272	
atc cag cag agg aag caa atg atc gct gtc aaa atc aaa gag aca aag				864
Ile Gln Gln Arg Lys Gln Met Ile Ala Val Lys Ile Lys Glu Thr Lys				
273	278	283	288	
gtt atg aaa ctg aga aag ttg gca cag cag gtt gct aat tgc cgc cag				912
Val Met Lys Leu Arg Lys Leu Ala Gln Gln Val Ala Asn Cys Arg Gln				
289	294	299	304	
tgt ctt gaa cgg tca aca gtc ctc atc aac caa gct gag cat atc ctg				960
Cys Leu Glu Arg Ser Thr Val Leu Ile Asn Gln Ala Glu His Ile Leu				
305	310	315	320	
aaa gaa aat gac cag gca cgg ttt cta cag tct gca aaa aat att gct				1008
Lys Glu Asn Asp Gln Ala Arg Phe Leu Gln Ser Ala Lys Asn Ile Ala				
321	326	331	336	
gag agg gtc gct atg gca act gca tct tct caa gtt ctg att cca gac				1056
Glu Arg Val Ala Met Ala Thr Ala Ser Ser Gln Val Leu Ile Pro Asp				
337	342	347	352	
atc aat ttt aat gat gcc ttt gaa aac ttt gct tta gat ttt tcc aga				1104
Ile Asn Phe Asn Asp Ala Phe Glu Asn Phe Ala Leu Asp Phe Ser Arg				
353	358	363	368	
gaa aag aaa ctg cta gag ggg tta gat tat tta aca gcc cca aac cca				1152
Glu Lys Lys Leu Leu Glu Gly Leu Asp Tyr Leu Thr Ala Pro Asn Pro				
369	374	379	384	
cca tct atc cga gaa gaa ctc tgt act gcc tcc cat gac acc att aca				1200
Pro Ser Ile Arg Glu Glu Leu Cys Thr Ala Ser His Asp Thr Ile Thr				
385	390	395	400	
gtc cac tgg atc tcg gat gat gag ttc agc atc agc tcc tat gag ctt				1248
Val His Trp Ile Ser Asp Asp Glu Phe Ser Ile Ser Ser Tyr Glu Leu				
401	406	411	416	
cag tac acc ata ttc act ggc cag gct aac ttc atc agc ctg tat aat				1296
Gln Tyr Thr Ile Phe Thr Gly Gln Ala Asn Phe Ile Ser Leu Tyr Asn				
417	422	427	432	
tca gta gac agc tgg atg att gtt ccc aac att aaa cag aac cat tac				1344
Ser Val Asp Ser Trp Met Ile Val Pro Asn Ile Lys Gln Asn His Tyr				
433	438	443	448	

aca gtg cat gga ctc cag agc ggg act cgc tac atc ttc atc gtt aaa	1392
Thr Val His Gly Leu Gln Ser Gly Thr Arg Tyr Ile Phe Ile Val Lys	
449 454 459 464	
gcc ata aac caa gcc ggc agc cgg aac agt gaa cct acc cga cta aaa	1440
Ala Ile Asn Gln Ala Gly Ser Arg Asn Ser Glu Pro Thr Arg Leu Lys	
465 470 475 480	
aca aac agc caa ccc ttt aaa ttg gat ccc aaa atg act cac aag aag	1488
Thr Asn Ser Gln Pro Phe Lys Leu Asp Pro Lys Met Thr His Lys Lys	
481 486 491 496	
ttg aag atc tcc aat gat gga ttg cag atg gag aag gat gaa agc tct	1536
Leu Lys Ile Ser Asn Asp Gly Leu Gln Met Glu Lys Asp Glu Ser Ser	
497 502 507 512	
cta aag aag agc cac acc cca gag agg ttt agt ggc aca ggg tgc tat	1584
Leu Lys Lys Ser His Thr Pro Glu Arg Phe Ser Gly Thr Gly Cys Tyr	
513 518 523 528	
ggg gca gca gga aat ata ttc att gac agt ggc tgc cac tat tgg gag	1632
Gly Ala Ala Gly Asn Ile Phe Ile Asp Ser Gly Cys His Tyr Trp Glu	
529 534 539 544	
gtg gtc atg ggt tcc tca aca tgg tat gca att ggc att gcc tac aaa	1680
Val Val Met Gly Ser Ser Thr Trp Tyr Ala Ile Gly Ile Ala Tyr Lys	
545 550 555 560	
tca gct cca aag aat gaa tgg att ggc aag aat gcc tcc tca tgg gtc	1728
Ser Ala Pro Lys Asn Glu Trp Ile Gly Lys Asn Ala Ser Ser Trp Val	
561 566 571 576	
ttc tct cgc tgc aat agt aac ttc gtg gtg aga cac aac aac aag gaa	1776
Phe Ser Arg Cys Asn Ser Asn Phe Val Val Arg His Asn Asn Lys Glu	
577 582 587 592	
atg ctg gtg gat gtg ccc cca cac ctg aag cgt ctg ggt gtc ctc ctg	1824
Met Leu Val Asp Val Pro Pro His Leu Lys Arg Leu Gly Val Leu Leu	
593 598 603 608	
gat tat gac aac aat atg ctg tct ttc tat gac cca gct aac tct ctc	1872
Asp Tyr Asp Asn Asn Met Leu Ser Phe Tyr Asp Pro Ala Asn Ser Leu	
609 614 619 624	
cat ctt cat act ttt gat gtg acc ttc att ctt cca gtt tgt cca aca	1920
His Leu His Thr Phe Asp Val Thr Phe Ile Leu Pro Val Cys Pro Thr	
625 630 635 640	
ttt aca atc tgg aac aaa tcc cta atg atc ctg tct ggc ttg cct gcc	1968
Phe Thr Ile Trp Asn Lys Ser Leu Met Ile Leu Ser Gly Leu Pro Ala	
641 646 651 656	
cca gat ttt att gat tac cct gag cgg cag gaa tgc aac tgc agg cct	2016
Pro Asp Phe Ile Asp Tyr Pro Glu Arg Gln Glu Cys Asn Cys Arg Pro	
657 662 667 672	

caa gaa tcc cct tat gtt tct ggg atg aaa acc tgt cat taa gtttcag	2065
Gln Glu Ser Pro Tyr Val Ser Gly Met Lys Thr Cys His *	
673 678 683	
gagagtatat aattcactgg ctctctagtt cagcagttct tccccctcta cacctaagtt	2125
agcgttcaat atacgagaca caaaataaag tttgtttgaa gcatccaaaa taactagata	2185
ttgcagattt aatttttgtg cattaaagct tgtatttgaa ttaatttatt gagtttttca	2245
gaacaaatta tctgagtagt ctgcgttcaa gccattggag aaaaatttag aaaatgcctc	2305
tgttgtcatt ggagaattaa aaattcccaa tgatttaaga atataaatta tattggaagc	2365
aattagggta attctagtta aataatgtgg aaagggtgcc tgaataagga gctagcaagc	2425
cagagcgggg ggtggtcagc ctttctagta ctggccagtt tggccatgta gaattttgaa	2485
cagtgtcaaa ttatcacata ttatatttta cttttgatga aaacctatca tcaagggttt	2545
gttaggaaac catgaatgtg tatatgtaat atataaagtg aacatatatg tactttatat	2605
atattcactt gtgtatgtat gtttatgcat attcacttta tatattacat atacacaaaa	2665
aacttttttt tccaaacacc acctcgaact agaacaaaaa actttttaat ttgctaattt	2725
gagtgagaaa tatactggaa gggaaaataa gttacaccat ccatttttgt cccctaaagg	2785
aaacatcaaa atcaatcaac atttatttcc tccctctatc catcattgcc ttccctccctc	2845
ctgtcacgca cacatacaca tgcaaccatg acacagataa tgggaagagc tttattggat	2905
tagcagagat ttacagacaa gattgcacaa gagatgctgt tgctggatag aaaattgatc	2965
aggtagaagt gatgctacct acttgaggat ggccatctga attgttaaaa attctgtcat	3025
agactattaa aaaaaaagtt ttactactcc caagtacaca cagttatgag aattaggctt	3085
ttaaaaagtt gcacagtga ggctcttttag gaacctactt tacttaatca gtaaaaattg	3145
agtattattg atgcaccaac tattcccata taaatgtact tgctttttca gataaaacac	3205
ttctgaagtg ctcaagaatg tctgaaaaca gtttgttttc ttaaataagga taaataatca	3265
ttccttttgc aatcttgttt acagtattca ttctcttagc caatccctcc acgcaaattg	3325
agacaaactt catcccagtc ctaaccagta tagttgaagg gaatggagcc ttgtagtcta	3385
tgattttttt ttttaaatth ccacgaagg gattggggat gtcagagagc cagagctttc	3445
ccctttccag gagctaagtt ggcttcggaa gtcttctggg atttggtgaaa atattactgt	3505
tgtaaaatta caaagtggta gccataacaa ctccctcaga ttggagactt gaaatgtcaa	3565
aactccccctc ttccctttccc ctagtttggg ggatgctcat ttattaattc attcaataaa	3625
ctattagatg ccaggtaacca aactactgcc atgggagtg acatattaac aaaatgctct	3685

cca ctg gcc act gct gag tct gga tca gtt act aaa tct aag ggc ctg	1070
Pro Leu Ala Thr Ala Glu Ser Gly Ser Val Thr Lys Ser Lys Gly Leu	
154 159 164 169	
tct atg gat aga gaa cta gtc aat gtg gat gct gaa acc ttt cct ggc	1118
Ser Met Asp Arg Glu Leu Val Asn Val Asp Ala Glu Thr Phe Pro Gly	
170 175 180 185	
acc cag ggt cag aaa gga atc cag ccc tgg ttt gga cca ggg gag gag	1166
Thr Gln Gly Gln Lys Gly Ile Gln Pro Trp Phe Gly Pro Gly Glu Glu	
186 191 196 201	
act aat atg ggg tct tgg tgc tat tcc agg ccc agg gcc aga gag gag	1214
Thr Asn Met Gly Ser Trp Cys Tyr Ser Arg Pro Arg Ala Arg Glu Glu	
202 207 212 217	
gcc tct aat gag tct ggg ttc tgg tca gca gat gag acc tct aca gcg	1262
Ala Ser Asn Glu Ser Gly Phe Trp Ser Ala Asp Glu Thr Ser Thr Ala	
218 223 228 233	
tct tct ttc tgg act gga gaa gag aca agt gtc aga tca tgg ccc agg	1310
Ser Ser Phe Trp Thr Gly Glu Glu Thr Ser Val Arg Ser Trp Pro Arg	
234 239 244 249	
gaa gag tcc aat acc agg tcc agg cac agg gct aaa cat cag act aat	1358
Glu Glu Ser Asn Thr Arg Ser Arg His Arg Ala Lys His Gln Thr Asn	
250 255 260 265	
ccc agg tcc agg ccc aga tcc aag caa gaa gcc tat gtt gat tcc tgg	1406
Pro Arg Ser Arg Pro Arg Ser Lys Gln Glu Ala Tyr Val Asp Ser Trp	
266 271 276 281	
tct gga tct gag gat gag gcc agc aac cca ttc tcc ttc tgg gtt gga	1454
Ser Gly Ser Glu Asp Glu Ala Ser Asn Pro Phe Ser Phe Trp Val Gly	
282 287 292 297	
gaa aat acc aat aac ttg ttc agg ccc aga gtc agg gag gag gca aat	1502
Glu Asn Thr Asn Asn Leu Phe Arg Pro Arg Val Arg Glu Glu Ala Asn	
298 303 308 313	
atc agg tcc aag ctc agg aca aat aga gaa gat tgt ttt gaa tct gag	1550
Ile Arg Ser Lys Leu Arg Thr Asn Arg Glu Asp Cys Phe Glu Ser Glu	
314 319 324 329	
tct gaa gat gag ttc tat aag cag tcc tgg gtt ttg cct gga gaa gag	1598
Ser Glu Asp Glu Phe Tyr Lys Gln Ser Trp Val Leu Pro Gly Glu Glu	
330 335 340 345	
gcc aat agt aga ttc agg cac aga gac aaa gaa gat cct aat act gcc	1646
Ala Asn Ser Arg Phe Arg His Arg Asp Lys Glu Asp Pro Asn Thr Ala	
346 351 356 361	
ttg aaa ctc agg gcc cag aaa gat gtt gac agt gat agg gtc aaa caa	1694
Leu Lys Leu Arg Ala Gln Lys Asp Val Asp Ser Asp Arg Val Lys Gln	
362 367 372 377	

gaa ccc agg ttt gag gag gaa gtc att att ggg tcc tgg ttc tgg gca	1742
Glu Pro Arg Phe Glu Glu Glu Val Ile Ile Gly Ser Trp Phe Trp Ala	
378 383 388 393	
gaa aaa gag gcc agt ttg gag ggt gga gct tca gca atc tgt gaa tct	1790
Glu Lys Glu Ala Ser Leu Glu Gly Gly Ala Ser Ala Ile Cys Glu Ser	
394 399 404 409	
gag cca gga act gag gag ggg gcc att ggc gga tcc gcg tac tgg gct	1838
Glu Pro Gly Thr Glu Glu Gly Ala Ile Gly Gly Ser Ala Tyr Trp Ala	
410 415 420 425	
gag gaa aag tcc agt ttg ggg gct gtg gcc aga gaa gag gcc aag ccg	1886
Glu Glu Lys Ser Ser Leu Gly Ala Val Ala Arg Glu Glu Ala Lys Pro	
426 431 436 441	
gag tct gaa gaa gag gcc ata ttt ggg tcc tgg ttc tgg gac aga gat	1934
Glu Ser Glu Glu Glu Ala Ile Phe Gly Ser Trp Phe Trp Asp Arg Asp	
442 447 452 457	
gag gcc tgc ttt gac cta aat ccc tgt cct gtg tac aag gtc agt gat	1982
Glu Ala Cys Phe Asp Leu Asn Pro Cys Pro Val Tyr Lys Val Ser Asp	
458 463 468 473	
agg ttc aga gat gca gct gag gag ctt aat gca tcc tcc agg ccc caa	2030
Arg Phe Arg Asp Ala Ala Glu Glu Leu Asn Ala Ser Ser Arg Pro Gln	
474 479 484 489	
acc tgg gac gag gtc act gtt gaa ttc aaa cct ggt ctt ttt cat ggg	2078
Thr Trp Asp Glu Val Thr Val Glu Phe Lys Pro Gly Leu Phe His Gly	
490 495 500 505	
gtt ggc ttc cga tcc aca agc ccc ttt gga att ccc gaa gag gct tct	2126
Val Gly Phe Arg Ser Thr Ser Pro Phe Gly Ile Pro Glu Glu Ala Ser	
506 511 516 521	
gaa atg ctt gag gca aag ccc aag aac ctg gaa ctt agc cca gaa gga	2174
Glu Met Leu Glu Ala Lys Pro Lys Asn Leu Glu Leu Ser Pro Glu Gly	
522 527 532 537	
gaa gag cag gaa tct ttg ctt cag cct gat cag cct agt cct gag ttc	2222
Glu Glu Gln Glu Ser Leu Leu Gln Pro Asp Gln Pro Ser Pro Glu Phe	
538 543 548 553	
aca ttt cag tat gat cct tcc tac cgg tca gtc cgg gaa att cga gag	2270
Thr Phe Gln Tyr Asp Pro Ser Tyr Arg Ser Val Arg Glu Ile Arg Glu	
554 559 564 569	
cat ctt agg gcc agg gag agt gca gag tct gag agt tgg tcc tgc agc	2318
His Leu Arg Ala Arg Glu Ser Ala Glu Ser Glu Ser Trp Ser Cys Ser	
570 575 580 585	
tgc ata caa tgt gag ctg aaa att ggt tct gaa gag ttt gaa gaa ttc	2366
Cys Ile Gln Cys Glu Leu Lys Ile Gly Ser Glu Glu Phe Glu Glu Phe	
586 591 596 601	
ctt tta tta atg gac aaa att cgg gat cct ttt att cat gaa ata tct	2414

Leu Leu Leu Met Asp Lys Ile Arg Asp Pro Phe Ile His Glu Ile Ser	
602 607 612 617	
aaa att gca atg ggt atg aga agt gct tct caa ttt acc cga gat ttc	2462
Lys Ile Ala Met Gly Met Arg Ser Ala Ser Gln Phe Thr Arg Asp Phe	
618 623 628 633	
att cga gat tca ggt gtt gtc tca ctt att gaa acc ttg ctt aat tat	2510
Ile Arg Asp Ser Gly Val Val Ser Leu Ile Glu Thr Leu Leu Asn Tyr	
634 639 644 649	
cca tcc tct aga gtt agg aca agt ttt ttg gaa aat atg att cac atg	2558
Pro Ser Ser Arg Val Arg Thr Ser Phe Leu Glu Asn Met Ile His Met	
650 655 660 665	
gct cca cct tat cca aat cta aac atg att gag aca ttc ata tgt caa	2606
Ala Pro Pro Tyr Pro Asn Leu Asn Met Ile Glu Thr Phe Ile Cys Gln	
666 671 676 681	
gtg tgt gag gaa acc ctt gca cat agt gtg gat tcc ctt gag cag ctg	2654
Val Cys Glu Glu Thr Leu Ala His Ser Val Asp Ser Leu Glu Gln Leu	
682 687 692 697	
act gga ata agg atg ctt aga cac ctc act atg act att gac tat cac	2702
Thr Gly Ile Arg Met Leu Arg His Leu Thr Met Thr Ile Asp Tyr His	
698 703 708 713	
aca ctg att gcc aac tat atg tcc ggg ttt ctc tcc tta tta acc aca	2750
Thr Leu Ile Ala Asn Tyr Met Ser Gly Phe Leu Ser Leu Leu Thr Thr	
714 719 724 729	
gcc aat gcg aga acg aag ttt cac gtt ctg aaa atg cta ttg aat ttg	2798
Ala Asn Ala Arg Thr Lys Phe His Val Leu Lys Met Leu Leu Asn Leu	
730 735 740 745	
tct gaa aat cct gct gtg gca aaa aaa cta ttc agt gcc aaa gct ctt	2846
Ser Glu Asn Pro Ala Val Ala Lys Lys Leu Phe Ser Ala Lys Ala Leu	
746 751 756 761	
tca ata ttt gtg ggt ctc ttt aac ata gaa gag aca aat gat aat att	2894
Ser Ile Phe Val Gly Leu Phe Asn Ile Glu Glu Thr Asn Asp Asn Ile	
762 767 772 777	
caa att gtt att aaa atg ttt cag aat atc agt aac att ata aaa agt	2942
Gln Ile Val Ile Lys Met Phe Gln Asn Ile Ser Asn Ile Ile Lys Ser	
778 783 788 793	
gga aag atg tcc tta att gat gat gat ttc agt ctt gag ccg ctt att	2990
Gly Lys Met Ser Leu Ile Asp Asp Asp Phe Ser Leu Glu Pro Leu Ile	
794 799 804 809	
tct gca ttt cgt gaa ttt gag gag tta gct aag caa cta caa gcc caa	3038
Ser Ala Phe Arg Glu Phe Glu Glu Leu Ala Lys Gln Leu Gln Ala Gln	
810 815 820 825	
ata gac aac caa aat gat cct gag gtg gga caa caa agt taa tatgatt	3087
Ile Asp Asn Gln Asn Asp Pro Glu Val Gly Gln Gln Ser *	

826	831	836	
aaccacctgc	cgctgatcag	ccttatgttc	ccaaagagcc ctgagtagtg ctttggtggt 3147
cacagtctgt	ttttttgttg	taacttatat	tttttaatgc tgatgttaac tttgtcaaac 3207
tcttgttttg	agctggatca	ttttgtggat	gccaaatgaa tatcaaaact gaaaacacat 3267
ttgttgatat	ttgtcttgct	gtccagattg	cggtatTTTT cagtattaag ttttcaatga 3327
actgtgtcac	ctaagtaagc	taccctgcta	ttcgttgttt aaatatatgg ttctctattt 3387
gagtctgtgt	tttcaataaa	gttctatggt	aaaattggaa aaaaaaaaaa 3437

<210> 15
 <211> 4603
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (846) .. (3911)

<400> 15	
ctggtggtcc agtacctcca aagatatgga atacactcct gaaatatacct gaaaactttt	60
ttttttcaga atcctttaat aagcagttat gtcaatctga aagttgctta cttgtacttt	120
atattaatag ctattcttgt ttttcttata caaagaaaaa tcctctaata cccttttcac	180
atgatagttg ttaccatggt taggcattag tcacatcaac cctctctctc tcccaaactt	240
ctcttcttca aatcaaactt tattagtccc tcctttataa tgattccttg cctcgtttta	300
tccagatcaa ttttttttca ctttgatgcc cagagctgaa gaaatggact actgtataaa	360
ttattcattg ccaagagaat aattgcattt taaaccata ttataacaaa gaataatgat	420
tatatattgt gatttgtaac aaataccctt tattttccct taactattga attaaatatt	480
ttaattattt gtattctctt taactatctt ggtatattaa agtattatct tttatatatt	540
tatcaatggg ggacactttt ataggacttc tgtgtcattt ttgatactgt aggtatctta	600
tttcatttat ctttattctt aatgtacgaa ttcataatat ttgattcaga acaaatttat	660
cactaattaa cagagtgtca attatgctaa catctcattt actgatttta atttaaaaca	720
gtttttgtta acatgcatgt ttaggggttg cttcttaata atttcttctt cctcttctct	780
ctctcctctt cttttggtca gtgtgtgctg ggttaataca acaaactgta acaagtgtac	840
ctggt atg gac ttg ttg tcc ggg acg tac att ttc gcg gtc ctg cta	887
Met Asp Leu Leu Ser Gly Thr Tyr Ile Phe Ala Val Leu Leu	

1					5					10						
gca	tgc	gtg	gtg	ttc	cac	tct	ggc	gcc	cag	gag	aaa	aac	tac	acc	atc	935
Ala	Cys	Val	Val	Phe	His	Ser	Gly	Ala	Gln	Glu	Lys	Asn	Tyr	Thr	Ile	
15					20					25					30	
cga	gaa	gaa	atg	cca	gaa	aac	gtc	ctg	ata	ggc	gac	ttg	ttg	aaa	gac	983
Arg	Glu	Glu	Met	Pro	Glu	Asn	Val	Leu	Ile	Gly	Asp	Leu	Leu	Lys	Asp	
31					36					41					46	
ctt	aac	ttg	tcg	ctg	att	cca	aac	aag	tcc	ttg	aca	act	gct	atg	cag	1031
Leu	Asn	Leu	Ser	Leu	Ile	Pro	Asn	Lys	Ser	Leu	Thr	Thr	Ala	Met	Gln	
47					52					57					62	
ttc	aag	cta	gtg	tac	aag	acc	gga	gat	gtg	cca	ctg	att	cga	att	gaa	1079
Phe	Lys	Leu	Val	Tyr	Lys	Thr	Gly	Asp	Val	Pro	Leu	Ile	Arg	Ile	Glu	
63					68					73					78	
gag	gat	act	ggg	gag	atc	ttc	act	act	ggc	gct	cgc	att	gat	cgt	gag	1127
Glu	Asp	Thr	Gly	Glu	Ile	Phe	Thr	Thr	Gly	Ala	Arg	Ile	Asp	Arg	Glu	
79					84					89					94	
aaa	tta	tgt	gct	ggg	atc	cca	agg	gat	gag	cat	tgc	ttt	tat	gaa	gtg	1175
Lys	Leu	Cys	Ala	Gly	Ile	Pro	Arg	Asp	Glu	His	Cys	Phe	Tyr	Glu	Val	
95					100					105					110	
gag	gtt	gcc	att	ttg	ccg	gat	gaa	ata	ttt	aga	ctg	gtt	aag	ata	cgt	1223
Glu	Val	Ala	Ile	Leu	Pro	Asp	Glu	Ile	Phe	Arg	Leu	Val	Lys	Ile	Arg	
111					116					121					126	
ttt	ctg	ata	gaa	gat	ata	aat	gat	aat	gca	cca	ttg	ttc	cca	gca	aca	1271
Phe	Leu	Ile	Glu	Asp	Ile	Asn	Asp	Asn	Ala	Pro	Leu	Phe	Pro	Ala	Thr	
127					132					137					142	
gtt	atc	aac	ata	tca	att	cca	gag	aac	tcg	gct	ata	aac	tct	aaa	tat	1319
Val	Ile	Asn	Ile	Ser	Ile	Pro	Glu	Asn	Ser	Ala	Ile	Asn	Ser	Lys	Tyr	
143					148					153					158	
act	ctc	cca	gcg	gct	gtt	gat	cct	gac	gta	gga	ata	aac	gga	gtt	caa	1367
Thr	Leu	Pro	Ala	Ala	Val	Asp	Pro	Asp	Val	Gly	Ile	Asn	Gly	Val	Gln	
159					164					169					174	
aac	tac	gaa	cta	att	aag	agt	caa	aac	att	ttt	ggc	ctc	gat	gtc	att	1415
Asn	Tyr	Glu	Leu	Ile	Lys	Ser	Gln	Asn	Ile	Phe	Gly	Leu	Asp	Val	Ile	
175					180					185					190	
gaa	aca	cca	gaa	gga	gac	aag	atg	cca	caa	ctg	att	gtt	caa	aag	gag	1463
Glu	Thr	Pro	Glu	Gly	Asp	Lys	Met	Pro	Gln	Leu	Ile	Val	Gln	Lys	Glu	
191					196					201					206	
tta	gat	agg	gaa	gag	aag	gat	acc	tac	gtg	atg	aaa	gta	aag	gtt	gaa	1511
Leu	Asp	Arg	Glu	Glu	Lys	Asp	Thr	Tyr	Val	Met	Lys	Val	Lys	Val	Glu	
207					212					217					222	
gat	ggg	ggc	ttt	cct	caa	aga	tcc	agt	act	gct	att	ttg	caa	gtg	agt	1559
Asp	Gly	Gly	Phe	Pro	Gln	Arg	Ser	Ser	Thr	Ala	Ile	Leu	Gln	Val	Ser	
223					228					233					238	

gtt act gat aca aat gac aac cac cca gtc ttt aag gag aca gag att	1607
Val Thr Asp Thr Asn Asp Asn His Pro Val Phe Lys Glu Thr Glu Ile	
239 244 249 254	
gaa gtc agt ata cca gaa aat gct cct gta ggc act tca gtg aca cag	1655
Glu Val Ser Ile Pro Glu Asn Ala Pro Val Gly Thr Ser Val Thr Gln	
255 260 265 270	
ctc cat gcc aca gat gct gac ata ggt gaa aat gcc aag atc cac ttc	1703
Leu His Ala Thr Asp Ala Asp Ile Gly Glu Asn Ala Lys Ile His Phe	
271 276 281 286	
tct ttc agc aat cta gtc tcc aac att gcc agg aga tta ttt cac ctc	1751
Ser Phe Ser Asn Leu Val Ser Asn Ile Ala Arg Arg Leu Phe His Leu	
287 292 297 302	
aat gcc acc act gga ctt atc aca atc aaa gaa cca ctg gat agg gaa	1799
Asn Ala Thr Thr Gly Leu Ile Thr Ile Lys Glu Pro Leu Asp Arg Glu	
303 308 313 318	
gaa aca cca aac cac aag tta ctg gtt ttg gca agt gat ggt gga ttg	1847
Glu Thr Pro Asn His Lys Leu Leu Val Leu Ala Ser Asp Gly Gly Leu	
319 324 329 334	
atg cca gca aga gca atg gtg ctg gta aat gtt aca gat gtc aat gat	1895
Met Pro Ala Arg Ala Met Val Leu Val Asn Val Thr Asp Val Asn Asp	
335 340 345 350	
aat gtc cca tcc att gac ata aga tac atc gtc aat cct gtc aat gac	1943
Asn Val Pro Ser Ile Asp Ile Arg Tyr Ile Val Asn Pro Val Asn Asp	
351 356 361 366	
aca gtt gtt ctt tca gaa aat att cca ctc aac acc aaa att gct ctc	1991
Thr Val Val Leu Ser Glu Asn Ile Pro Leu Asn Thr Lys Ile Ala Leu	
367 372 377 382	
ata act gtg acg gat aag gat gcg gac cat aat ggc agg gtg aca tgc	2039
Ile Thr Val Thr Asp Lys Asp Ala Asp His Asn Gly Arg Val Thr Cys	
383 388 393 398	
ttc aca gat cat gaa atc cct ttc aga tta agg cca gta ttc agt aat	2087
Phe Thr Asp His Glu Ile Pro Phe Arg Leu Arg Pro Val Phe Ser Asn	
399 404 409 414	
cag ttc ctc ctg gag act gca gca tat ctt gac tat gag tcc aca aaa	2135
Gln Phe Leu Leu Glu Thr Ala Ala Tyr Leu Asp Tyr Glu Ser Thr Lys	
415 420 425 430	
gaa tat gcc att aaa tta ctg gct gca gat gct ggc aaa cct cct ttg	2183
Glu Tyr Ala Ile Lys Leu Leu Ala Ala Asp Ala Gly Lys Pro Pro Leu	
431 436 441 446	
aat cag tca gca atg ctc ttc atc aaa gtg aaa gat gaa aat gac aat	2231
Asn Gln Ser Ala Met Leu Phe Ile Lys Val Lys Asp Glu Asn Asp Asn	
447 452 457 462	

Pro Ser Thr Asn Pro Gly Thr Val Val Phe Gln Val Ile Ala Val Asp	
687 692 697 702	
aat gac act ggc atg aat gca gag gtt cgt tac agc att gta gga gga	2999
Asn Asp Thr Gly Met Asn Ala Glu Val Arg Tyr Ser Ile Val Gly Gly	
703 708 713 718	
aac aca aga gat ctg ttt gca atc gac caa gaa aca ggc aac ata aca	3047
Asn Thr Arg Asp Leu Phe Ala Ile Asp Gln Glu Thr Gly Asn Ile Thr	
719 724 729 734	
ttg atg gag aaa tgt gat gtt aca gac ctt ggt tta cac aga gtg ttg	3095
Leu Met Glu Lys Cys Asp Val Thr Asp Leu Gly Leu His Arg Val Leu	
735 740 745 750	
gtc aaa gct aat gac tta gga cag cct gat tct ctc ttc agt gtt gta	3143
Val Lys Ala Asn Asp Leu Gly Gln Pro Asp Ser Leu Phe Ser Val Val	
751 756 761 766	
att gtc aat ctg ttc gtg aat gag tcg gtg acc aat gct aca ctg att	3191
Ile Val Asn Leu Phe Val Asn Glu Ser Val Thr Asn Ala Thr Leu Ile	
767 772 777 782	
aat gaa ctg gtg cgc aaa agc act gaa gca cca gtg acc cca aat act	3239
Asn Glu Leu Val Arg Lys Ser Thr Glu Ala Pro Val Thr Pro Asn Thr	
783 788 793 798	
gag ata gct gat gta tcc tca cca act agt gac tat gtc aag atc ctg	3287
Glu Ile Ala Asp Val Ser Ser Pro Thr Ser Asp Tyr Val Lys Ile Leu	
799 804 809 814	
gtt gca gct gtt gct ggc acc ata act gtc gtt gta gtt att ttc atc	3335
Val Ala Ala Val Ala Gly Thr Ile Thr Val Val Val Val Ile Phe Ile	
815 820 825 830	
act gct gta gta aga tgt cgc cag gca cca cac ctt aag gct gct cag	3383
Thr Ala Val Val Arg Cys Arg Gln Ala Pro His Leu Lys Ala Ala Gln	
831 836 841 846	
aaa aac aag cag aat tct gaa tgg gct acc cca aac cca gaa aac agg	3431
Lys Asn Lys Gln Asn Ser Glu Trp Ala Thr Pro Asn Pro Glu Asn Arg	
847 852 857 862	
cag atg ata atg atg aag aaa aag aaa aag aag aag aag cat tcc cct	3479
Gln Met Ile Met Met Lys Lys Lys Lys Lys Lys Lys Lys His Ser Pro	
863 868 873 878	
aag aac ttg ctg ctt aat ttt gtc act att gaa gaa act aag gca gat	3527
Lys Asn Leu Leu Leu Asn Phe Val Thr Ile Glu Glu Thr Lys Ala Asp	
879 884 889 894	
gat gtt gac agt gat gga aac aga gtc aca cta gac ctt cct att gat	3575
Asp Val Asp Ser Asp Gly Asn Arg Val Thr Leu Asp Leu Pro Ile Asp	
895 900 905 910	
cta gaa gag caa aca atg gga aag tac aat tgg gta act aca cct act	3623
Leu Glu Glu Gln Thr Met Gly Lys Tyr Asn Trp Val Thr Thr Pro Thr	

911	916	921	926	
act ttc aag ccc gac	agc cct gat ttg gcc	cga cac tac aaa tct gcc		3671
Thr Phe Lys Pro Asp	Ser Pro Asp Leu Ala	Arg His Tyr Lys Ser	Ala	
927	932	937	942	
tct cca cag cct gcc	ttc caa att cag cct	gaa act ccc ctg aat tcg		3719
Ser Pro Gln Pro Ala	Phe Gln Ile Gln Pro	Glu Thr Pro Leu Asn Ser		
943	948	953	958	
aag cac cac atc atc	caa gaa ctg cct ctc	gat aac acc ttt gtg gcc		3767
Lys His His Ile Ile	Gln Glu Leu Pro Leu	Asp Asn Thr Phe Val	Ala	
959	964	969	974	
tgt gac tct atc tcc	aag tgt tcc tca agc	agt tca gat ccc tac agc		3815
Cys Asp Ser Ile Ser	Lys Cys Ser Ser Ser	Ser Ser Asp Pro Tyr Ser		
975	980	985	990	
gtt tct gac tgt ggc	tat cca gtg acg acc	ttc gag gta cct gtg tcc		3863
Val Ser Asp Cys Gly	Tyr Pro Val Thr Thr	Phe Glu Val Pro Val	Ser	
991	996	1001	1006	
gta cac acc aga ccg	gta ggt atc caa gtt	tct aac aca act ttc	taa	3911
Val His Thr Arg Pro	Val Gly Ile Gln Val	Ser Asn Thr Thr Phe	*	
1007	1012	1017	1022	
ctattttttt attattattt tcagttgatg tagaacttta caaaatctat tgacttcaaa				3971
gagggatcaa aacaatcata ttctacagat gtaccaata gatatatgga ttcaattaag				4031
tttggtagaa gatgagaaca aaataactac tgatttagga aaattggatg cagaataata				4091
attatagtag gggcaatttt gtctgtagat ggcagtatga caattcttgc tagagaatat				4151
attgaaaaaa acttcaacac aaagggttgt agcactgtcc tcagtaccat tgtgtgcatg				4211
aggatcagaa tagtctgggc tagatacatc acattaaagc ttttcagaat ctgataaata				4271
gctctaaata ctaatgatat tgagaagcct agcttcactt gggaaaatct gtggctgttc				4331
acagaaattc agcaccaagt tattcccccc atactctacc aggccttcag gtccctcataa				4391
agaaaagtgt cgttttcaga ttaggaactc aaaattattt tgggtgcatca aatctacagt				4451
cacacaatat aacaagaatg ggattagaaa aatgaaagcc tactcattct catctttaag				4511
ccagagaatg aaatatatat gaggtctctg gatagctatt taaatatttg catatttatg				4571
caaggtattt tgagcccttc agaagacatt ct				4603

<210> 16
 <211> 1312
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (60)..(866)

<400> 16

tgcaggatcc catcgattcg aattcggcac gaggccagga catctaccgg ctccttctg	59
atg gat ttt gtg ttc tct tta gtc aat tcc ttc ctg ggg gag ttt ctg	107
Met Asp Phe Val Phe Ser Leu Val Asn Ser Phe Leu Gly Glu Phe Leu	
1 5 10 15	
agg aga atc att ggg atg caa ctg atc aca agt ctt ggc ctt cag gag	155
Arg Arg Ile Ile Gly Met Gln Leu Ile Thr Ser Leu Gly Leu Gln Glu	
17 22 27 32	
ttt gac att gcc agg aac gtt cta gaa ctg atc tat gca caa act ctg	203
Phe Asp Ile Ala Arg Asn Val Leu Glu Leu Ile Tyr Ala Gln Thr Leu	
33 38 43 48	
gtg tgg att ggc atc ttc ttc tgc ccc ctg ctg ccc ttt atc caa atg	251
Val Trp Ile Gly Ile Phe Phe Cys Pro Leu Leu Pro Phe Ile Gln Met	
49 54 59 64	
att atg ctt ttc atc atg ttc tac tcc aaa aat atc agc ctg atg atg	299
Ile Met Leu Phe Ile Met Phe Tyr Ser Lys Asn Ile Ser Leu Met Met	
65 70 75 80	
aat ttc cag cct ccg agc aaa gcc tgg cgg gcc tca cag atg atg act	347
Asn Phe Gln Pro Pro Ser Lys Ala Trp Arg Ala Ser Gln Met Met Thr	
81 86 91 96	
ttc ttc atc ttc ttg ctc ttt ttc cca tcc ttc acc ggg gtc ttg tgc	395
Phe Phe Ile Phe Leu Leu Phe Phe Pro Ser Phe Thr Gly Val Leu Cys	
97 102 107 112	
acc ctg gcc atc acc atc tgg aga ttg aag cct tca gct gac tgt ggc	443
Thr Leu Ala Ile Thr Ile Trp Arg Leu Lys Pro Ser Ala Asp Cys Gly	
113 118 123 128	
cct ttt cga ggt ctg cct ctc ttc att cac tcc atc tac agc tgg atc	491
Pro Phe Arg Gly Leu Pro Leu Phe Ile His Ser Ile Tyr Ser Trp Ile	
129 134 139 144	
gac acc cta agt aca cgg cct ggc tac ctg tgg gtt gtt tgg atc tat	539
Asp Thr Leu Ser Thr Arg Pro Gly Tyr Leu Trp Val Val Trp Ile Tyr	
145 150 155 160	
cgg aac ctc att gga agt gtg cac ttc ttt ttc atc ctc acc ctc att	587
Arg Asn Leu Ile Gly Ser Val His Phe Phe Phe Ile Leu Thr Leu Ile	
161 166 171 176	
gtg cta atc atc acc tat ctt tac tgg cag atc aca gag gga agg aag	635
Val Leu Ile Ile Thr Tyr Leu Tyr Trp Gln Ile Thr Glu Gly Arg Lys	
177 182 187 192	
att atg ata agg ctg ctc cat gag cag atc att aat gag ggc aaa gat	683
Ile Met Ile Arg Leu Leu His Glu Gln Ile Ile Asn Glu Gly Lys Asp	

ggc aag gcc gcc gcg acc cag ccc gcg aag tct ccg ggc gca cag ctc	212
Gly Lys Ala Ala Ala Thr Gln Pro Ala Lys Ser Pro Gly Ala Gln Leu	
18 23 28 33	
tgg ctc ttt ccc agc gcc gcg ggc ctc cac cgc gcg ctg ctc cgg agg	260
Trp Leu Phe Pro Ser Ala Ala Gly Leu His Arg Ala Leu Leu Arg Arg	
34 39 44 49	
gtg gag gtg acg cgc caa ctc tgc tgc tcg ccg ggg cgc ctc gcg gtc	308
Val Glu Val Thr Arg Gln Leu Cys Cys Ser Pro Gly Arg Leu Ala Val	
50 55 60 65	
ttg gaa cgc ggc ggg gcg ggc gtc cag gtt cac cag ctg ctc gcc ggg	356
Leu Glu Arg Gly Gly Ala Gly Val Gln Val His Gln Leu Leu Ala Gly	
66 71 76 81	
agc ggc ggc gcc cgg acg ccg aaa tgc att aaa tta gga aaa aac atg	404
Ser Gly Gly Ala Arg Thr Pro Lys Cys Ile Lys Leu Gly Lys Asn Met	
82 87 92 97	
aag ata cat tcc gtg gac caa gga gca gag cac atg ctg att ctc tca	452
Lys Ile His Ser Val Asp Gln Gly Ala Glu His Met Leu Ile Leu Ser	
98 103 108 113	
tca gat gga aaa cca ttt gag tat gac aac tat agc atg aaa cat cta	500
Ser Asp Gly Lys Pro Phe Glu Tyr Asp Asn Tyr Ser Met Lys His Leu	
114 119 124 129	
agg ttt gaa agc att tta caa gaa aaa aaa ata att cag atc aca tgt	548
Arg Phe Glu Ser Ile Leu Gln Glu Lys Lys Ile Ile Gln Ile Thr Cys	
130 135 140 145	
gga gat tac cat tct ctt gca ctc tca aaa ggc ggt gag ctt ttt gcc	596
Gly Asp Tyr His Ser Leu Ala Leu Ser Lys Gly Gly Glu Leu Phe Ala	
146 151 156 161	
tgg gga cag aac ctg cat ggg cag ctt gga gtt gga agg aaa ttt ccc	644
Trp Gly Gln Asn Leu His Gly Gln Leu Gly Val Gly Arg Lys Phe Pro	
162 167 172 177	
tca acc acc aca cca cag att gtg gag cac ctc gca gga gta ccc ttg	692
Ser Thr Thr Thr Pro Gln Ile Val Glu His Leu Ala Gly Val Pro Leu	
178 183 188 193	
gct cag att tct gcc gga gaa gcc cac agc atg gcc tta tcc atg tct	740
Ala Gln Ile Ser Ala Gly Glu Ala His Ser Met Ala Leu Ser Met Ser	
194 199 204 209	
ggc aac att tat tca tgg gga aaa aat gaa tgt gga caa cta ggc ctg	788
Gly Asn Ile Tyr Ser Trp Gly Lys Asn Glu Cys Gly Gln Leu Gly Leu	
210 215 220 225	
ggc cac act gag agt aaa gat gat cca tcc ctt att gaa gga cta gac	836
Gly His Thr Glu Ser Lys Asp Asp Pro Ser Leu Ile Glu Gly Leu Asp	
226 231 236 241	
aat cag aaa gtt gaa ttt gtc gct tgt ggt ggc tct cac agt gcc cta	884

Asn	Gln	Lys	Val	Glu	Phe	Val	Ala	Cys	Gly	Gly	Ser	His	Ser	Ala	Leu	
242					247					252					257	
ctc	aca	cag	gat	ggg	ctg	ctg	ttt	act	ttc	ggt	gct	gga	aaa	cat	ggg	932
Leu	Thr	Gln	Asp	Gly	Leu	Leu	Phe	Thr	Phe	Gly	Ala	Gly	Lys	His	Gly	
258					263					268					273	
caa	ctt	ggt	cat	aat	tca	aca	cag	aat	gag	cta	aga	ccc	tgt	ttg	gtg	980
Gln	Leu	Gly	His	Asn	Ser	Thr	Gln	Asn	Glu	Leu	Arg	Pro	Cys	Leu	Val	
274					279					284					289	
gct	gag	ctt	gtt	ggg	tat	aga	gtg	act	cag	ata	gca	tgt	gga	agg	tgg	1028
Ala	Glu	Leu	Val	Gly	Tyr	Arg	Val	Thr	Gln	Ile	Ala	Cys	Gly	Arg	Trp	
290					295					300					305	
cac	aca	ctt	gcc	tat	gtt	tct	gat	ttg	gga	aag	gtc	ttt	tcc	ttt	ggg	1076
His	Thr	Leu	Ala	Tyr	Val	Ser	Asp	Leu	Gly	Lys	Val	Phe	Ser	Phe	Gly	
306					311					316					321	
tct	gga	aaa	gat	gga	caa	ctg	gga	aat	ggt	gga	aca	cgt	gac	cag	ctg	1124
Ser	Gly	Lys	Asp	Gly	Gln	Leu	Gly	Asn	Gly	Gly	Thr	Arg	Asp	Gln	Leu	
322					327					332					337	
atg	ccg	ctt	cca	gtg	aaa	gta	tca	tca	agt	gaa	gaa	ctc	aaa	ctt	gaa	1172
Met	Pro	Leu	Pro	Val	Lys	Val	Ser	Ser	Ser	Glu	Glu	Leu	Lys	Leu	Glu	
338					343					348					353	
agc	cat	acc	tca	gaa	aag	gag	tta	ata	atg	att	gct	gga	ggg	aat	caa	1220
Ser	His	Thr	Ser	Glu	Lys	Glu	Leu	Ile	Met	Ile	Ala	Gly	Gly	Asn	Gln	
354					359					364					369	
agc	att	ttg	ctc	tgg	ata	aag	aaa	gag	aat	tca	tat	gtt	aat	ctg	aag	1268
Ser	Ile	Leu	Leu	Trp	Ile	Lys	Lys	Glu	Asn	Ser	Tyr	Val	Asn	Leu	Lys	
370					375					380					385	
agg	aca	att	cct	act	ctg	aat	gaa	ggg	act	gta	aag	aga	tgg	att	gct	1316
Arg	Thr	Ile	Pro	Thr	Leu	Asn	Glu	Gly	Thr	Val	Lys	Arg	Trp	Ile	Ala	
386					391					396					401	
gat	gtg	gag	act	aaa	cgg	tgg	cag	agc	aca	aaa	agg	gaa	atc	caa	gag	1364
Asp	Val	Glu	Thr	Lys	Arg	Trp	Gln	Ser	Thr	Lys	Arg	Glu	Ile	Gln	Glu	
402					407					412					417	
ata	ttt	tca	tct	cct	gct	tgt	cta	act	gga	agt	ttt	tta	agg	aaa	aga	1412
Ile	Phe	Ser	Ser	Pro	Ala	Cys	Leu	Thr	Gly	Ser	Phe	Leu	Arg	Lys	Arg	
418					423					428					433	
aga	act	aca	gaa	atg	atg	cct	gtt	tat	ttg	gac	tta	aat	aaa	gca	aga	1460
Arg	Thr	Thr	Glu	Met	Met	Pro	Val	Tyr	Leu	Asp	Leu	Asn	Lys	Ala	Arg	
434					439					444					449	
aac	atc	ttc	agg	gag	tta	acc	caa	aag	gac	tgg	att	act	aac	atg	ata	1508
Asn	Ile	Phe	Arg	Glu	Leu	Thr	Gln	Lys	Asp	Trp	Ile	Thr	Asn	Met	Ile	
450					455					460					465	
acc	acc	tgc	ctc	aaa	gat	aat	ctg	ctc	aaa	aga	ctt	cca	ttt	cat	tct	1556
Thr	Thr	Cys	Leu	Lys	Asp	Asn	Leu	Leu	Lys	Arg	Leu	Pro	Phe	His	Ser	

466	471	476	481	
cca ccc caa gaa gct tta gaa att ttc ttc ctt ctc cca gaa tgt cct				1604
Pro Pro Gln Glu Ala Leu Glu Ile Phe Phe Leu Leu Pro Glu Cys Pro				
482	487	492	497	
gtg atg cat att tcc aac aac tgg gag agc ctt gtg gtt cca ttt gca				1652
Val Met His Ile Ser Asn Asn Trp Glu Ser Leu Val Val Pro Phe Ala				
498	503	508	513	
aag gtt gtt tgt aaa atg agt gac cag tct tca ctg gtt ctg gaa gag				1700
Lys Val Val Cys Lys Met Ser Asp Gln Ser Ser Leu Val Leu Glu Glu				
514	519	524	529	
tat tgg gca act ctg caa gaa tcc act ttc agc aaa ctg gtc cag atg				1748
Tyr Trp Ala Thr Leu Gln Glu Ser Thr Phe Ser Lys Leu Val Gln Met				
530	535	540	545	
ttt aaa aca gcc gtc ata tgc cag ttg gat tac tgg gat gaa agt gct				1796
Phe Lys Thr Ala Val Ile Cys Gln Leu Asp Tyr Trp Asp Glu Ser Ala				
546	551	556	561	
gag gag aat ggt aat gtt caa gct ctc cta gaa atg ttg aag aag ctg				1844
Glu Glu Asn Gly Asn Val Gln Ala Leu Leu Glu Met Leu Lys Lys Leu				
562	567	572	577	
cac agg gta aac cag gtg aaa tgt caa cta cct gaa agt att ttc caa				1892
His Arg Val Asn Gln Val Lys Cys Gln Leu Pro Glu Ser Ile Phe Gln				
578	583	588	593	
gta gac gaa ctc ttg cac cgt ctc aat ttt ttt gta gaa gta tgc aga				1940
Val Asp Glu Leu Leu His Arg Leu Asn Phe Phe Val Glu Val Cys Arg				
594	599	604	609	
agg tac ttg tgg aaa atg act gtg gac gct tca gaa aat gta caa tgc				1988
Arg Tyr Leu Trp Lys Met Thr Val Asp Ala Ser Glu Asn Val Gln Cys				
610	615	620	625	
tgc gtc ata ttc agt cac ttt cca ttt atc ttt aat aat ctg tcg aaa				2036
Cys Val Ile Phe Ser His Phe Pro Phe Ile Phe Asn Asn Leu Ser Lys				
626	631	636	641	
att aaa cta cta cat aca gac aca ctt tta aaa ata gag agt aaa aaa				2084
Ile Lys Leu Leu His Thr Asp Thr Leu Leu Lys Ile Glu Ser Lys Lys				
642	647	652	657	
cat aaa gct tat ctt agg tcg gca gca att gag gaa gaa aga gag tct				2132
His Lys Ala Tyr Leu Arg Ser Ala Ala Ile Glu Glu Glu Arg Glu Ser				
658	663	668	673	
gaa ttc gct ttg agg ccc acg ttt gat cta aca gtc aga agg aat cac				2180
Glu Phe Ala Leu Arg Pro Thr Phe Asp Leu Thr Val Arg Arg Asn His				
674	679	684	689	
ttg att gag gat gtt ttg aat cag cta agt caa ttt gag aat gaa gac				2228
Leu Ile Glu Asp Val Leu Asn Gln Leu Ser Gln Phe Glu Asn Glu Asp				
690	695	700	705	

ctg Leu 706	agg Arg	aaa Lys	gag Glu	tta Leu	tgg Trp 711	gtt Val	tca Ser	ttt Phe	agt Ser	gga Gly 716	gaa Glu	att Ile	ggg Gly	tat Tyr	gac Asp 721	2276
ctc Leu 722	gga Gly	gga Gly	gtc Val	aag Lys	aaa Lys 727	gag Glu	ttc Phe	ttc Phe	tac Tyr	tgt Cys 732	ctg Leu	ttt Phe	gca Ala	gag Glu	atg Met 737	2324
atc Ile 738	cag Gln	ccg Pro	gaa Glu	tat Tyr	ggg Gly 743	atg Met	ttc Phe	atg Met	tat Tyr	cct Pro 748	gaa Glu	ggg Gly	gct Ala	tcc Ser	tgc Cys 753	2372
atg Met 754	tgg Trp	ttt Phe	cct Pro	gtc Val	aag Lys 759	cct Pro	aaa Lys	ttt Phe	gag Glu	aag Lys 764	aaa Lys	aga Arg	tac Tyr	ttc Phe	ttt Phe 769	2420
ttt Phe 770	ggg Gly	gtt Val	cta Leu	tgt Cys	gga Gly 775	ctt Leu	tcc Ser	ctg Leu	ttc Phe	aat Asn 780	tgc Cys	aat Asn	gtt Val	gcc Ala	aac Asn 785	2468
ctc Leu 786	cct Pro	ttc Phe	cca Pro	ctg Leu	gca Ala 791	ctg Leu	ttt Phe	aag Lys	aaa Lys	ctt Leu 796	ttg Leu	gac Asp	caa Gln	atg Met	cca Pro 801	2516
tca Ser 802	ttg Leu	gaa Glu	gac Asp	ttg Leu	aaa Lys 807	gaa Glu	ctc Leu	agt Ser	cct Pro	gat Asp 812	ttg Leu	gga Gly	aag Lys	aat Asn	ttg Leu 817	2564
caa Gln 818	aca Thr	ctt Leu	ctg Leu	gat Asp	gat Asp 823	gaa Glu	ggt Gly	gat Asp	aac Asn	ttt Phe 828	gag Glu	gaa Glu	gta Val	ttt Phe	tac Tyr 833	2612
atc Ile 834	cat His	ttt Phe	aat Asn	gtg Val	cac His 839	tgg Trp	gac Asp	aga Arg	aac Asn	gac Asp 844	aca Thr	aac Asn	tta Leu	att Ile	cct Pro 849	2660
aat Asn 850	gga Gly	agt Ser	agc Ser	ata Ile	act Thr 855	gtc Val	aac Asn	cag Gln	act Thr	aac Asn 860	aag Lys	aga Arg	gac Asp	tat Tyr	gtt Val 865	2708
tct Ser 866	aag Lys	tat Tyr	atc Ile	aat Asn	tac Tyr 871	att Ile	ttc Phe	aac Asn	gac Asp	tct Ser 876	gta Val	aag Lys	gcg Ala	gtt Val	tat Tyr 881	2756
gaa Glu 882	gaa Glu	ttt Phe	cgg Arg	aga Arg	gga Gly 887	ttt Phe	tat Tyr	aaa Lys	atg Met	tgc Cys 892	gac Asp	gaa Glu	gac Asp	att Ile	atc Ile 897	2804
aaa Lys 898	tta Leu	ttc Phe	cac His	ccc Pro	gaa Glu 903	gaa Glu	ctg Leu	aag Lys	gat Asp	gtg Val 908	att Ile	gtt Val	gga Gly	aat Asn	aca Thr 913	2852
gat Asp 914	tat Tyr	gat Asp	tgg Trp	aaa Lys	aca Thr 919	ttt Phe	gaa Glu	aag Lys	aat Asn	gca Ala 924	cgt Arg	tat Tyr	gaa Glu	cca Pro	gga Gly 929	2900

tat aac agt tca cat ccc acc ata gtg atg ttt tgg aag gct ttc cac	2948
Tyr Asn Ser Ser His Pro Thr Ile Val Met Phe Trp Lys Ala Phe His	
930 935 940 945	
aaa ttg act ctg gaa gaa aag aaa aaa ttc ctt gta ttt ctt aca gga	2996
Lys Leu Thr Leu Glu Glu Lys Lys Lys Phe Leu Val Phe Leu Thr Gly	
946 951 956 961	
act gac aga cta caa atg aaa gat tta aat aat atg aaa ata aca ttt	3044
Thr Asp Arg Leu Gln Met Lys Asp Leu Asn Asn Met Lys Ile Thr Phe	
962 967 972 977	
tgc tgt cct gaa agt tgg aat gaa aga gac cct ata aga gca ctg aca	3092
Cys Cys Pro Glu Ser Trp Asn Glu Arg Asp Pro Ile Arg Ala Leu Thr	
978 983 988 993	
tgt ttc agt gtc ctc ttc ctc cct aaa tat tct aca atg gaa aca gtt	3140
Cys Phe Ser Val Leu Phe Leu Pro Lys Tyr Ser Thr Met Glu Thr Val	
994 999 1004 1009	
gaa gaa gcg ctt caa gaa gcc atc aac aac aac aga gga ttt ggc tga	3188
Glu Glu Ala Leu Gln Glu Ala Ile Asn Asn Asn Arg Gly Phe Gly *	
1010 1015 1020 1025	
ccagcttgct tgtccaacag ccttattttg ttgttggtat cgttggtggt gttggtggtg	3248
ttgttggttc tctactttgt ttgttttag gcttttagca gcctgaagcc atggtttttc	3308
atttctgtct ctagtgataa gcaggaaaga gggatgaaga agagggttta ctggccggtt	3368
agaaccctg actgtattct ctcccttga taccctatg cctacatcat attccttacc	3428
tcttttggga aatatttttc aaaaataaaa taaccgaaaa actaaaaaaaa g	3479
<210> 18	
<211> 2140	
<212> DNA	
<213> Homo sapiens	
<220>	
<221> CDS	
<222> (39) .. (1796)	
<400> 18	
tgaactctca cccgagcggg ttctctttcc gggacaac atg gcg ccg tcc acg	53
Met Ala Pro Ser Thr	
1	
ccg ctc ttg aca gtc cga gga tca gaa gga ctg tac atg gtg aat gga	101
Pro Leu Leu Thr Val Arg Gly Ser Glu Gly Leu Tyr Met Val Asn Gly	
6 11 16 21	
cca cca cat ttt aca gaa agc aca gtg ttt cca agg gaa tct ggg aag	149
Pro Pro His Phe Thr Glu Ser Thr Val Phe Pro Arg Glu Ser Gly Lys	

22	27	32	37	
aat tgc aaa gtc tgt atc ttt agt aag gat ggg acc ttg ttt gcc tgg	197			
Asn Cys Lys Val Cys Ile Phe Ser Lys Asp Gly Thr Leu Phe Ala Trp				
38 43 48 53				
ggc aat gga gaa aaa gta aat att atc agt gtc act aac aag gga cta	245			
Gly Asn Gly Glu Lys Val Asn Ile Ile Ser Val Thr Asn Lys Gly Leu				
54 59 64 69				
ctg cac tcc ttc gac ctc ctg aag gca gtt tgc ctt gaa ttc tca ccc	293			
Leu His Ser Phe Asp Leu Leu Lys Ala Val Cys Leu Glu Phe Ser Pro				
70 75 80 85				
aaa aat act gtc ctg gca acg tgg cag cct tac agt act tct aaa gat	341			
Lys Asn Thr Val Leu Ala Thr Trp Gln Pro Tyr Ser Thr Ser Lys Asp				
86 91 96 101				
ggc aca gct ggg ata ccc aac cta caa ctt tat gat gtg aaa act ggg	389			
Gly Thr Ala Gly Ile Pro Asn Leu Gln Leu Tyr Asp Val Lys Thr Gly				
102 107 112 117				
aca tgt ttg aaa tct ttc atc cag aaa aaa atg caa aat tgg tgt cca	437			
Thr Cys Leu Lys Ser Phe Ile Gln Lys Lys Met Gln Asn Trp Cys Pro				
118 123 128 133				
tcc tgg tca gaa gat gaa act ctt tgt gcc cgc aat gtt aac aat gaa	485			
Ser Trp Ser Glu Asp Glu Thr Leu Cys Ala Arg Asn Val Asn Asn Glu				
134 139 144 149				
gtt cac ttc ttt gaa aac aac aat ttt aac aca att gca aat aaa ttg	533			
Val His Phe Phe Glu Asn Asn Asn Phe Asn Thr Ile Ala Asn Lys Leu				
150 155 160 165				
cat ttg caa aaa att aat gat ttt gta tta tca cct gga ccc caa cca	581			
His Leu Gln Lys Ile Asn Asp Phe Val Leu Ser Pro Gly Pro Gln Pro				
166 171 176 181				
tac aag gtg gct gtc tat gtt cca gga agt aaa ggt gca cct tca ttt	629			
Tyr Lys Val Ala Val Tyr Val Pro Gly Ser Lys Gly Ala Pro Ser Phe				
182 187 192 197				
gtt aga tta tat cag tac ccc aac ttt gct gga cct cat gca gct tta	677			
Val Arg Leu Tyr Gln Tyr Pro Asn Phe Ala Gly Pro His Ala Ala Leu				
198 203 208 213				
gct aat aaa agt ttc ttt aag gca gat aaa gtt aca atg ctg tgg aat	725			
Ala Asn Lys Ser Phe Phe Lys Ala Asp Lys Val Thr Met Leu Trp Asn				
214 219 224 229				
aaa aaa gct act gct gtg ttg gta ata gct agc aca gat gtt gac aag	773			
Lys Lys Ala Thr Ala Val Leu Val Ile Ala Ser Thr Asp Val Asp Lys				
230 235 240 245				
aca gga gct tcc tac tat gga gaa caa act cta cac tac att gca aca	821			
Thr Gly Ala Ser Tyr Tyr Gly Glu Gln Thr Leu His Tyr Ile Ala Thr				
246 251 256 261				

aat gga gaa agt gct gta gtg caa tta cca aaa aat ggc ccc att tat	869
Asn Gly Glu Ser Ala Val Val Gln Leu Pro Lys Asn Gly Pro Ile Tyr	
262 267 272 277	
gat gta gtt tgg aat tct agt tct act gag ttt tgt gct gta tat ggt	917
Asp Val Val Trp Asn Ser Ser Ser Thr Glu Phe Cys Ala Val Tyr Gly	
278 283 288 293	
ttt atg cct gcc aaa gcg aca att ttc aac ttg aaa tgt gat cct gta	965
Phe Met Pro Ala Lys Ala Thr Ile Phe Asn Leu Lys Cys Asp Pro Val	
294 299 304 309	
ttt gac ttt gga act ggt cct cgt aat gca gcc tac tat agc cct cat	1013
Phe Asp Phe Gly Thr Gly Pro Arg Asn Ala Ala Tyr Tyr Ser Pro His	
310 315 320 325	
gga cat ata tta gta tta gct gga ttt gga aat ctg agg gga caa atg	1061
Gly His Ile Leu Val Leu Ala Gly Phe Gly Asn Leu Arg Gly Gln Met	
326 331 336 341	
gaa gtg tgg gat gtg aaa aac tac aaa ctt att tct aaa ccg gtg gct	1109
Glu Val Trp Asp Val Lys Asn Tyr Lys Leu Ile Ser Lys Pro Val Ala	
342 347 352 357	
tct gat tct aca tat ttt gct tgg tgc ccg gat ggt gag cat att tta	1157
Ser Asp Ser Thr Tyr Phe Ala Trp Cys Pro Asp Gly Glu His Ile Leu	
358 363 368 373	
aca gct aca tgt gct ccc agg tta cgg gtt aat aat gga tac aaa att	1205
Thr Ala Thr Cys Ala Pro Arg Leu Arg Val Asn Asn Gly Tyr Lys Ile	
374 379 384 389	
tgg cat tat act ggc tct atc ttg cac aag tat gat gtg cca tca aat	1253
Trp His Tyr Thr Gly Ser Ile Leu His Lys Tyr Asp Val Pro Ser Asn	
390 395 400 405	
gca gaa tta tgg cag gtt tct tgg cag cca ttt ttg gat gga ata ttt	1301
Ala Glu Leu Trp Gln Val Ser Trp Gln Pro Phe Leu Asp Gly Ile Phe	
406 411 416 421	
cca gca aaa aca ata act tac caa gca gtt cca agt gaa gta ccc aat	1349
Pro Ala Lys Thr Ile Thr Tyr Gln Ala Val Pro Ser Glu Val Pro Asn	
422 427 432 437	
gag gaa cct aaa gtt gca aca gct tat aga ccc cca gct tta aga aat	1397
Glu Glu Pro Lys Val Ala Thr Ala Tyr Arg Pro Pro Ala Leu Arg Asn	
438 443 448 453	
aaa cca atc acc aat tcc aaa ttg cat gaa gag gaa cca cct cag aat	1445
Lys Pro Ile Thr Asn Ser Lys Leu His Glu Glu Glu Pro Pro Gln Asn	
454 459 464 469	
atg aaa cca caa tca gga aac gat aag cca tta tca aaa aca gct ctt	1493
Met Lys Pro Gln Ser Gly Asn Asp Lys Pro Leu Ser Lys Thr Ala Leu	
470 475 480 485	

[illegible]

```
<210> 19
<211> 3159
<212> DNA
<213> Homo sapiens
```

```
<400> 19
cgccgggca ggtcggagac ggaggaaagg tggcagccag attacttaga gaggcacaga      60
ggagagagat cggggtgagt cgcc    atg ggg act ccc agg gcc cag cac ccg      111
           Met Gly Thr Pro Arg Ala Gln His Pro
```

1

5

ccg cct ccc cag ctg ctg ttc cta att ctg ctg agc tgt ccc tgg atc	159
Pro Pro Pro Gln Leu Leu Phe Leu Ile Leu Leu Ser Cys Pro Trp Ile	
10 15 20 25	
cag ggt ctg ccc ctg aag gag gag gag ata ttg cca gag cct gga agt	207
Gln Gly Leu Pro Leu Lys Glu Glu Glu Ile Leu Pro Glu Pro Gly Ser	
26 31 36 41	
gag acc ccc acg gtg gcc tct gag gcc ctg gct gaa ctg ctt cat ggg	255
Glu Thr Pro Thr Val Ala Ser Glu Ala Leu Ala Glu Leu Leu His Gly	
42 47 52 57	
gcc ctg ctg agg agg ggc cca gag atg ggc tac ctg cca ggg cct ccc	303
Ala Leu Leu Arg Arg Gly Pro Glu Met Gly Tyr Leu Pro Gly Pro Pro	
58 63 68 73	
ctt ggg cct gag gga gga gag gag gag acg acg acc acc atc atc acc	351
Leu Gly Pro Glu Gly Gly Glu Glu Glu Thr Thr Thr Thr Ile Ile Thr	
74 79 84 89	
acg aca act gtt acc act acg gtg acc agc cca gtt ctg tgt aat aac	399
Thr Thr Thr Val Thr Thr Thr Val Thr Ser Pro Val Leu Cys Asn Asn	
90 95 100 105	
aac atc tcc gag ggc gaa ggg tat gtg gag tct cca gat ctg ggg agc	447
Asn Ile Ser Glu Gly Glu Gly Tyr Val Glu Ser Pro Asp Leu Gly Ser	
106 111 116 121	
ccc gtc agc cgc acc ctg ggg ctc ctg gac tgc act tac agc atc cat	495
Pro Val Ser Arg Thr Leu Gly Leu Leu Asp Cys Thr Tyr Ser Ile His	
122 127 132 137	
gtc tac cct ggc tac ggc att gag atc cag gtg cag acg ctg aac ctg	543
Val Tyr Pro Gly Tyr Gly Ile Glu Ile Gln Val Gln Thr Leu Asn Leu	
138 143 148 153	
tca cag gaa gag gag ctc ctg gtg ctg gct ggt ggg gga tcc cca ggc	591
Ser Gln Glu Glu Glu Leu Leu Val Leu Ala Gly Gly Gly Ser Pro Gly	
154 159 164 169	
ctg gcc ccc cga ctc ctg gcc aac tca tcc atg ctt gga gaa gga caa	639
Leu Ala Pro Arg Leu Leu Ala Asn Ser Ser Met Leu Gly Glu Gly Gln	
170 175 180 185	
gtc ctt cgg agc cca acc aac cgg ctg ctt ctg cac ttc cag agc cca	687
Val Leu Arg Ser Pro Thr Asn Arg Leu Leu Leu His Phe Gln Ser Pro	
186 191 196 201	
cgg gtc cca agg ggc ggt ggc ttc agg atc cac tat cag gcc tac ctc	735
Arg Val Pro Arg Gly Gly Gly Phe Arg Ile His Tyr Gln Ala Tyr Leu	
202 207 212 217	
ctg agc tgt ggc ttc cct ccc cgg ccg gcc cat ggg gac gtg agt gtg	783
Leu Ser Cys Gly Phe Pro Pro Arg Pro Ala His Gly Asp Val Ser Val	
218 223 228 233	

acg gac ctg cac cct ggg ggc act gcc acc ttt cac tgt gat tcg ggc Thr Asp Leu His Pro Gly Gly Thr Ala Thr Phe His Cys Asp Ser Gly 234 239 244 249	831
tac cag ctg cag gga gag gag acc ctc atc tgc ctc aat ggc acc cgg Tyr Gln Leu Gln Gly Glu Glu Thr Leu Ile Cys Leu Asn Gly Thr Arg 250 255 260 265	879
cca tcc tgg aac ggt gaa acc ccc agc tgc atg gca tcc tgt ggt ggc Pro Ser Trp Asn Gly Glu Thr Pro Ser Cys Met Ala Ser Cys Gly Gly 266 271 276 281	927
acc atc cac aat gcc acc ctg ggc cgc atc gtg tcc cca gag cct ggg Thr Ile His Asn Ala Thr Leu Gly Arg Ile Val Ser Pro Glu Pro Gly 282 287 292 297	975
gga gcc gta ggg ccc aac ctc acc tgc cgt tgg gtc att gaa gca gct Gly Ala Val Gly Pro Asn Leu Thr Cys Arg Trp Val Ile Glu Ala Ala 298 303 308 313	1023
gag ggg cgc cgg ctg cac ctg cac ttt gaa agg gtc tcg ctg gat gag Glu Gly Arg Arg Leu His Leu His Phe Glu Arg Val Ser Leu Asp Glu 314 319 324 329	1071
gac aat gac cgg ctg atg gtg cgc tca ggg ggc agc ccc cta tcc ccc Asp Asn Asp Arg Leu Met Val Arg Ser Gly Gly Ser Pro Leu Ser Pro 330 335 340 345	1119
gtg atc tat gat tcg gac atg gac gat gtc ccc gag cgg ggt ctc atc Val Ile Tyr Asp Ser Asp Met Asp Asp Val Pro Glu Arg Gly Leu Ile 346 351 356 361	1167
agt gac gcc cag tcc ctc tac gtg gag ctg ctg tca gag aca cct gcc Ser Asp Ala Gln Ser Leu Tyr Val Glu Leu Leu Ser Glu Thr Pro Ala 362 367 372 377	1215
aat ccc ctg ctg tta agc ctt cga ttt gaa gcc ttt gag gag gat cgc Asn Pro Leu Leu Leu Ser Leu Arg Phe Glu Ala Phe Glu Glu Asp Arg 378 383 388 393	1263
tgc ttc gcc ccc ttc ctg gca cat gga aat gtc act acc acg gac cct Cys Phe Ala Pro Phe Leu Ala His Gly Asn Val Thr Thr Thr Asp Pro 394 399 404 409	1311
gag tat cgc cca ggg gca ctg gca acc ttc tcg tgc ctc cca gga tat Glu Tyr Arg Pro Gly Ala Leu Ala Thr Phe Ser Cys Leu Pro Gly Tyr 410 415 420 425	1359
gcc ctg gag ccc cct ggg ccc ccc aat gcc atc gaa tgt gtg gat ccc Ala Leu Glu Pro Pro Gly Pro Pro Asn Ala Ile Glu Cys Val Asp Pro 426 431 436 441	1407
aca gaa ccc cac tgg aac gac aca gag ccg gcc tgc aaa gcc atg tgt Thr Glu Pro His Trp Asn Asp Thr Glu Pro Ala Cys Lys Ala Met Cys 442 447 452 457	1455

gga ggg gag ctg tcg gaa cca gct ggc gtg gtc ctc tct ccc gac tgg Gly Gly Glu Leu Ser Glu Pro Ala Gly Val Val Leu Ser Pro Asp Trp 458 463 468 473	1503
ccc cag agc tat agc ccg ggc caa gac tgc gtg tgg ggc gtg cac gtc Pro Gln Ser Tyr Ser Pro Gly Gln Asp Cys Val Trp Gly Val His Val 474 479 484 489	1551
cag gaa gag aag cgc atc ttg ctc caa gtt gag ata ttg aat gtg cgg Gln Glu Glu Lys Arg Ile Leu Leu Gln Val Glu Ile Leu Asn Val Arg 490 495 500 505	1599
gaa ggg gac atg ctg acg ctg ttt gac ggg gac ggt ccc agc gcc cga Glu Gly Asp Met Leu Thr Leu Phe Asp Gly Asp Gly Pro Ser Ala Arg 506 511 516 521	1647
gtc ttg gcc cag ctg cgg gga cct cag ccg cgc cgc cgc ctt ctc tcc Val Leu Ala Gln Leu Arg Gly Pro Gln Pro Arg Arg Arg Leu Leu Ser 522 527 532 537	1695
tct ggg ccc gac ctc aca ctg cag ttt cag gca ccg ccc ggg ccc cca Ser Gly Pro Asp Leu Thr Leu Gln Phe Gln Ala Pro Pro Gly Pro Pro 538 543 548 553	1743
aat cca ggc ctg ggc cag ggc ttc gta ttg cac ttc aaa gag gtc ccg Asn Pro Gly Leu Gly Gln Gly Phe Val Leu His Phe Lys Glu Val Pro 554 559 564 569	1791
agg aac gac acg tgc ccc gag ctg cca cct ccg gag tgg ggc tgg aga Arg Asn Asp Thr Cys Pro Glu Leu Pro Pro Pro Glu Trp Gly Trp Arg 570 575 580 585	1839
acg gca tcc cac ggg gac ctg atc cgg ggc acg gtg ctc acc tac cag Thr Ala Ser His Gly Asp Leu Ile Arg Gly Thr Val Leu Thr Tyr Gln 586 591 596 601	1887
tgc gag cct ggc tac gag ctg cta ggc tcc gac att ctc act tgc cag Cys Glu Pro Gly Tyr Glu Leu Leu Gly Ser Asp Ile Leu Thr Cys Gln 602 607 612 617	1935
tgg gac ctg tct tgg agc gcc gcg ccg ccc gcc tgc caa aag atc atg Trp Asp Leu Ser Trp Ser Ala Ala Pro Pro Ala Cys Gln Lys Ile Met 618 623 628 633	1983
act tgt gct gac cct ggc gag att gcc aac ggg cac cgc acc gcc tcg Thr Cys Ala Asp Pro Gly Glu Ile Ala Asn Gly His Arg Thr Ala Ser 634 639 644 649	2031
gac gcc ggc ttc ccc gtt ggc tcc cac gtc cag tac cgc tgc ctg cca Asp Ala Gly Phe Pro Val Gly Ser His Val Gln Tyr Arg Cys Leu Pro 650 655 660 665	2079
ggg tac agc ctc gag ggg gca gcc atg ctc acc tgc tac agc cgg gac Gly Tyr Ser Leu Glu Gly Ala Ala Met Leu Thr Cys Tyr Ser Arg Asp 666 671 676 681	2127
aca ggc aca ccc aag tgg agc gat agg gtc ccc aaa tgc gcc ttg aag	2175

Thr Gly Thr Pro Lys Trp Ser Asp Arg Val Pro Lys Cys Ala Leu Lys	
682 687 692 697	
tac gag ccg tgc ctg aac ccg ggg gtt ccc gag aat ggc tac cag acg	2223
Tyr Glu Pro Cys Leu Asn Pro Gly Val Pro Glu Asn Gly Tyr Gln Thr	
698 703 708 713	
ctg tac aag cac cac tac cag gcg ggc gag tct ctg cgc ttc ttc tgc	2271
Leu Tyr Lys His His Tyr Gln Ala Gly Glu Ser Leu Arg Phe Phe Cys	
714 719 724 729	
tat gag ggc ttt gag ctt atc ggc gag gtc acc atc acc tgt gtg ccc	2319
Tyr Glu Gly Phe Glu Leu Ile Gly Glu Val Thr Ile Thr Cys Val Pro	
730 735 740 745	
ggc cac ccc tcc cag tgg acc agc cag ccc cca ctc tgc aaa gtg acc	2367
Gly His Pro Ser Gln Trp Thr Ser Gln Pro Pro Leu Cys Lys Val Thr	
746 751 756 761	
cag acc aca gat cca tca cgg cag ctg gaa ggg ggg aac ctg gcc ctg	2415
Gln Thr Thr Asp Pro Ser Arg Gln Leu Glu Gly Gly Asn Leu Ala Leu	
762 767 772 777	
gcc atc ctg ctg cct cta ggc ttg gtc att gtc ctc ggc agt ggc gtt	2463
Ala Ile Leu Leu Pro Leu Gly Leu Val Ile Val Leu Gly Ser Gly Val	
778 783 788 793	
tac atc tac tac acc aag ctt cag gga aag tcc ctt ttc ggc ttc tcg	2511
Tyr Ile Tyr Tyr Thr Lys Leu Gln Gly Lys Ser Leu Phe Gly Phe Ser	
794 799 804 809	
ggc tcc cac tcc tac agc ccc atc acc gtg gag tcg gac ttc agc aac	2559
Gly Ser His Ser Tyr Ser Pro Ile Thr Val Glu Ser Asp Phe Ser Asn	
810 815 820 825	
ccg ctg tat gaa gct ggg gat acg cgg gag tat gaa gtt tcc atc tga	2607
Pro Leu Tyr Glu Ala Gly Asp Thr Arg Glu Tyr Glu Val Ser Ile *	
826 831 836 841	
acccaagac tacagctgca ggaccagga cgccctccc ctctcatc gggcagaggg	2667
aaatacggga cccggtctct gctcctggc tgccctcctc cctggtctgtg taaatagtct	2727
ccctatccca cgagggggct ttgatggccc tggagatcct acagtaaata aaccagcatc	2787
ctgccgcca aagccgcctc ttctcagttg ccaaacgagg ggcctgcccc ccgccctacc	2847
ggcttttggg ttctgggagg ggaactctgc ctccctgcaa atcttgacgc ccctcctgcc	2907
cagggcaccc ctcaaggact gccccgata gctctactgt tcccttgccc acgaagggtgc	2967
ccccctccca gatgccctgg ccctaggcct gactccggcc aggagggtca gaagaaggac	3027
aaaggggaga gctgggacaa ggccttgccc ccttctgccc atctcccca cccacagtct	3087
ctccaccttt gcttctgaat tcttggtttt gagcaataaa cagaaaatcg ccacttgtaa	3147

aaaaaaaaaa aa

3159

<210> 20
 <211> 3198
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (85)..(2646)

<400> 20

cgcccgggca ggtcgggagac ggaggaaagg tggcagccag attacttaga gaggcacaga	60
ggagagagat cggggtgagt cgcc atg ggg act ccc agg gcc cag cac ccg	111
Met Gly Thr Pro Arg Ala Gln His Pro	
1 5	
ccg cct ccc cag ctg ctg ttc cta att ctg ctg agc tgt ccc tgg atc	159
Pro Pro Pro Gln Leu Leu Phe Leu Ile Leu Leu Ser Cys Pro Trp Ile	
10 15 20 25	
cag ggt ctg ccc ctg aag gag gag gag ata ttg cca gag cct gga agt	207
Gln Gly Leu Pro Leu Lys Glu Glu Glu Ile Leu Pro Glu Pro Gly Ser	
26 31 36 41	
gag acc ccc acg gtg gcc tct gag gcc ctg gct gaa ctg ctt cat ggg	255
Glu Thr Pro Thr Val Ala Ser Glu Ala Leu Ala Glu Leu Leu His Gly	
42 47 52 57	
gcc ctg ctg agg agg ggc cca gag atg ggc tac ctg cca ggg cct ccc	303
Ala Leu Leu Arg Arg Gly Pro Glu Met Gly Tyr Leu Pro Gly Pro Pro	
58 63 68 73	
ctt ggg cct gag gga gga gag gag gag acg acg acc acc atc atc acc	351
Leu Gly Pro Glu Gly Gly Glu Glu Glu Thr Thr Thr Thr Ile Ile Thr	
74 79 84 89	
acg aca act gtt acc act acg gtg acc agc cca gtt ctg tgt aat aac	399
Thr Thr Thr Val Thr Thr Thr Val Thr Ser Pro Val Leu Cys Asn Asn	
90 95 100 105	
aac atc tcc gag ggc gaa ggg tat gtg gag tct cca gat ctg ggg agc	447
Asn Ile Ser Glu Gly Glu Gly Tyr Val Glu Ser Pro Asp Leu Gly Ser	
106 111 116 121	
ccc gtc agc cgc acc ctg ggg ctc ctg gac tgc act tac agc atc cat	495
Pro Val Ser Arg Thr Leu Gly Leu Leu Asp Cys Thr Tyr Ser Ile His	
122 127 132 137	
gtc tac cct ggc tac ggc att gag atc cag gtg cag acg ctg aac ctg	543
Val Tyr Pro Gly Tyr Gly Ile Glu Ile Gln Val Gln Thr Leu Asn Leu	
138 143 148 153	

tca Ser 154	cag Gln	gaa Glu	gag Glu	gag Glu	ctc Leu 159	ctg Leu	gtg Val	ctg Leu	gct Ala	ggg Gly 164	ggg Gly	gga Gly	tcc Ser	cca Pro	ggc Gly 169	591
ctg Leu 170	gcc Ala	ccc Pro	cga Arg	ctc Leu	ctg Leu 175	gcc Ala	aac Asn	tca Ser	tcc Ser	atg Met 180	ctt Leu	gga Gly	gaa Glu	gga Gly	caa Gln 185	639
gtc Val 186	ctt Leu	cgg Arg	agc Ser	cca Pro	acc Thr 191	aac Asn	cgg Arg	ctg Leu	ctt Leu	ctg Leu 196	cac His	ttc Phe	cag Gln	agc Ser	cca Pro 201	687
cgg Arg 202	gtc Val	cca Pro	agg Arg	ggc Gly	ggg Gly 207	ggc Gly	ttc Phe	agg Arg	atc Ile	cac His 212	tat Tyr	cag Gln	gcc Ala	tac Tyr	ctc Leu 217	735
ctg Leu 218	agc Ser	tgt Cys	ggc Gly	ttc Phe	cct Pro 223	ccc Pro	cgg Arg	ccg Pro	gcc Ala	cat His 228	ggg Gly	gac Asp	gtg Val	agt Ser	gtg Val 233	783
acg Thr 234	gac Asp	ctg Leu	cac His	cct Pro	ggg Gly 239	ggc Gly	act Thr	gcc Ala	acc Thr	ttt Phe 244	cac His	tgt Cys	gat Asp	tcg Ser	ggc Gly 249	831
tac Tyr 250	cag Gln	ctg Leu	cag Gln	gga Gly	gag Glu 255	gag Glu	acc Thr	ctc Leu	atc Ile	tgc Cys 260	ctc Leu	aat Asn	ggc Gly	acc Thr	cgg Arg 265	879
cca Pro 266	tcc Ser	tgg Trp	aac Asn	ggg Gly	gaa Glu 271	acc Thr	ccc Pro	agc Ser	tgc Cys	atg Met 276	gca Ala	tcc Ser	tgt Cys	ggg Gly	ggc Gly 281	927
acc Thr 282	atc Ile	cac His	aat Asn	gcc Ala	acc Thr 287	ctg Leu	ggc Gly	cgc Arg	atc Ile	gtg Val 292	tcc Ser	cca Pro	gag Glu	cct Pro	ggg Gly 297	975
gga Gly 298	gcc Ala	gta Val	ggg Gly	ccc Pro	aac Asn 303	ctc Leu	acc Thr	tgc Cys	cgt Arg	tgg Trp 308	gtc Val	att Ile	gaa Glu	gca Ala	gct Ala 313	1023
gag Glu 314	ggg Gly	cgc Arg	cgg Arg	ctg Leu	cac His 319	ctg Leu	cac His	ttt Phe	gaa Glu	agg Arg 324	gtc Val	tcg Ser	ctg Leu	gat Asp	gag Glu 329	1071
gac Asp 330	aat Asn	gac Asp	cgg Arg	ctg Leu	atg Met 335	gtg Val	cgc Arg	tca Ser	ggg Gly	ggc Gly 340	agc Ser	ccc Pro	cta Leu	tcc Ser	ccc Pro 345	1119
gtg Val 346	atc Ile	tat Tyr	gat Asp	tcg Ser	gac Asp 351	atg Met	gac Asp	gat Asp	gtc Val	ccc Pro 356	gag Glu	cgg Arg	ggg Gly	ctc Leu	atc Ile 361	1167
agt Ser 362	gac Asp	gcc Ala	cag Gln	tcc Ser	ctc Leu 367	tac Tyr	gtg Val	gag Glu	ctg Leu	ctg Leu 372	tca Ser	gag Glu	aca Thr	cct Pro	gcc Ala 377	1215
aat	ccc	ctg	ctg	tta	agc	ctt	cga	ttt	gaa	gcc	ttt	gag	gag	gat	cgc	1263

Asn Pro Leu Leu Leu Ser Leu Arg Phe Glu Ala Phe Glu Glu Asp Arg	
378 383 388 393	
tgc ttc gcc ccc ttc ctg gca cat gga aat gtc act acc acg gac cct	1311
Cys Phe Ala Pro Phe Leu Ala His Gly Asn Val Thr Thr Thr Asp Pro	
394 399 404 409	
gag tat cgc cca ggg gca ctg gca acc ttc tcg tgc ctc cca gga tat	1359
Glu Tyr Arg Pro Gly Ala Leu Ala Thr Phe Ser Cys Leu Pro Gly Tyr	
410 415 420 425	
gcc ctg gag ccc cct ggg ccc ccc aat gcc atc gaa tgt gtg gat ccc	1407
Ala Leu Glu Pro Pro Gly Pro Pro Asn Ala Ile Glu Cys Val Asp Pro	
426 431 436 441	
aca gaa ccc cac tgg aac gac aca gag ccg gcc tgc aaa gcc atg tgt	1455
Thr Glu Pro His Trp Asn Asp Thr Glu Pro Ala Cys Lys Ala Met Cys	
442 447 452 457	
gga ggg gag ctg tcg gaa cca gct ggc gtg gtc ctc tct ccc gac tgg	1503
Gly Gly Glu Leu Ser Glu Pro Ala Gly Val Val Leu Ser Pro Asp Trp	
458 463 468 473	
ccc cag agc tat agc ccg ggc caa gac tgc gtg tgg ggc gtg cac gtc	1551
Pro Gln Ser Tyr Ser Pro Gly Gln Asp Cys Val Trp Gly Val His Val	
474 479 484 489	
cag gaa gag aag cgc atc ttg ctc caa gtt gag ata ttg aat gtg cgg	1599
Gln Glu Glu Lys Arg Ile Leu Leu Gln Val Glu Ile Leu Asn Val Arg	
490 495 500 505	
gaa ggg gac atg ctg acg ctg ttt gac ggg gac ggt ccc agc gcc cga	1647
Glu Gly Asp Met Leu Thr Leu Phe Asp Gly Asp Gly Pro Ser Ala Arg	
506 511 516 521	
gtc ttg gcc cag ctg ccg gga cct cag ccg cgc cgc cgc ctt ctc tcc	1695
Val Leu Ala Gln Leu Arg Gly Pro Gln Pro Arg Arg Arg Leu Leu Ser	
522 527 532 537	
tct ggg ccc gac ctc aca ctg cag ttt cag gca ccg ccc ggg ccc cca	1743
Ser Gly Pro Asp Leu Thr Leu Gln Phe Gln Ala Pro Pro Gly Pro Pro	
538 543 548 553	
aat cca ggc ctg ggc cag ggc ttc gta ttg cac ttc aaa gag gtc ccg	1791
Asn Pro Gly Leu Gly Gln Gly Phe Val Leu His Phe Lys Glu Val Pro	
554 559 564 569	
agg aac gac acg tgc ccc gag ctg cca cct ccg gag tgg ggc tgg aga	1839
Arg Asn Asp Thr Cys Pro Glu Leu Pro Pro Pro Glu Trp Gly Trp Arg	
570 575 580 585	
acg gca tcc cac ggg gac ctg atc ccg ggc acg gtg ctc acc tac cag	1887
Thr Ala Ser His Gly Asp Leu Ile Arg Gly Thr Val Leu Thr Tyr Gln	
586 591 596 601	
tgc gag cct ggc tac gag ctg cta ggc tcc gac att ctc act tgc cag	1935
Cys Glu Pro Gly Tyr Glu Leu Leu Gly Ser Asp Ile Leu Thr Cys Gln	

602	607	612	617	
tgg gac ctg tct tgg agc gcc gcg ccg ccc gcc tgc caa aag atc atg				1983
Trp Asp Leu Ser Trp Ser Ala Ala Pro Pro Ala Cys Gln Lys Ile Met				
618	623	628	633	
act tgt gct gac cct ggc gag att gcc aac ggg cac cgc acc gcc tcg				2031
Thr Cys Ala Asp Pro Gly Glu Ile Ala Asn Gly His Arg Thr Ala Ser				
634	639	644	649	
gac gcc ggc ttc ccc gtt ggc tcc cac gtc cag tac cgc tgc ctg cca				2079
Asp Ala Gly Phe Pro Val Gly Ser His Val Gln Tyr Arg Cys Leu Pro				
650	655	660	665	
ggg tac agc ctc gag ggg gca gcc atg ctc acc tgc tac agc cgg gac				2127
Gly Tyr Ser Leu Glu Gly Ala Ala Met Leu Thr Cys Tyr Ser Arg Asp				
666	671	676	681	
aca ggc aca ccc aag tgg agc gat agg gtc ccc aaa tgc gcc ttg aag				2175
Thr Gly Thr Pro Lys Trp Ser Asp Arg Val Pro Lys Cys Ala Leu Lys				
682	687	692	697	
tac gag ccg tgc ctg aac ccg ggg gtt ccc gag aat ggc tac cag acg				2223
Tyr Glu Pro Cys Leu Asn Pro Gly Val Pro Glu Asn Gly Tyr Gln Thr				
698	703	708	713	
ctg tac aag cac cac tac cag gcg ggc gag tct ctg cgc ttc ttc tgc				2271
Leu Tyr Lys His His Tyr Gln Ala Gly Glu Ser Leu Arg Phe Phe Cys				
714	719	724	729	
tat gag ggc ttt gag ctt atc ggc gag gtc acc atc acc tgt gtg ccc				2319
Tyr Glu Gly Phe Glu Leu Ile Gly Glu Val Thr Ile Thr Cys Val Pro				
730	735	740	745	
ggc cac ccc tcc cag tgg acc agc cag ccc cca ctc tgc aaa gtt gcc				2367
Gly His Pro Ser Gln Trp Thr Ser Gln Pro Pro Leu Cys Lys Val Ala				
746	751	756	761	
tat gag gag ctc ctg gac aac cga aaa ctg gaa gtg acc cag acc aca				2415
Tyr Glu Glu Leu Leu Asp Asn Arg Lys Leu Glu Val Thr Gln Thr Thr				
762	767	772	777	
gat cca tca cgg cag ctg gaa ggg ggg aac ctg gcc ctg gcc atc ctg				2463
Asp Pro Ser Arg Gln Leu Glu Gly Gly Asn Leu Ala Leu Ala Ile Leu				
778	783	788	793	
ctg cct cta ggc ttg gtc att gtc ctc ggc agt ggc gtt tac atc tac				2511
Leu Pro Leu Gly Leu Val Ile Val Leu Gly Ser Gly Val Tyr Ile Tyr				
794	799	804	809	
tac acc aag ctt cag gga aag tcc ctt ttc ggc ttc tcg ggc tcc cac				2559
Tyr Thr Lys Leu Gln Gly Lys Ser Leu Phe Gly Phe Ser Gly Ser His				
810	815	820	825	
tcc tac agc ccc atc acc gtg gag tcg gac ttc agc aac ccg ctg tat				2607
Ser Tyr Ser Pro Ile Thr Val Glu Ser Asp Phe Ser Asn Pro Leu Tyr				
826	831	836	841	

gaa gct ggg gat acg cgg gag tat gaa gtt tcc atc tga accccaagac 2656
 Glu Ala Gly Asp Thr Arg Glu Tyr Glu Val Ser Ile *
 842 847 852

tacagctgca ggacccagga cgccccctccc ctctctcattc gggcagaggg aaatacggga 2716

cccgggtctct gctccttggc tgccctcctc cctggctgtg taaatagtct ccctatccca 2776

cgaggggggct ttgatggccc tggagatcct acagtaaata aaccagcatc ctgccgcca 2836

aagccgcctc ttctcagttg ccaaacgagg ggcctgcccc ccgccctacc ggctttttgga 2896

ttctgggagg ggaactctgc ctccctgcaa atcttgacgc ccctcctgcc cagggcacccc 2956

ctcaaggact gccccgata gctctactgt tcccttggcc acgaagggtgc ccccctccca 3016

gatgccctgg ccctaggcct gactccggcc aggaggggtca gaagaaggac aaaggggaga 3076

gctgggacaa ggccttgccc ccttcctgcc atctcccaa cccacagtct ctccaccttt 3136

gcttctgaat tcttggtttt gagcaataaa cagaaaatcg ccacttgtaa aaaaaaaaaa 3196

aa 3198

<210> 21
 <211> 3238
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (172)..(2121)

<400> 21

ttgtaaacgc cgggccagtg aattgaattt aggtgacact atagaagagc tatgacgtcg 60

catgcacgcg tacgtaagct tggatcctct agagcggccg cgggagccgg ggccgcccgcg 120

ccggcttctc agcaccgccg aaccggcacc ggcgctgtcc agaccgaggc c atg aag 177
 Met Lys
 1

cag att ctc ggg gtg atc gac aag aaa ctt cgg aac ctg gag aag aaa 225
 Gln Ile Leu Gly Val Ile Asp Lys Lys Leu Arg Asn Leu Glu Lys Lys
 3 8 13 18

aag ggt aag ctt gat gat tac cag gaa cga atg aac aaa ggg gaa agg 273
 Lys Gly Lys Leu Asp Asp Tyr Gln Glu Arg Met Asn Lys Gly Glu Arg
 19 24 29 34

ctt aat caa gat cag ctg gat gcc gtt tct aag tac cag gaa gtc aca 321
 Leu Asn Gln Asp Gln Leu Asp Ala Val Ser Lys Tyr Gln Glu Val Thr
 35 40 45 50

aat Asn 51	aat Asn	ttg Leu	gag Glu	ttt Phe	gca Ala 56	aaa Lys	gaa Glu	tta Leu	cag Gln	agg Arg 61	agt Ser	ttc Phe	atg Met	gca Ala	cta Leu 66	369
agt Ser 67	caa Gln	gat Asp	att Ile	cag Gln	aaa Lys 72	aca Thr	ata Ile	aag Lys	aag Lys	aca Thr 77	gca Ala	cgt Arg	cgg Arg	gag Glu	cag Gln 82	417
ctt Leu 83	atg Met	aga Arg	gaa Glu	gaa Glu	gct Ala 88	gaa Glu	cag Gln	aaa Lys	cgt Arg	tta Leu 93	aaa Lys	act Thr	gta Val	ctt Leu	gag Glu 98	465
cta Leu 99	cag Gln	tat Tyr	gtt Val	ttg Leu	gac Asp 104	aaa Lys	ttg Leu	gga Gly	gat Asp	gat Asp 109	gaa Glu	gtg Val	cgg Arg	act Thr	gac Asp 114	513
ctg Leu 115	aaa Lys	caa Gln	ggg Gly	ttg Leu	aat Asn 120	gga Gly	gtg Val	cca Pro	ata Ile	ttg Leu 125	tcc Ser	gaa Glu	gag Glu	gag Glu	ttg Leu 130	561
tca Ser 131	ttg Leu	ttg Leu	gat Asp	gaa Glu	ttc Phe 136	tat Tyr	aag Lys	cta Leu	gta Val	gac Asp 141	cct Pro	gaa Glu	cgg Arg	gac Asp	atg Met 146	609
agc Ser 147	ttg Leu	agg Arg	ttg Leu	aat Asn	gaa Glu 152	cag Gln	tat Tyr	gaa Glu	cat His	gcc Ala 157	tcc Ser	att Ile	cac His	ctg Leu	tgg Trp 162	657
gac Asp 163	ctg Leu	ctg Leu	gaa Glu	ggg Gly	aag Lys 168	gaa Glu	aaa Lys	cct Pro	gta Val	tgt Cys 173	gga Gly	acc Thr	acc Thr	tat Tyr	aaa Lys 178	705
gtt Val 179	cta Leu	aag Lys	gaa Glu	att Ile	gtt Val 184	gag Glu	cgt Arg	gtt Val	ttt Phe	cag Gln 189	tca Ser	aac Asn	tac Tyr	ttt Phe	gac Asp 194	753
agc Ser 195	acc Thr	cac His	aac Asn	cac His	cag Gln 200	aat Asn	ggg Gly	ctg Leu	tgt Cys	gag Glu 205	gaa Glu	gaa Glu	gag Glu	gca Ala	gcc Ala 210	801
tca Ser 211	gca Ala	cct Pro	gca Ala	gtt Val	gaa Glu 216	gac Asp	cag Gln	gta Val	cct Pro	gaa Glu 221	gct Ala	gaa Glu	cct Pro	gag Glu	cca Pro 226	849
gca Ala 227	gaa Glu	gag Glu	tac Tyr	act Thr	gag Glu 232	caa Gln	agt Ser	gaa Glu	gtt Val	gaa Glu 237	tca Ser	aca Thr	gag Glu	tat Tyr	gta Val 242	897
aat Asn 243	aga Arg	cag Gln	ttc Phe	atg Met	gca Ala 248	gaa Glu	aca Thr	cag Gln	ttc Phe	acc Thr 253	agt Ser	ggg Gly	gaa Glu	aag Lys	gag Glu 258	945
cag Gln 259	gta Val	gat Asp	gag Glu	tgg Trp	aca Thr 264	gtt Val	gaa Glu	acg Thr	gtt Val	gag Glu 269	gtg Val	gta Val	aat Asn	tca Ser	ctc Leu 274	993

cag cag caa cct cag gct gca tcc cct tca gta cca gag ccc cac tct	1041
Gln Gln Gln Pro Gln Ala Ala Ser Pro Ser Val Pro Glu Pro His Ser	
275 280 285 290	
ttg act cca gtg gct cag gca gat ccc ctt gtg aga aga cag cga gta	1089
Leu Thr Pro Val Ala Gln Ala Asp Pro Leu Val Arg Arg Gln Arg Val	
291 296 301 306	
caa gac ctt atg gca caa atg cag ggt ccc gat aat ttc ata cag gat	1137
Gln Asp Leu Met Ala Gln Met Gln Gly Pro Asp Asn Phe Ile Gln Asp	
307 312 317 322	
tca atg ctg gat ttt gaa aat cag aca ctt gat cct gcc att gta tct	1185
Ser Met Leu Asp Phe Glu Asn Gln Thr Leu Asp Pro Ala Ile Val Ser	
323 328 333 338	
gca cag cct atg aat cca aca caa aac atg gac atg ccc cag ctg gtt	1233
Ala Gln Pro Met Asn Pro Thr Gln Asn Met Asp Met Pro Gln Leu Val	
339 344 349 354	
tgc cct cca gtt cat tct gaa tct aga ctt gct cag cct aat caa gtt	1281
Cys Pro Pro Val His Ser Glu Ser Arg Leu Ala Gln Pro Asn Gln Val	
355 360 365 370	
cct gta caa cca gaa gcg aca cag gtt cct ttg gta tca tcc aca agt	1329
Pro Val Gln Pro Glu Ala Thr Gln Val Pro Leu Val Ser Ser Thr Ser	
371 376 381 386	
gag ggg tac aca gca tct caa ccc ttg tac cag cct tct cat gct aca	1377
Glu Gly Tyr Thr Ala Ser Gln Pro Leu Tyr Gln Pro Ser His Ala Thr	
387 392 397 402	
gag caa cga cca cag aag gaa cca att gat cag att cag gca aca atc	1425
Glu Gln Arg Pro Gln Lys Glu Pro Ile Asp Gln Ile Gln Ala Thr Ile	
403 408 413 418	
tct tta aat aca gac cag act aca gca tca tca tcc ctt cct gct gcg	1473
Ser Leu Asn Thr Asp Gln Thr Thr Ala Ser Ser Ser Leu Pro Ala Ala	
419 424 429 434	
tct cag cct caa gta ttt cag gct ggg aca agc aaa cct tta cat agc	1521
Ser Gln Pro Gln Val Phe Gln Ala Gly Thr Ser Lys Pro Leu His Ser	
435 440 445 450	
agt gga atc aat gta aat gca gct cca ttc caa tcc atg caa acg gtg	1569
Ser Gly Ile Asn Val Asn Ala Ala Pro Phe Gln Ser Met Gln Thr Val	
451 456 461 466	
ttc aat atg aat gcc cca gtt cct cct gtt aat gaa cca gaa act tta	1617
Phe Asn Met Asn Ala Pro Val Pro Pro Val Asn Glu Pro Glu Thr Leu	
467 472 477 482	
aaa cag caa aat cag tac cag gcc agt tat aac cag agc ttt tct agt	1665
Lys Gln Gln Asn Gln Tyr Gln Ala Ser Tyr Asn Gln Ser Phe Ser Ser	
483 488 493 498	
cag cct cac caa gta gaa caa aca gag ctt cag caa gaa cag ctt caa	1713

Gln Pro His Gln Val Glu Gln Thr Glu Leu Gln Gln Glu Gln Leu Gln	
499 504 509 514	
aca gtg gtt ggc act tac cat ggt tcc cca gac cag tcc cat caa gtg	1761
Thr Val Val Gly Thr Tyr His Gly Ser Pro Asp Gln Ser His Gln Val	
515 520 525 530	
act ggt aac cac cag cag cct cct cag cag aac act gga ttt cca cgt	1809
Thr Gly Asn His Gln Gln Pro Pro Gln Gln Asn Thr Gly Phe Pro Arg	
531 536 541 546	
agc aat cag ccc tat tac aat agt cgt ggt gtg tct cgt gga ggc tcc	1857
Ser Asn Gln Pro Tyr Tyr Asn Ser Arg Gly Val Ser Arg Gly Gly Ser	
547 552 557 562	
cgt ggt gct aga ggc ttg atg aat gga tac cgg ggc cct gca atg gat	1905
Arg Gly Ala Arg Gly Leu Met Asn Gly Tyr Arg Gly Pro Ala Met Asp	
563 568 573 578	
tca gag gag gat atg atg gtt acc gcc ctt cat tct cta aca ctc caa	1953
Ser Glu Glu Asp Met Met Val Thr Ala Leu His Ser Leu Thr Leu Gln	
579 584 589 594	
aca gtg gtt ata cac agt ctc agt tca gtg ctc ccc ggg att act ctg	2001
Thr Val Val Ile His Ser Leu Ser Ser Val Leu Pro Gly Ile Thr Leu	
595 600 605 610	
gct atc aac ggg atg gat atc agc aga att tca agc gag gct ctg ggc	2049
Ala Ile Asn Gly Met Asp Ile Ser Arg Ile Ser Ser Glu Ala Leu Gly	
611 616 621 626	
aga gtg gac cac ggg gag ccc cac gag gtc gtg gag ggc ccc caa gac	2097
Arg Val Asp His Gly Glu Pro His Glu Val Val Glu Gly Pro Gln Asp	
627 632 637 642	
cca aca gag gga tgc cgc aaa tga acactcagca agtgaattaa tctgattcac	2151
Pro Thr Glu Gly Cys Arg Lys *	
643 648	
aggattatgt ttaatcgcca aaaacacact ggccagtgtg ccataatatg ttaccagaag	2211
agttattatc tatttgttct ccctttcagg aaacttattg taaagggact gttttcatcc	2271
cataaagaca ggactacaat tgtcagcttt ctattacctg gatatggaag gaaactatct	2331
ttactctgca tggtctgtcc taagcgcat cttgagcctt gcacatgata ctcagattcc	2391
tcacccttgc ttaggagtaa aacaatatac tttacagggt gataataatc tccatagtta	2451
tttgaagtgg cttgaaaaag gcaagattga cttttatgac attggataaa atctacaaat	2511
cagccctcga gttattcaat gataactgac aaactaaatt atttccctag aaaggaagat	2571
gaaaggagtg gagtgtggtt tggccagaac aactgcattt cacagctttt ccagttaa	2631
tggagcactg aacgttcaga tgcataccaa attatgcatg ggtcctaatac acacataata	2691

ggctggctac cagctttgac acagcactgt tcctctggcc aaacaactgt gggtaaaaaac 2751
 acatgtaaaa tggcttttta acagctgata ctgtataaga caaagccaag atgcaaaatt 2811
 aggctttgat tggcactttt tgaaaaatat gcaacaaata tgggatgtaa tccggatggc 2871
 cgcttctgta cttaatgtga aatatttaga tacctttttg aacacttaac agtttctttg 2931
 agacaatgac tttgtaagga ttggtactat ctatcattcc ttatgacatg tacattgtct 2991
 gtcactaatc cttggatttt gctgtattgt caccgggatt ggtacaggta ctgatgaaaa 3051
 tctctagtgg ataatacataa cactctcggt cacatgtttt tccttcagct tgaaagcttt 3111
 ttttaaaagg aaaagatacc aaatgcctgc tgctaccacc cttttcaatt gctatgtttt 3171
 gaaaggcacc agtatgtgtt ttagattgat ttccctgttt cagggaaatc acggacagta 3231
 gtttccg 3238

<210> 22
 <211> 1826
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (2)..(1723)

<400> 22
 g atg gct cac tat att aca ttt ctc tgc atg gtt ttg gtg ctg ctt 46
 Met Ala His Tyr Ile Thr Phe Leu Cys Met Val Leu Val Leu Leu
 1 5 10
 ctt cag aat tct gtg tta gct gaa gat ggg gaa gta aga tca agt tgt 94
 Leu Gln Asn Ser Val Leu Ala Glu Asp Gly Glu Val Arg Ser Ser Cys
 16 21 26 31
 cgt act gct ccg aca gat tta gtt ttc atc tta gat ggc tct tat agt 142
 Arg Thr Ala Pro Thr Asp Leu Val Phe Ile Leu Asp Gly Ser Tyr Ser
 32 37 42 47
 gtt ggc cca gaa aac ttt gaa ata gtg aaa aag tgg ctt gtc aat atc 190
 Val Gly Pro Glu Asn Phe Glu Ile Val Lys Lys Trp Leu Val Asn Ile
 48 53 58 63
 aca aaa aac ttt gac ata ggg ccg aag ttt att caa gtt gga gtg gtt 238
 Thr Lys Asn Phe Asp Ile Gly Pro Lys Phe Ile Gln Val Gly Val Val
 64 69 74 79
 caa tat agt gac tac cct gtg ctg gag att cct ctc gga agc tat gat 286
 Gln Tyr Ser Asp Tyr Pro Val Leu Glu Ile Pro Leu Gly Ser Tyr Asp
 80 85 90 95

tca gga gaa cat ttg acg gca gca gtg gaa tcc ata ctc tac tta gga	334
Ser Gly Glu His Leu Thr Ala Ala Val Glu Ser Ile Leu Tyr Leu Gly	
96 101 106 111	
gga aac aca aag aca ggg aag gcc atc cag ttt gcg ctc gat tac ctt	382
Gly Asn Thr Lys Thr Gly Lys Ala Ile Gln Phe Ala Leu Asp Tyr Leu	
112 117 122 127	
ttt gcc aag tcc tca cga ttt ctg act aag ata gca gtg gta ctt acg	430
Phe Ala Lys Ser Ser Arg Phe Leu Thr Lys Ile Ala Val Val Leu Thr	
128 133 138 143	
gat ggc aaa tcc caa gat gac gtc aag gat gca gct caa gca gca aga	478
Asp Gly Lys Ser Gln Asp Asp Val Lys Asp Ala Ala Gln Ala Ala Arg	
144 149 154 159	
gat agt aag ata aca tta ttt gct att ggt gtt ggt tca gaa aca gaa	526
Asp Ser Lys Ile Thr Leu Phe Ala Ile Gly Val Gly Ser Glu Thr Glu	
160 165 170 175	
gat gcc gaa ctt aga gct att gcc aac aag cct tcg tct act tat gtg	574
Asp Ala Glu Leu Arg Ala Ile Ala Asn Lys Pro Ser Ser Thr Tyr Val	
176 181 186 191	
ttt tat gtg gaa gac tat att gca ata tcc aaa ata agg gaa gtg atg	622
Phe Tyr Val Glu Asp Tyr Ile Ala Ile Ser Lys Ile Arg Glu Val Met	
192 197 202 207	
aag cag aaa ctt tgt gaa gaa tct gtc tgt cca aca cga att cca gtg	670
Lys Gln Lys Leu Cys Glu Glu Ser Val Cys Pro Thr Arg Ile Pro Val	
208 213 218 223	
gca gct cgt gat gaa agg gga ttt gat att ctt tta ggt tta gat gta	718
Ala Ala Arg Asp Glu Arg Gly Phe Asp Ile Leu Leu Gly Leu Asp Val	
224 229 234 239	
aat aaa aag gtt aag aaa aga ata cag ctt tca cca aaa aag ata aaa	766
Asn Lys Lys Val Lys Lys Arg Ile Gln Leu Ser Pro Lys Lys Ile Lys	
240 245 250 255	
gga tat gaa gta aca tca aaa gtt gat tta tca gaa ctc aca agc aat	814
Gly Tyr Glu Val Thr Ser Lys Val Asp Leu Ser Glu Leu Thr Ser Asn	
256 261 266 271	
gtt ttc cca gaa ggt ctt cct cca tca tat gta ttt gtg tct act caa	862
Val Phe Pro Glu Gly Leu Pro Pro Ser Tyr Val Phe Val Ser Thr Gln	
272 277 282 287	
aga ttt aaa gtc aag aaa att tgg gat tta tgg aga ata tta act att	910
Arg Phe Lys Val Lys Lys Ile Trp Asp Leu Trp Arg Ile Leu Thr Ile	
288 293 298 303	
gat gga agg cca caa ata gca gtt acc tta aat ggt gtg gac aaa atc	958
Asp Gly Arg Pro Gln Ile Ala Val Thr Leu Asn Gly Val Asp Lys Ile	
304 309 314 319	
tta tta ttt aca aca acc agc gta att aat ggc tca caa gtg gtt acc	1006

Leu 320	Phe	Thr	Thr	Thr	Ser	Val	Ile	Asn	Gly	Ser	Gln	Val	Val	Thr		
325					330				335							
ttt Phe 336	gct Ala	aac Asn	cct Pro	caa Gln	gtt Val	aag Lys	acg Thr	ttg Leu	ttt Phe	gat Asp	gaa Glu	ggc Gly	tgg Trp	cac His	caa Gln	1054
341					346				351							
att Ile 352	cgt Arg	ctc Leu	tta Leu	gta Val	aca Thr	gaa Glu	caa Gln	gat Asp	gtg Val	act Thr	ttg Leu	tat Tyr	att Ile	gat Asp	gac Asp	1102
357					362				367							
caa Gln 368	caa Gln	att Ile	gaa Glu	aac Asn	aag Lys	ccc Pro	tta Leu	cat His	cca Pro	gtt Val	tta Leu	ggg Gly	atc Ile	ttg Leu	atc Ile	1150
373					378				383							
aat Asn 384	ggg Gly	caa Gln	acc Thr	caa Gln	att Ile	gga Gly	aaa Lys	tat Tyr	tct Ser	gga Gly	aaa Lys	gaa Glu	gaa Glu	act Thr	gtt Val	1198
389					394				399							
cag Gln 400	ttt Phe	gat Asp	gtc Val	caa Gln	aag Lys	ttg Leu	cga Arg	atc Ile	tac Tyr	tgt Cys	gac Asp	cca Pro	gaa Glu	cag Gln	aac Asn	1246
405					410				415							
aac Asn 416	cgg Arg	gag Glu	aca Thr	gca Ala	tgt Cys	gag Glu	att Ile	cct Pro	gga Gly	ttt Phe	tgc Cys	ctt Leu	aat Asn	ggg Gly	ccc Pro	1294
421					426				431							
agt Ser 432	gat Asp	gta Val	ggg Gly	tca Ser	act Thr	cca Pro	gct Ala	ccc Pro	tgt Cys	att Ile	tgt Cys	cct Pro	ccg Pro	gga Gly	aaa Lys	1342
437					442				447							
cca Pro 448	gga Gly	ctt Leu	caa Gln	ggc Gly	ccc Pro	aaa Lys	ggg Gly	gac Asp	cct Pro	gga Gly	ctg Leu	cct Pro	ggg Gly	aac Asn	cct Pro	1390
453					458				463							
ggc Gly 464	tac Tyr	cct Pro	gga Gly	caa Gln	cct Pro	ggg Gly	caa Gln	gat Asp	ggg Gly	aag Lys	cct Pro	gtg Val	agt Ser	act Thr	gaa Glu	1438
469					474				479							
agc Ser 480	tta Leu	gtc Val	atc Ile	tcc Ser	ggg Gly	ata Ile	tct Ser	ggg Gly	att Ile	aca Thr	gga Gly	tat Tyr	cag Gln	gga Gly	att Ile	1486
485					490				495							
gca Ala 496	ggg Gly	aca Thr	cca Pro	ggg Gly	gtt Val	cca Pro	gga Gly	tct Ser	cca Pro	gga Gly	ata Ile	caa Gln	gga Gly	gct Ala	cga Arg	1534
501					506				511							
gga Gly 512	cta Leu	cca Pro	ggg Gly	tac Tyr	aaa Lys	gga Gly	gaa Glu	cca Pro	ggg Gly	cga Arg	gat Asp	ggg Gly	gac Asp	aag Lys	ggg Gly	1582
517					522				527							
gat Asp 528	cgt Arg	gga Gly	ctt Leu	cct Pro	ggg Gly	ttt Phe	cct Pro	ggg Gly	ctt Leu	cat His	ggc Gly	atg Met	cca Pro	gga Gly	tca Ser	1630
533					538				543							
aag Lys	ggg Gly	gaa Glu	atg Met	ggg Gly	gcc Ala	aaa Lys	gga Gly	gac Asp	aaa Lys	gga Gly	tca Ser	cct Pro	gga Gly	ttt Phe	tat Tyr	1678

544	549	554	559	
ggc aaa aag gga agt ata gat cac aca aca aag tat tca tat tga act				1726
Gly Lys Lys Gly Ser Ile Asp His Thr Thr Lys Tyr Ser Tyr *				
560	565	570		
tttaatgtaa tggaaacaga aaactagaat tgcagttcta acccagcatt agaacagtta				1786
gctctgttca cccttcttag gggattaatt cagaacaatg				1826

<210> 23
 <211> 4759
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (156) .. (3962)

<400> 23	
cgcggagaag cttgggtacc tgagccgcgg tcccgggtga caccctcagt gacgccaggc	60
gcgttccctc ctcttctct ctctctccg gcccgcctt cccttccctc cgcccacctc	120
cctgaagcgg agccgccgtc gccaccagcg ccgtc atg tcg gcc ccc gcc ggg	173
Met Ser Ala Pro Ala Gly	
1	
tcc tct cac ccg gcc gcc agc gcc cgg atc ccg ccc aag ttc ggc gga	221
Ser Ser His Pro Ala Ala Ser Ala Arg Ile Pro Pro Lys Phe Gly Gly	
7 12 17 22	
tcg gcc gtc tca gga gcc gca gcg ccc gcg ggc ccg ggt gcg ggc ccg	269
Ser Ala Val Ser Gly Ala Ala Ala Pro Ala Gly Pro Gly Ala Gly Pro	
23 28 33 38	
gcg ccg cac cag cag aac ggt cca gcc cag aat caa atg cag gtt cca	317
Ala Pro His Gln Gln Asn Gly Pro Ala Gln Asn Gln Met Gln Val Pro	
39 44 49 54	
tct gga tat gga ttg cat cat caa aac tat att gct ccc tca gga cat	365
Ser Gly Tyr Gly Leu His His Gln Asn Tyr Ile Ala Pro Ser Gly His	
55 60 65 70	
tac tct caa gga cct ggg aaa atg acc tca ttg cca ttg gat acc cag	413
Tyr Ser Gln Gly Pro Gly Lys Met Thr Ser Leu Pro Leu Asp Thr Gln	
71 76 81 86	
tgt ggt gat tac tac tct gct ctc tat aca gta cca aca caa aat gtg	461
Cys Gly Asp Tyr Tyr Ser Ala Leu Tyr Thr Val Pro Thr Gln Asn Val	
87 92 97 102	
act cct aac aca gtg aac cag caa cca gga gca cag cag ttg tac agc	509
Thr Pro Asn Thr Val Asn Gln Gln Pro Gly Ala Gln Gln Leu Tyr Ser	

103	108	113	118	
agg ggt cct cct gcc cct cat att gtg gga tcc act cta gga tct ttc				557
Arg Gly Pro Pro Ala Pro His Ile Val Gly Ser Thr Leu Gly Ser Phe				
119	124	129	134	
caa ggt gct gca tcg tca gca tcc cat ttg cat acg agt gcc tcc caa				605
Gln Gly Ala Ala Ser Ser Ala Ser His Leu His Thr Ser Ala Ser Gln				
135	140	145	150	
cca tac tcc tct ttt gtg aat cac tac aat agt cca gcc atg tac tct				653
Pro Tyr Ser Ser Phe Val Asn His Tyr Asn Ser Pro Ala Met Tyr Ser				
151	156	161	166	
gcc agc tct tct gtt gcg tct cag gga ttt ccc tct act tgt ggt cat				701
Ala Ser Ser Ser Val Ala Ser Gln Gly Phe Pro Ser Thr Cys Gly His				
167	172	177	182	
tat gct atg tca act gtt tct aat gcc gcg tat cct agt gtt tca tat				749
Tyr Ala Met Ser Thr Val Ser Asn Ala Ala Tyr Pro Ser Val Ser Tyr				
183	188	193	198	
ccc tct ctg cct gct ggt gat aca tat ggg caa atg ttt acc tca cag				797
Pro Ser Leu Pro Ala Gly Asp Thr Tyr Gly Gln Met Phe Thr Ser Gln				
199	204	209	214	
aat gct ccg act gtt agg cca gtt aaa gat aat tca ttc tct ggt caa				845
Asn Ala Pro Thr Val Arg Pro Val Lys Asp Asn Ser Phe Ser Gly Gln				
215	220	225	230	
aat aca gct atc agc cat cca tcg cca ctt cca cct cta cca tca caa				893
Asn Thr Ala Ile Ser His Pro Ser Pro Leu Pro Pro Leu Pro Ser Gln				
231	236	241	246	
cag cac cac cag cag caa agt ctt tca gga tac agt act cta acg tgg				941
Gln His His Gln Gln Gln Ser Leu Ser Gly Tyr Ser Thr Leu Thr Trp				
247	252	257	262	
tca tct cca ggc ctt cca tcg act caa gac aat ctc atc cga aac cac				989
Ser Ser Pro Gly Leu Pro Ser Thr Gln Asp Asn Leu Ile Arg Asn His				
263	268	273	278	
aca gga tcc ctg gct gta gcg aac aac aac cca acc att act gtt gca				1037
Thr Gly Ser Leu Ala Val Ala Asn Asn Asn Pro Thr Ile Thr Val Ala				
279	284	289	294	
gat tct tta tcc tgt cct gtt atg caa aat gtt cag cct ccc aag tcc				1085
Asp Ser Leu Ser Cys Pro Val Met Gln Asn Val Gln Pro Pro Lys Ser				
295	300	305	310	
agc cca gtg gta tcc act gtt tta tca gga tcc tca gga tcc tca tca				1133
Ser Pro Val Val Ser Thr Val Leu Ser Gly Ser Ser Gly Ser Ser Ser				
311	316	321	326	
aca aga aca cct ccc act gca aat cac cca gtt gag cct gtg acc tca				1181
Thr Arg Thr Pro Pro Thr Ala Asn His Pro Val Glu Pro Val Thr Ser				
327	332	337	342	

gtt	aca	cag	cca	tca	gag	cta	tta	caa	caa	aaa	ggc	gtg	cag	tat	ggc	1229
Val	Thr	Gln	Pro	Ser	Glu	Leu	Leu	Gln	Gln	Lys	Gly	Val	Gln	Tyr	Gly	
343					348					353					358	
gaa	tat	gtt	aat	aac	caa	gct	agc	tcc	gca	cca	act	ccc	ttg	tca	tca	1277
Glu	Tyr	Val	Asn	Asn	Gln	Ala	Ser	Ser	Ala	Pro	Thr	Pro	Leu	Ser	Ser	
359					364					369					374	
act	tcc	gat	gat	gag	gaa	gag	gag	gag	gag	gat	gag	gaa	gca	ggc	gtt	1325
Thr	Ser	Asp	Asp	Glu	Glu	Glu	Glu	Glu	Glu	Asp	Glu	Glu	Ala	Gly	Val	
375					380					385					390	
gac	agc	tct	tct	acc	aca	agc	agt	gct	tct	cca	atg	ccc	aac	agt	tat	1373
Asp	Ser	Ser	Ser	Thr	Thr	Ser	Ser	Ala	Ser	Pro	Met	Pro	Asn	Ser	Tyr	
391					396					401					406	
gat	gcc	ctg	gaa	gga	ggc	agt	tac	cca	gat	atg	ctt	tct	tca	tca	gca	1421
Asp	Ala	Leu	Glu	Gly	Gly	Ser	Tyr	Pro	Asp	Met	Leu	Ser	Ser	Ser	Ala	
407					412					417					422	
agc	agt	cct	gct	cct	gat	ccc	gcc	cct	gaa	cct	gat	cct	gct	tct	gct	1469
Ser	Ser	Pro	Ala	Pro	Asp	Pro	Ala	Pro	Glu	Pro	Asp	Pro	Ala	Ser	Ala	
423					428					433					438	
cca	gct	cca	gct	tca	gct	cca	gct	cct	gtc	gtc	cct	cag	cct	tca	aaa	1517
Pro	Ala	Pro	Ala	Ser	Ala	Pro	Ala	Pro	Val	Val	Pro	Gln	Pro	Ser	Lys	
439					444					449					454	
atg	gct	aag	cct	ttg	gct	atg	gct	atc	caa	cac	ttc	agc	ctg	gtt	atc	1565
Met	Ala	Lys	Pro	Leu	Ala	Met	Ala	Ile	Gln	His	Phe	Ser	Leu	Val	Ile	
455					460					465					470	
aga	atg	cta	cag	cac	cac	tta	ttt	ctg	gag	tac	agc	ccc	agt	aac	ccg	1613
Arg	Met	Leu	Gln	His	His	Leu	Phe	Leu	Glu	Tyr	Ser	Pro	Ser	Asn	Pro	
471					476					481					486	
gta	tat	tct	gga	ttc	cag	cag	tat	cct	caa	cag	tat	cct	ggc	gtg	aac	1661
Val	Tyr	Ser	Gly	Phe	Gln	Gln	Tyr	Pro	Gln	Gln	Tyr	Pro	Gly	Val	Asn	
487					492					497					502	
cag	cta	tcc	tcc	agt	ata	gga	gga	ttg	agt	ctt	cag	agt	tct	cca	caa	1709
Gln	Leu	Ser	Ser	Ser	Ile	Gly	Gly	Leu	Ser	Leu	Gln	Ser	Ser	Pro	Gln	
503					508					513					518	
cca	gaa	agc	ctg	aga	cct	gta	aac	ctt	act	cag	gag	agg	aat	att	tta	1757
Pro	Glu	Ser	Leu	Arg	Pro	Val	Asn	Leu	Thr	Gln	Glu	Arg	Asn	Ile	Leu	
519					524					529					534	
cct	atg	act	cct	gtt	tgg	gct	cct	gta	cct	aac	ttg	aat	gca	gac	ctc	1805
Pro	Met	Thr	Pro	Val	Trp	Ala	Pro	Val	Pro	Asn	Leu	Asn	Ala	Asp	Leu	
535					540					545					550	
aaa	aaa	tta	aac	tgt	agc	cca	gat	tca	ttt	cgg	tgt	act	ttg	aca	aat	1853
Lys	Lys	Leu	Asn	Cys	Ser	Pro	Asp	Ser	Phe	Arg	Cys	Thr	Leu	Thr	Asn	
551					556					561					566	

att cca cag aca cag gct tta ctg aat aaa gct aag ctt cct tta gga Ile Pro Gln Thr Gln Ala Leu Leu Asn Lys Ala Lys Leu Pro Leu Gly 567 572 577 582	1901
ttg ttg tta cat ccc ttc aga gac cta acg caa tta cca gtg ata aca Leu Leu Leu His Pro Phe Arg Asp Leu Thr Gln Leu Pro Val Ile Thr 583 588 593 598	1949
tca aat acc att gtg agg tgc cga tcc tgt cga acg tat att aac ccc Ser Asn Thr Ile Val Arg Cys Arg Ser Cys Arg Thr Tyr Ile Asn Pro 599 604 609 614	1997
ttt gta tcc ttc att gat caa cgt aga tgg aaa tgc aat ttg tgc tat Phe Val Ser Phe Ile Asp Gln Arg Arg Trp Lys Cys Asn Leu Cys Tyr 615 620 625 630	2045
aga gta aac gat gtt cct gaa gaa ttt atg tat aac ccc ctt acc cga Arg Val Asn Asp Val Pro Glu Glu Phe Met Tyr Asn Pro Leu Thr Arg 631 636 641 646	2093
tct tat gga gag cct cat aaa cga cca gaa gtt cag aat tca act gtg Ser Tyr Gly Glu Pro His Lys Arg Pro Glu Val Gln Asn Ser Thr Val 647 652 657 662	2141
gag ttc att gct tct tca gat tac atg ctg cgt cct cct caa cct gca Glu Phe Ile Ala Ser Ser Asp Tyr Met Leu Arg Pro Pro Gln Pro Ala 663 668 673 678	2189
gtt tac ttg ttt gtt tta gat gtg tct cat aat gca gtg gaa gct gga Val Tyr Leu Phe Val Leu Asp Val Ser His Asn Ala Val Glu Ala Gly 679 684 689 694	2237
tat ttg aca att ttg tgc cag tca ctc cta gaa aat cta gac aag ctt Tyr Leu Thr Ile Leu Cys Gln Ser Leu Leu Glu Asn Leu Asp Lys Leu 695 700 705 710	2285
cct gga gat tca cga aca aga ata gga ttc atg acc ttt gat agc act Pro Gly Asp Ser Arg Thr Arg Ile Gly Phe Met Thr Phe Asp Ser Thr 711 716 721 726	2333
att cat ttc tac aat tta caa gaa gga tta tca cag cct caa atg ttg Ile His Phe Tyr Asn Leu Gln Glu Gly Leu Ser Gln Pro Gln Met Leu 727 732 737 742	2381
att gtg tct gat ata gat gat gtt ttt cta cct aca ccg gat agt tta Ile Val Ser Asp Ile Asp Asp Val Phe Leu Pro Thr Pro Asp Ser Leu 743 748 753 758	2429
ctt gtg aat cta tat gaa agt aaa gag ctt ata aaa gac tta ctg aat Leu Val Asn Leu Tyr Glu Ser Lys Glu Leu Ile Lys Asp Leu Leu Asn 759 764 769 774	2477
gca tta cca aac atg ttc acc aat aca aga gaa aca cac agt gcc ctt Ala Leu Pro Asn Met Phe Thr Asn Thr Arg Glu Thr His Ser Ala Leu 775 780 785 790	2525
ggg cct gca ctt cag gct gcc ttt aaa tta atg tct cca aca ggt ggc	2573

Gly 791	Pro	Ala	Leu	Gln	Ala 796	Ala	Phe	Lys	Leu	Met 801	Ser	Pro	Thr	Gly	Gly 806	
cgt	gtg	tct	gta	ttt	cag	aca	cag	tta	cct	tcc	ttg	ggt	gca	gga	ctt	2621
Arg 807	Val	Ser	Val	Phe	Gln 812	Thr	Gln	Leu	Pro	Ser 817	Leu	Gly	Ala	Gly	Leu 822	
ctg	caa	tcc	aga	gaa	gat	cct	aat	cag	aga	tca	agt	aca	aag	gtg	gta	2669
Leu 823	Gln	Ser	Arg	Glu	Asp 828	Pro	Asn	Gln	Arg	Ser 833	Ser	Thr	Lys	Val	Val 838	
caa	cat	ctt	ggc	cct	gca	act	gat	ttt	tat	aag	aaa	ctt	gca	tta	gat	2717
Gln 839	His	Leu	Gly	Pro	Ala 844	Thr	Asp	Phe	Tyr	Lys 849	Lys	Leu	Ala	Leu	Asp 854	
tgc	tcg	gga	cag	caa	act	gca	gtg	gat	ttg	ttc	ctt	tta	agt	tca	cag	2765
Cys 855	Ser	Gly	Gln	Gln	Thr 860	Ala	Val	Asp	Leu	Phe 865	Leu	Leu	Ser	Ser	Gln 870	
tat	tct	gat	ctt	gct	tct	cta	gct	tgc	atg	tcc	aag	tat	tct	gca	ggg	2813
Tyr 871	Ser	Asp	Leu	Ala	Ser 876	Leu	Ala	Cys	Met	Ser 881	Lys	Tyr	Ser	Ala	Gly 886	
tgc	atc	tat	tat	tat	cca	tca	ttc	cac	tat	act	cac	aat	cct	tca	caa	2861
Cys 887	Ile	Tyr	Tyr	Tyr	Pro 892	Ser	Phe	His	Tyr	Thr 897	His	Asn	Pro	Ser	Gln 902	
gca	gaa	aag	tta	caa	aaa	gac	cta	aaa	cgg	tat	ctc	aca	aga	aaa	att	2909
Ala 903	Glu	Lys	Leu	Gln	Lys 908	Asp	Leu	Lys	Arg	Tyr 913	Leu	Thr	Arg	Lys	Ile 918	
ggg	ttt	gaa	gct	ggt	atg	aga	ata	agg	tgt	act	aaa	ggt	ctt	tca	atg	2957
Gly 919	Phe	Glu	Ala	Val	Met 924	Arg	Ile	Arg	Cys	Thr 929	Lys	Gly	Leu	Ser	Met 934	
cac	act	ttt	cac	ggt	aac	ttc	ttt	gtc	cgt	tct	act	gat	ttg	tta	tcc	3005
His 935	Thr	Phe	His	Gly	Asn 940	Phe	Phe	Val	Arg	Ser 945	Thr	Asp	Leu	Leu	Ser 950	
ctt	gcc	aac	atc	aat	cct	gat	gct	gga	ttt	gcg	gtg	cag	ttg	tca	att	3053
Leu 951	Ala	Asn	Ile	Asn	Pro 956	Asp	Ala	Gly	Phe	Ala 961	Val	Gln	Leu	Ser	Ile 966	
gaa	gaa	agt	tta	aca	gat	act	tcc	tta	gta	tgt	ttt	caa	aca	gcc	cta	3101
Glu 967	Glu	Ser	Leu	Thr	Asp 972	Thr	Ser	Leu	Val	Cys 977	Phe	Gln	Thr	Ala	Leu 982	
tta	tat	aca	tca	agc	aaa	ggt	gag	cgg	aga	att	aga	gta	cat	aca	ctt	3149
Leu 983	Tyr	Thr	Ser	Ser	Lys 988	Gly	Glu	Arg	Arg	Ile 993	Arg	Val	His	Thr	Leu 998	
tgt	ttg	cca	gtg	gta	agt	tca	cta	gca	gat	gta	tat	gcg	gga	gtg	gat	3197
Cys 999	Leu	Pro	Val	Val	Ser 1004	Ser	Leu	Ala	Asp	Val 1009	Tyr	Ala	Gly	Val	Asp 1014	
gta	caa	gct	gcc	atc	tgc	ctt	ctg	gca	aac	atg	gct	gtg	gat	cgg	tcc	3245
Val	Gln	Ala	Ala	Ile	Cys	Leu	Leu	Ala	Asn	Met	Ala	Val	Asp	Arg	Ser	

1015	1020	1025	1030	
gtt tca tca agt ctg tca gat gca aga gat gcc tta gtg aat gct gta				3293
Val Ser Ser Ser Leu Ser Asp Ala Arg Asp Ala Leu Val Asn Ala Val				
1031	1036	1041	1046	
gtg gac tca ttg tct gca tat ggc tca act gtc tca aat tta cag cac				3341
Val Asp Ser Leu Ser Ala Tyr Gly Ser Thr Val Ser Asn Leu Gln His				
1047	1052	1057	1062	
tct gca ttg atg gcg ccc agc tcc ctc aag ttg ttt cct ctc tat gtt				3389
Ser Ala Leu Met Ala Pro Ser Ser Leu Lys Leu Phe Pro Leu Tyr Val				
1063	1068	1073	1078	
ttg gcc ctt ctc aaa cag aaa gca ttt aga acg ggt aca agc aca cgg				3437
Leu Ala Leu Leu Lys Gln Lys Ala Phe Arg Thr Gly Thr Ser Thr Arg				
1079	1084	1089	1094	
ctg gat gat cgt gta tat gcc atg tgt cag ata aag tct cag cca ctt				3485
Leu Asp Asp Arg Val Tyr Ala Met Cys Gln Ile Lys Ser Gln Pro Leu				
1095	1100	1105	1110	
gtt cat cta atg aaa atg att cat ccc aac tta tac agg ata gac aga				3533
Val His Leu Met Lys Met Ile His Pro Asn Leu Tyr Arg Ile Asp Arg				
1111	1116	1121	1126	
ttg aca gat gag ggt gca gta cat gtt aat gac agg att gta cca cag				3581
Leu Thr Asp Glu Gly Ala Val His Val Asn Asp Arg Ile Val Pro Gln				
1127	1132	1137	1142	
cca cct ctt caa aaa ttg tct gca gag aag ctg aca aga gaa ggt gct				3629
Pro Pro Leu Gln Lys Leu Ser Ala Glu Lys Leu Thr Arg Glu Gly Ala				
1143	1148	1153	1158	
ttc ctt atg gac tgt ggc tct gtt ttt tac att tgg gtt ggg aaa ggc				3677
Phe Leu Met Asp Cys Gly Ser Val Phe Tyr Ile Trp Val Gly Lys Gly				
1159	1164	1169	1174	
tgt gac aat aac ttc ata gag gat gtg ctt gga tat act aat ttt gca				3725
Cys Asp Asn Asn Phe Ile Glu Asp Val Leu Gly Tyr Thr Asn Phe Ala				
1175	1180	1185	1190	
tca ata cca cag aaa atg aca cat ctt cca gag cta gat aca ctt tca				3773
Ser Ile Pro Gln Lys Met Thr His Leu Pro Glu Leu Asp Thr Leu Ser				
1191	1196	1201	1206	
tca gaa aga gcc aga tcc ttc ata act tgg ctt aga gac agc aga cca				3821
Ser Glu Arg Ala Arg Ser Phe Ile Thr Trp Leu Arg Asp Ser Arg Pro				
1207	1212	1217	1222	
tta agt cca atc ctt cac ata gta aaa gat gag agt cct gcc aaa gca				3869
Leu Ser Pro Ile Leu His Ile Val Lys Asp Glu Ser Pro Ala Lys Ala				
1223	1228	1233	1238	
gaa ttt ttt cag cat ttg att gaa gac cgg aca gag gct gca ttt tct				3917
Glu Phe Phe Gln His Leu Ile Glu Asp Arg Thr Glu Ala Ala Phe Ser				
1239	1244	1249	1254	

tac tat gaa ttt ttg ctt cat gtt cag cag cag att tgt aag tga agt 3965
 Tyr Tyr Glu Phe Leu Leu His Val Gln Gln Gln Ile Cys Lys *
 1255 1260 1265

agaataaaat tgaataagaa aaagatctat aacctaggta aagcataatc tgtcagagaa 4025
 gcgcgtgaga aatttgaaat gaaggcattt gttaatacaa gatgcaacgc acagcactct 4085
 gtctgaggct ttggtaaaaa gtaaagggga agaaagaact tgacagatct ttttcaactc 4145
 aaattaatgg taacgatgat gctgtttcac caagtatatt ttgaattggg ttctacacat 4205
 ttccagtagt atggcagtag agtgctctgt tcattgcaag ctggcaaatt tatgtagcta 4265
 tgtggaatga tatgtcataa tgtaaaatta gataaattct tttttcttat aattaatata 4325
 acatttctgg acttgaactc tggcaagaga tgccaaaagg cattggtacc gtgttatttg 4385
 tttatatgaa ttacttttta acaaggaatg tttcttattc attaaatgaa ttcaacattt 4445
 tctctgtaaa aacaatagag tttcagtaca tgaactatag aaaaaaatct atatataatg 4505
 tacataaatg ttacatttgt aaagaaaatg taaaaatgta actatagcat atgaattgct 4565
 taaactgtgc tgcattgttg gatgacaact ctttttgtca cagttagaga atgaggttga 4625
 ctaatgcata ttatgaattg agtccacaaa ggaacacaaa actctttgta attctgttaa 4685
 atcttttatg tagatttatt tatgatcagc ctactaatta aaactatttc gcttgacagt 4745
 aaaaaaaaaa aaaa 4759

<210> 24
 <211> 1800
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (379) .. (1701)

<400> 24
 ggcgctctgc cagccccggg aacagcagag gcggcggcac tggctggacc catgcgcgcg 60
 cctccggggc tgaagaagga aggagtgagc cgagccgagc accccacatc tggagggggac 120
 agccagccgt gggccccgcc ccggcgtccg gagcaggaga actccgagct tcttgcccag 180
 gcagagagag caggagcgga ccgcgcgccc gggattgaga gtccttgccg tccagacccc 240
 caccagtggt ccgccagggt cccgcctgt ccggaccctc gccgcgccc ggcagggcgcg 300
 ccagggcggg gctgacctgc ccgcgaagtt gcggacagtg cgtgagaaac cagcaccccc 360

ttccgcccgc tccagctt	atg gaa act ggt caa aga act cat gca agt gga	411
	Met Glu Thr Gly Gln Arg Thr His Ala Ser Gly	
	1 5	
act tac agc ttc ctt gat cgg act cag cat tca gat atc aaa gca gac	459	
Thr Tyr Ser Phe Leu Asp Arg Thr Gln His Ser Asp Ile Lys Ala Asp		
12 17 22 27		
tgc aat acc tgc gtg gaa ata gaa gac aga aag gtt tca aga caa cag	507	
Cys Asn Thr Cys Val Glu Ile Glu Asp Arg Lys Val Ser Arg Gln Gln		
28 33 38 43		
atg aat tgt gaa aga gag cag cta agg ggt aat cag gaa gca gcc gct	555	
Met Asn Cys Glu Arg Glu Gln Leu Arg Gly Asn Gln Glu Ala Ala Ala		
44 49 54 59		
gcc cct gac aca atg gct cag cct tac gct tcg gcc cag ttt gct ccc	603	
Ala Pro Asp Thr Met Ala Gln Pro Tyr Ala Ser Ala Gln Phe Ala Pro		
60 65 70 75		
ccg cag aac ggt atc ccc gcg gaa tac acg gcc cct cat ccc cac ccc	651	
Pro Gln Asn Gly Ile Pro Ala Glu Tyr Thr Ala Pro His Pro His Pro		
76 81 86 91		
gcg cca gag tac aca ggc cag acc acg gtt ccc gag cac aca tta aac	699	
Ala Pro Glu Tyr Thr Gly Gln Thr Thr Val Pro Glu His Thr Leu Asn		
92 97 102 107		
ctg tac cct ccc gcc cag acg cac tcc gag cag agc ccg gcg gac acg	747	
Leu Tyr Pro Pro Ala Gln Thr His Ser Glu Gln Ser Pro Ala Asp Thr		
108 113 118 123		
agc gct cag acc gtc tct ggc acc gcc aca cag aca gat gac gca gca	795	
Ser Ala Gln Thr Val Ser Gly Thr Ala Thr Gln Thr Asp Asp Ala Ala		
124 129 134 139		
ccg acg gat ggc cag ccc cag aca caa cct tct gaa aac acg gaa aac	843	
Pro Thr Asp Gly Gln Pro Gln Thr Gln Pro Ser Glu Asn Thr Glu Asn		
140 145 150 155		
aag tct cag ccc aag cgg ctg cat gtc tcc aat atc ccc ttc agg ttc	891	
Lys Ser Gln Pro Lys Arg Leu His Val Ser Asn Ile Pro Phe Arg Phe		
156 161 166 171		
cgg gat ccg gac ctc aga caa atg ttt ggt caa ttt ggt aaa atc tta	939	
Arg Asp Pro Asp Leu Arg Gln Met Phe Gly Gln Phe Gly Lys Ile Leu		
172 177 182 187		
gat gtt gaa att att ttt aat gag cga ggc tca aag gga ttt ggt ttc	987	
Asp Val Glu Ile Ile Phe Asn Glu Arg Gly Ser Lys Gly Phe Gly Phe		
188 193 198 203		
gta act ttc gaa aat agt gcc gat gcg gac agg gcg agg gag aaa tta	1035	
Val Thr Phe Glu Asn Ser Ala Asp Ala Asp Arg Ala Arg Glu Lys Leu		
204 209 214 219		

cac ggc acc gtg gta gag ggc cgt aaa atc gag gta aat aat gcc aca His Gly Thr Val Val Glu Gly Arg Lys Ile Glu Val Asn Asn Ala Thr 220 225 230 235	1083
gca cgt gta atg aca aat aaa aag acc gtc aac cct tat aca aat ggc Ala Arg Val Met Thr Asn Lys Lys Thr Val Asn Pro Tyr Thr Asn Gly 236 241 246 251	1131
tgg aaa ttg aat cca gtt gtg ggt gca gtc tac agt ccc gaa ttc tat Trp Lys Leu Asn Pro Val Val Gly Ala Val Tyr Ser Pro Glu Phe Tyr 252 257 262 267	1179
gca ggc acg gtc ctg ttg tgc cag gcc aac cag gag gga tct tcc atg Ala Gly Thr Val Leu Leu Cys Gln Ala Asn Gln Glu Gly Ser Ser Met 268 273 278 283	1227
tac agt gcc ccc agt tca ctt gta tat act tct gca atg cca ggc ttc Tyr Ser Ala Pro Ser Ser Leu Val Tyr Thr Ser Ala Met Pro Gly Phe 284 289 294 299	1275
ccg tat cca gca gcc acc gcc gcg gcc gcc tac cga ggg gcg cac ctg Pro Tyr Pro Ala Ala Thr Ala Ala Ala Ala Tyr Arg Gly Ala His Leu 300 305 310 315	1323
cga ggc cgc ggt cgc acc gtg tac aac acc ttc agg gcc gcg gcg ccc Arg Gly Arg Gly Arg Thr Val Tyr Asn Thr Phe Arg Ala Ala Ala Pro 316 321 326 331	1371
ccg ccc ccg atc ccg gcc tac ggc ggt gtt gtt tac cag gat gga ttt Pro Pro Pro Ile Pro Ala Tyr Gly Gly Val Val Tyr Gln Asp Gly Phe 332 337 342 347	1419
tat ggt gca gac att tat ggt ggt tat gct gca tac cgc tac gcc cag Tyr Gly Ala Asp Ile Tyr Gly Gly Tyr Ala Ala Tyr Arg Tyr Ala Gln 348 353 358 363	1467
cct acc cct gcc act gcc gct gcc tac agt gac agt tac gga cga gtt Pro Thr Pro Ala Thr Ala Ala Ala Tyr Ser Asp Ser Tyr Gly Arg Val 364 369 374 379	1515
tat gct gcc gac ccc tac cac cac gca ctt gct cca gcc ccc acc tac Tyr Ala Ala Asp Pro Tyr His His Ala Leu Ala Pro Ala Pro Thr Tyr 380 385 390 395	1563
ggc gtt ggt gcc atg aat gct ttt gca cct ttg act gat gcc aag act Gly Val Gly Ala Met Asn Ala Phe Ala Pro Leu Thr Asp Ala Lys Thr 396 401 406 411	1611
agg agc cat gct gat gat gtg ggt ctc gtt ctt tct tca ttg cag gct Arg Ser His Ala Asp Asp Val Gly Leu Val Leu Ser Ser Leu Gln Ala 412 417 422 427	1659
agt ata tac cga ggg gga tac aac cgt ttt gct cca tac taa atgacaa Ser Ile Tyr Arg Gly Gly Tyr Asn Arg Phe Ala Pro Tyr * 428 433 438	1708
aaccataaaa accttccaat gtggggagaa aggaagcttt ccgaggcctg agtattgcaa	1768

tacatgcagt agtacatcat tttagcaact ct

1800

<210> 25
<211> 2296
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (27) .. (2267)

<400> 25
ggaaagatga atcaaagtaa attgaa atg aca att cca ggt tta gat tgg gga 53
Met Thr Ile Pro Gly Leu Asp Trp Gly
1 5

atg gag gaa gtg atg caa aag gat cag aaa aaa gta cct cag aag aaa 101
Met Glu Glu Val Met Gln Lys Asp Gln Lys Lys Val Pro Gln Lys Lys
10 15 20 25

gtt cct tat gca aaa ccc att cct gct cag ttc cag cag gct tgg atg 149
Val Pro Tyr Ala Lys Pro Ile Pro Ala Gln Phe Gln Gln Ala Trp Met
26 31 36 41

caa aat aaa gtt cca att cct gct cca aat gag gtg ctg aat gac aga 197
Gln Asn Lys Val Pro Ile Pro Ala Pro Asn Glu Val Leu Asn Asp Arg
42 47 52 57

aaa gaa gac att aaa ttg gaa gag aag aaa aaa aca caa gca gaa att 245
Lys Glu Asp Ile Lys Leu Glu Glu Lys Lys Lys Thr Gln Ala Glu Ile
58 63 68 73

gag caa gaa atg gct aca tta caa tat act aac cca caa ctt ctg gag 293
Glu Gln Glu Met Ala Thr Leu Gln Tyr Thr Asn Pro Gln Leu Leu Glu
74 79 84 89

caa ctt aaa att gaa aga ctt gca cag aaa caa gtt gag caa att cag 341
Gln Leu Lys Ile Glu Arg Leu Ala Gln Lys Gln Val Glu Gln Ile Gln
90 95 100 105

cct cct ccc tca tct ggc acc cct ctc ctc gga ccc cag cct ttt cca 389
Pro Pro Pro Ser Ser Gly Thr Pro Leu Leu Gly Pro Gln Pro Phe Pro
106 111 116 121

gga caa ggt cca atg tct cag att cct caa ggt ttt caa cag ccc cat 437
Gly Gln Gly Pro Met Ser Gln Ile Pro Gln Gly Phe Gln Gln Pro His
122 127 132 137

cca tct cag cag atg cca atg aac atg gct caa atg ggg cct cca ggt 485
Pro Ser Gln Gln Met Pro Met Asn Met Ala Gln Met Gly Pro Pro Gly
138 143 148 153

cca cag gga cag ttt agg cct cct gga ccc cag gga caa atg gga cca 533

Pro 154	Gln	Gly	Gln	Phe	Arg 159	Pro	Pro	Gly	Pro	Gln 164	Gly	Gln	Met	Gly	Pro 169	
caa Gln 170	ggt Gly	cct Pro	cca Pro	ctg Leu	cat His 175	cag Gln	gga Gly	ggt Gly	ggg Gly	ggg Gly 180	cca Pro	caa Gln	gga Gly	ttc Phe	atg Met 185	581
gga Gly 186	cca Pro	cag Gln	ggg Gly	ccc Pro	cag Gln 191	ggc Gly	ccg Pro	ccc Pro	cag Gln	ggg Gly 196	ttg Leu	cca Pro	cgg Arg	cct Pro	cag Gln 201	629
gac Asp 202	atg Met	cat His	ggg Gly	ccc Pro	caa Gln 207	gga Gly	atg Met	cag Gln	agg Arg	cat His 212	cct Pro	gga Gly	cct Pro	cat His	ggc Gly 217	677
cct Pro 218	ttg Leu	gga Gly	cct Pro	caa Gln	ggg Gly 223	cca Pro	cct Pro	gga Gly	cca Pro	caa Gln 228	ggt Gly	agt Ser	tct Ser	ggt Gly	cct Pro 233	725
caa Gln 234	ggt Gly	cat His	atg Met	ggt Gly	cct Pro 239	cag Gln	ggt Gly	cca Pro	cct Pro	ggc Gly 244	cca Pro	cag Gln	ggt Gly	cac His	ata Ile 249	773
ggc Gly 250	ccc Pro	caa Gln	ggc Gly	ccg Pro	cct Pro 255	ggc Gly	cct Pro	cag Gln	ggt Gly	cac His 260	ttg Leu	ggc Gly	cca Pro	cag Gln	ggg Gly 265	821
cct Pro 266	ccg Pro	ggt Gly	act Thr	caa Gln	ggt Gly 271	atg Met	cag Gln	gga Gly	cca Pro	cct Pro 276	ggt Gly	ccc Pro	aga Arg	gga Gly	atg Met 281	869
caa Gln 282	ggg Gly	cct Pro	cct Pro	cat His	cct Pro 287	cat His	ggg Gly	atc Ile	caa Gln	ggc Gly 292	gga Gly	cca Pro	ggg Gly	tct Ser	caa Gln 297	917
ggg Gly 298	atc Ile	caa Gln	ggt Gly	cct Pro	gtg Val 303	tct Ser	cag Gln	gga Gly	cct Pro	ctg Leu 308	atg Met	gga Gly	ttg Leu	aat Asn	cca Pro 313	965
aga Arg 314	gga Gly	atg Met	cag Gln	ggg Gly	cct Pro 319	cca Pro	ggc Gly	ccc Pro	cgg Arg	gag Glu 324	aac Asn	cag Gln	ggt Gly	cct Pro	gct Ala 329	1013
ccc Pro 330	caa Gln	ggg Gly	atg Met	att Ile	atg Met 335	ggc Gly	cac His	ccg Pro	cct Pro	caa Gln 340	gag Glu	atg Met	aga Arg	gga Gly	cct Pro 345	1061
cac His 346	cct Pro	cca Pro	ggt Gly	gga Gly	cta Leu 351	ctg Leu	gga Gly	cac His	ggc Gly	cct Pro 356	cag Gln	gaa Glu	atg Met	aga Arg	ggt Gly 361	1109
cct Pro 362	cag Gln	gag Glu	atc Ile	cga Arg	ggc Gly 367	atg Met	cag Gln	ggg Gly	cct Pro	cca Pro 372	ccc Pro	caa Gln	gga Gly	tca Ser	atg Met 377	1157
ctg Leu	gga Gly	cct Pro	ccc Pro	cag Gln	gaa Glu	ttg Leu	cga Arg	ggg Gly	cct Pro	cca Pro	ggc Gly	tca Ser	caa Gln	agt Ser	cag Gln	1205

378	383	388	393	
cag ggg ccg ccc cag ggc tct tta gga cct cca ccc cag ggt ggc atg				1253
Gln Gly Pro Pro Gln Gly Ser Leu Gly Pro Pro Pro Gln Gly Gly Met				
394	399	404	409	
caa gga ccc ccc gga cct cag gga cag cag aac cca gca aga ggg cca				1301
Gln Gly Pro Pro Gly Pro Gln Gly Gln Gln Asn Pro Ala Arg Gly Pro				
410	415	420	425	
cat cca tct caa ggg cca ata cca ttc cag caa cag aaa acg cct ctg				1349
His Pro Ser Gln Gly Pro Ile Pro Phe Gln Gln Gln Lys Thr Pro Leu				
426	431	436	441	
cta ggt gat ggg ccc cgg gcc ccc ttc aac cag gaa gga cag agc aca				1397
Leu Gly Asp Gly Pro Arg Ala Pro Phe Asn Gln Glu Gly Gln Ser Thr				
442	447	452	457	
ggc ccc cca ccc ctg ata cca ggc cta ggg cag cag gga gca caa ggt				1445
Gly Pro Pro Pro Leu Ile Pro Gly Leu Gly Gln Gln Gly Ala Gln Gly				
458	463	468	473	
cgc att ccc cct ctg aac ccc gga caa gga cct ggc ccc aac aaa gtt				1493
Arg Ile Pro Pro Leu Asn Pro Gly Gln Gly Pro Gly Pro Asn Lys Val				
474	479	484	489	
tca gaa gag gag ccc cgc cga ggc atg agg gcc gtg ctc ccc cca gag				1541
Ser Glu Glu Glu Pro Arg Arg Gly Met Arg Ala Val Leu Pro Pro Glu				
490	495	500	505	
gaa ggg atg gtt ttc ctg gtc ctg aag act tta gtc cag agg aga att				1589
Glu Gly Met Val Phe Leu Val Leu Lys Thr Leu Val Gln Arg Arg Ile				
506	511	516	521	
ttg atg ctt atg agg gaa gcg gcc cga gga cga gat ctc aga ggt cga				1637
Leu Met Leu Met Arg Glu Ala Ala Arg Gly Arg Asp Leu Arg Gly Arg				
522	527	532	537	
ggt cgg ggt acc cca cga gga gga agg aag ggt tta ctt ccc act cct				1685
Gly Arg Gly Thr Pro Arg Gly Gly Arg Lys Gly Leu Leu Pro Thr Pro				
538	543	548	553	
gac gag ttc cct cgc ttt gaa gga ggg cgg aag cca gat tcc tgg gat				1733
Asp Glu Phe Pro Arg Phe Glu Gly Gly Arg Lys Pro Asp Ser Trp Asp				
554	559	564	569	
gga aac aga gag cct ggg cca ggt cat gaa cat ttt cgt gat act ccc				1781
Gly Asn Arg Glu Pro Gly Pro Gly His Glu His Phe Arg Asp Thr Pro				
570	575	580	585	
cgc cct gat cat ccc cct cac gac ggt cat tcc cca gcc agc aga gaa				1829
Arg Pro Asp His Pro Pro His Asp Gly His Ser Pro Ala Ser Arg Glu				
586	591	596	601	
cgc tcc tct tct ctc caa ggc atg gac atg gca tcc cta cct ccc cga				1877
Arg Ser Ser Ser Leu Gln Gly Met Asp Met Ala Ser Leu Pro Pro Arg				
602	607	612	617	

cctgcaggga acctcaggct tcagagagcc gaaaagtgtg gaggcgtaac cacttacagg	240
ccggaagtgt ccggggtgga cgcattcggg tagccgaaga agtcccagga ttgccgaaga	300
agtcccagga tttccgaagc gagccgaagc atcgcgacag ttttcagaga cagctgatcg	360
gttggagctg ttgcgccgag cagtc atg gcg gcg gcc aga gct act acg ccg	412
Met Ala Ala Ala Arg Ala Thr Thr Pro	
1 5	
gcc gat ggc gag gag ccc gcc ccg gag gct gag gct ctg gcc gca gcc	460
Ala Asp Gly Glu Glu Pro Ala Pro Glu Ala Glu Ala Leu Ala Ala Ala	
10 15 20 25	
cgg gag cgg agc agc cgc ttc ttg agc ggc ctg gag ctg gtg aag cag	508
Arg Glu Arg Ser Ser Arg Phe Leu Ser Gly Leu Glu Leu Val Lys Gln	
26 31 36 41	
ggt gcc gag gcg cgc gtg ttc cgt ggc cgc ttc cag ggc cgc gcg gcg	556
Gly Ala Glu Ala Arg Val Phe Arg Gly Arg Phe Gln Gly Arg Ala Ala	
42 47 52 57	
gtg atc aag cac cgc ttc ccc aag ggc tac cgg cac ccg gcg ctg gag	604
Val Ile Lys His Arg Phe Pro Lys Gly Tyr Arg His Pro Ala Leu Glu	
58 63 68 73	
gcg cgg ctt ggc aga cgg cgg acg gtg cag gag gcc cgg gcg ctc ctc	652
Ala Arg Leu Gly Arg Arg Arg Thr Val Gln Glu Ala Arg Ala Leu Leu	
74 79 84 89	
cgc tgt cgc cgc gct gga ata tct gcc cca gtt gtc ttt ttt gtg gac	700
Arg Cys Arg Arg Ala Gly Ile Ser Ala Pro Val Val Phe Phe Val Asp	
90 95 100 105	
tat gct tcc aac tgc tta tat atg gaa gaa att gaa ggc tca gtg act	748
Tyr Ala Ser Asn Cys Leu Tyr Met Glu Glu Ile Glu Gly Ser Val Thr	
106 111 116 121	
gtt cga gat tat att cag tcc act atg gag act gaa aaa act ccc cag	796
Val Arg Asp Tyr Ile Gln Ser Thr Met Glu Thr Glu Lys Thr Pro Gln	
122 127 132 137	
ggt ctc tcc aac tta gcc aag aca att ggg cag gtt ttg gct cga atg	844
Gly Leu Ser Asn Leu Ala Lys Thr Ile Gly Gln Val Leu Ala Arg Met	
138 143 148 153	
cac gat gaa gac ctc att cat ggt gat ctc acc acc tcc aac atg ctc	892
His Asp Glu Asp Leu Ile His Gly Asp Leu Thr Thr Ser Asn Met Leu	
154 159 164 169	
ctg aaa ccc ccc ctg gaa cag ctg aac att gtg ctc ata gac ttt ggg	940
Leu Lys Pro Pro Leu Glu Gln Leu Asn Ile Val Leu Ile Asp Phe Gly	
170 175 180 185	
ctg agt ttc att tca gca ctt cca gag gat aag gga gta gac ctc tat	988
Leu Ser Phe Ile Ser Ala Leu Pro Glu Asp Lys Gly Val Asp Leu Tyr	
186 191 196 201	

```

gtc ctg gag aag gcc ttc ctc agt acc cat ccc aac act gaa act gtg 1036
Val Leu Glu Lys Ala Phe Leu Ser Thr His Pro Asn Thr Glu Thr Val
202                207                212                217

ttt gaa gcc ttt ctg aag agc tac tcc acc tcc tcc aaa aag gcc agg 1084
Phe Glu Ala Phe Leu Lys Ser Tyr Ser Thr Ser Ser Lys Lys Ala Arg
218                223                228                233

cca gtg cta aaa aaa tta gat gaa gtg cgc ctg aga gga aga aag agg 1132
Pro Val Leu Lys Lys Leu Asp Glu Val Arg Leu Arg Gly Arg Lys Arg
234                239                244                249

tcc atg gtt ggg tag aagaatgtgt atgacaacca cacacagtga agctcttttt 1187
Ser Met Val Gly *
250

tcaaagtaaa tttgaagaaa tgctacaagt atgagatgag atctaagtaa aggtgttaag 1247

atatttttaa aaaaaaaaaa 1267

```

```

<210> 27
<211> 1506
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (218)..(1399)

```

```

<400> 27
tttttaggaat gacgtaccgg tccggaattc ccgggtcgac gatttcgtgt ccggcctccc 60

tgacatgcat atttccaccc agaagacaga gaaggagcca gtggatcatgg aatgggctgg 120

gggtcaaagac tgggtgcctg ggagctgagg cagccaccgt ttcagcctgg ccagccctct 180

ggacccccgag gttggaccct actgtgacac acctacc atg cgg aca ctc ttc aac 235
Met Arg Thr Leu Phe Asn
1

ctc ctc tgg ctt gcc ctg gcc tgc agc cct gtt cac act acc ctg tca 283
Leu Leu Trp Leu Ala Leu Ala Cys Ser Pro Val His Thr Thr Leu Ser
7                12                17                22

aag tca gat gcc aaa aaa gcc gcc tca aag acg ctg ctg gag aag agt 331
Lys Ser Asp Ala Lys Lys Ala Ala Ser Lys Thr Leu Leu Glu Lys Ser
23                28                33                38

cag ttt tca gat aag ccg gtg caa gac cgg ggt ttg gtg gtg acg gac 379
Gln Phe Ser Asp Lys Pro Val Gln Asp Arg Gly Leu Val Val Thr Asp
39                44                49                54

ctc aaa gct gag agt gtg gtt ctt gag cat cgc agc tac tgc tcg gca 427

```

Leu	Lys	Ala	Glu	Ser	Val	Val	Leu	Glu	His	Arg	Ser	Tyr	Cys	Ser	Ala		
55					60					65					70		
aag	gcc	cgg	gac	aga	cac	ttt	gct	ggg	gat	gta	ctg	ggc	tat	gtc	act		475
Lys	Ala	Arg	Asp	Arg	His	Phe	Ala	Gly	Asp	Val	Leu	Gly	Tyr	Val	Thr		
71					76					81					86		
cca	tgg	aac	agc	cat	ggc	tac	tat	gtc	acc	aag	gtc	ttt	ggg	agc	aag		523
Pro	Trp	Asn	Ser	His	Gly	Tyr	Tyr	Val	Thr	Lys	Val	Phe	Gly	Ser	Lys		
87					92					97					102		
ttc	aca	cag	atc	tca	ccc	gtc	tgg	ctg	cag	ctg	aag	aga	cgt	ggc	cgt		571
Phe	Thr	Gln	Ile	Ser	Pro	Val	Trp	Leu	Gln	Leu	Lys	Arg	Arg	Gly	Arg		
103					108					113					118		
gag	atg	ttt	gag	gtc	acg	ggc	ctc	cac	gac	gtg	gac	caa	ggg	tgg	atg		619
Glu	Met	Phe	Glu	Val	Thr	Gly	Leu	His	Asp	Val	Asp	Gln	Gly	Trp	Met		
119					124					129					134		
cga	gct	gtc	agg	aag	cat	gcc	aag	ggc	ctg	cac	ata	gtg	cct	cgg	ctc		667
Arg	Ala	Val	Arg	Lys	His	Ala	Lys	Gly	Leu	His	Ile	Val	Pro	Arg	Leu		
135					140					145					150		
ctg	ttt	gag	gac	tgg	act	tac	gat	gat	ttc	cgg	aac	gtc	tta	tac	agt		715
Leu	Phe	Glu	Asp	Trp	Thr	Tyr	Asp	Asp	Phe	Arg	Asn	Val	Leu	Tyr	Ser		
151					156					161					166		
gag	gat	gag	ata	gag	gag	ctg	agc	aag	acc	gtg	gtc	cag	gtg	gca	aag		763
Glu	Asp	Glu	Ile	Glu	Glu	Leu	Ser	Lys	Thr	Val	Val	Gln	Val	Ala	Lys		
167					172					177					182		
aac	cag	cat	ttc	gat	ggc	ttc	gtg	gtg	gag	gtc	tgg	aac	cag	ctg	cta		811
Asn	Gln	His	Phe	Asp	Gly	Phe	Val	Val	Glu	Val	Trp	Asn	Gln	Leu	Leu		
183					188					193					198		
agc	cag	aag	cgc	gtg	ggc	ctc	atc	cac	atg	ctc	acc	cac	ttg	gcc	gag		859
Ser	Gln	Lys	Arg	Val	Gly	Leu	Ile	His	Met	Leu	Thr	His	Leu	Ala	Glu		
199					204					209					214		
gct	ctg	cac	cag	gcc	cgg	ctg	ctg	gcc	ctc	ctg	gtc	atc	ccg	cct	gcc		907
Ala	Leu	His	Gln	Ala	Arg	Leu	Leu	Ala	Leu	Leu	Val	Ile	Pro	Pro	Ala		
215					220					225					230		
atc	acc	ccc	ggg	acc	gac	cag	ctg	ggc	atg	ttc	acg	cac	aag	gag	ttt		955
Ile	Thr	Pro	Gly	Thr	Asp	Gln	Leu	Gly	Met	Phe	Thr	His	Lys	Glu	Phe		
231					236					241					246		
gag	cag	ctg	gcc	ccc	gtg	ctg	gat	ggt	ttc	agc	ctc	atg	acc	tac	gac		1003
Glu	Gln	Leu	Ala	Pro	Val	Leu	Asp	Gly	Phe	Ser	Leu	Met	Thr	Tyr	Asp		
247					252					257					262		
tac	tct	aca	gcg	cat	cag	cct	ggc	cct	aat	gca	ccc	ctg	tcc	tgg	gtt		1051
Tyr	Ser	Thr	Ala	His	Gln	Pro	Gly	Pro	Asn	Ala	Pro	Leu	Ser	Trp	Val		
263					268					273					278		
cga	gcc	tgc	gtc	cag	gtc	ctg	gac	ccg	aag	tcc	aag	tgg	cga	agc	aaa		1099
Arg	Ala	Cys	Val	Gln	Val	Leu	Asp	Pro	Lys	Ser	Lys	Trp	Arg	Ser	Lys		

279	284	289	294	
atc ctc ctg ggg ctc aac ttc tat ggt atg gac tac gcg acc tcc aag				1147
Ile Leu Leu Gly Leu Asn Phe Tyr Gly Met Asp Tyr Ala Thr Ser Lys				
295	300	305	310	
gat gcc cgt gag cct gtt gtc ggg gcc agg tac atc cag aca ctg aag				1195
Asp Ala Arg Glu Pro Val Val Gly Ala Arg Tyr Ile Gln Thr Leu Lys				
311	316	321	326	
gac cac agg ccc cgg atg gtg tgg gac agc cag gcc tca gag cac ttc				1243
Asp His Arg Pro Arg Met Val Trp Asp Ser Gln Ala Ser Glu His Phe				
327	332	337	342	
ttc gag tac aag aag agc cgc agt ggg agg cac gtc gtc ttc tac cca				1291
Phe Glu Tyr Lys Lys Ser Arg Ser Gly Arg His Val Val Phe Tyr Pro				
343	348	353	358	
acc ctg aag tcc ctg cag gtg cgg ctg gag ctg gcc cgg gag ctg ggc				1339
Thr Leu Lys Ser Leu Gln Val Arg Leu Glu Leu Ala Arg Glu Leu Gly				
359	364	369	374	
gtt ggg gtc tct atc tgg gag ctg ggc cag ggc ctg gac tac ttc tac				1387
Val Gly Val Ser Ile Trp Glu Leu Gly Gln Gly Leu Asp Tyr Phe Tyr				
375	380	385	390	
gac ctg ctc tag gtg ggcattgcgg cctccgcggt ggacgtgttc ttttctaagc				1442
Asp Leu Leu *				
391				
catggagtga gtgagcaggt gtgaaataca ggccctccact ccgtttgctg tgaaaaaaaa				1502
aaaa				1506
<210> 28				
<211> 1770				
<212> DNA				
<213> Homo sapiens				
<220>				
<221> CDS				
<222> (277) .. (1515)				
<400> 28				
atttggccct cgaggccaag aattcggcac gaggaccgtc catccagagg aaggcaagtt				60
tttggctcgg gcggctgaga agaccgcgcg gggctggaga caggtagcag tacggggggcg				120
gggcttcatg ccggatgtga tagtctgcag tcgtttcgggt tggcagcctg gcggggtggga				180
gatgcggcgg ccacctgctg caaagaaccg aagggaaggt tagaagtacg aaggcagttt				240
ggagctgggg ctaagcagct gtcgcacggt cagatc atg ggc tcc acc aag cac				294
			Met Gly Ser Thr Lys His	

tgg ggc gaa tgg ctc ctg aac ttg aag gtg gct cca gcc ggc gtc ttt	342
Trp Gly Glu Trp Leu Leu Asn Leu Lys Val Ala Pro Ala Gly Val Phe	
7 12 17 22	
ggt gtg gcc ttt cta gcc aga gtc gcc ctg gtt ttc tat ggc gtc ttc	390
Gly Val Ala Phe Leu Ala Arg Val Ala Leu Val Phe Tyr Gly Val Phe	
23 28 33 38	
cag gac cgg acc ctg cac gtg agg tat acg gac atc gac tac cag gtc	438
Gln Asp Arg Thr Leu His Val Arg Tyr Thr Asp Ile Asp Tyr Gln Val	
39 44 49 54	
ttc acc gac gcc gcg cgc ttc gtc acg gag ggg cgc tcg cct tac ctg	486
Phe Thr Asp Ala Ala Arg Phe Val Thr Glu Gly Arg Ser Pro Tyr Leu	
55 60 65 70	
aga gcc acg tac cgt tac acc ccg ctg ctg ggt tgg ctc ctc act ccc	534
Arg Ala Thr Tyr Arg Tyr Thr Pro Leu Leu Gly Trp Leu Leu Thr Pro	
71 76 81 86	
aac atc tac ctc agc gag ctc ttt gga aag ttt ctc ttc atc agc tgc	582
Asn Ile Tyr Leu Ser Glu Leu Phe Gly Lys Phe Leu Phe Ile Ser Cys	
87 92 97 102	
gac ctc ctc acc gct ttc ctc tta tac cgc ctg ctg ctg ctg aag ggg	630
Asp Leu Leu Thr Ala Phe Leu Leu Tyr Arg Leu Leu Leu Leu Lys Gly	
103 108 113 118	
ctg ggg cgc cgc cag gct tgt ggc tac tgt gtc ttt tgg ctt ctt aac	678
Leu Gly Arg Arg Gln Ala Cys Gly Tyr Cys Val Phe Trp Leu Leu Asn	
119 124 129 134	
ccc ctg cct atg gca gta tcc agc cgc ggt aat gcg gac tct att gtc	726
Pro Leu Pro Met Ala Val Ser Ser Arg Gly Asn Ala Asp Ser Ile Val	
135 140 145 150	
gcc tcc ctg gtc ctg atg gtc ctc tac ttg ata aag aaa aga ctc gtc	774
Ala Ser Leu Val Leu Met Val Leu Tyr Leu Ile Lys Lys Arg Leu Val	
151 156 161 166	
gcg tgt gca gct gta ttc tat ggt ttc gcg gtg cat atg aag ata tat	822
Ala Cys Ala Ala Val Phe Tyr Gly Phe Ala Val His Met Lys Ile Tyr	
167 172 177 182	
cca gag act tac atc ctt ccc ata acc ctc cac ctg ctt cca gat cgc	870
Pro Glu Thr Tyr Ile Leu Pro Ile Thr Leu His Leu Leu Pro Asp Arg	
183 188 193 198	
gac aat gac aaa agc ctc cgt caa ttc cgg aca agg ctg tgt aat cgg	918
Asp Asn Asp Lys Ser Leu Arg Gln Phe Arg Thr Arg Leu Cys Asn Arg	
199 204 209 214	
act gcg ctg atg ttt gta gca gtt gct gga ctc acg ttt ttt gcc ctg	966
Thr Ala Leu Met Phe Val Ala Val Ala Gly Leu Thr Phe Phe Ala Leu	
215 220 225 230	

agc ttt ggt ttt tac tat gag tac ggc tgg gaa ttt ttg gaa cac acc	1014
Ser Phe Gly Phe Tyr Tyr Glu Tyr Gly Trp Glu Phe Leu Glu His Thr	
231 236 241 246	
tac ttt tat cac ctg act agg cgg gat atc cgt cac aac ttt tct ccg	1062
Tyr Phe Tyr His Leu Thr Arg Arg Asp Ile Arg His Asn Phe Ser Pro	
247 252 257 262	
tac ttc tac atg ctg tat ttg act gca gag agc aag tgg agt ttt tcc	1110
Tyr Phe Tyr Met Leu Tyr Leu Thr Ala Glu Ser Lys Trp Ser Phe Ser	
263 268 273 278	
ctg gga att gct gca ttc ctg cca cag ctc atc ttg ctt tca gct gtg	1158
Leu Gly Ile Ala Ala Phe Leu Pro Gln Leu Ile Leu Leu Ser Ala Val	
279 284 289 294	
tct ttc gcc tat tac aga gac ctc gtt ttt tgt tgt ttt ctt cat acg	1206
Ser Phe Ala Tyr Tyr Arg Asp Leu Val Phe Cys Cys Phe Leu His Thr	
295 300 305 310	
tcc att ttt gtg act ttt aac aaa gtc tgc acc tcc cag tac ttt ctt	1254
Ser Ile Phe Val Thr Phe Asn Lys Val Cys Thr Ser Gln Tyr Phe Leu	
311 316 321 326	
tgg tac ctc tgc tta ctg cct ctt gtg atg cca cta gtc aga atg cct	1302
Trp Tyr Leu Cys Leu Leu Pro Leu Val Met Pro Leu Val Arg Met Pro	
327 332 337 342	
tgg aaa aga gct gta gtt ctc cta atg tta tgg ttt ata ggg cag gcc	1350
Trp Lys Arg Ala Val Val Leu Leu Met Leu Trp Phe Ile Gly Gln Ala	
343 348 353 358	
atg tgg ctg gct cct gcc tat gtt cta gag ttt caa gga aag aac acc	1398
Met Trp Leu Ala Pro Ala Tyr Val Leu Glu Phe Gln Gly Lys Asn Thr	
359 364 369 374	
ttt ctg ttt att tgg tta gct ggt ttg ttc ttt ctt ctt atc aat tgt	1446
Phe Leu Phe Ile Trp Leu Ala Gly Leu Phe Phe Leu Leu Ile Asn Cys	
375 380 385 390	
tcc atc ctg att caa att att tcc cat tac aaa gaa gaa ccc ctg aca	1494
Ser Ile Leu Ile Gln Ile Ile Ser His Tyr Lys Glu Glu Pro Leu Thr	
391 396 401 406	
gag aga atc aaa tat gac tag tg tatgttccac accctctgct actgtgttac	1547
Glu Arg Ile Lys Tyr Asp *	
407 412	
attctgattg tcttgtatgg accagaagag agctttggga cattttttct gaacattcta	1607
agcattctag tgaaagttcc catgttccaa cagaacttaa aagcaatggt tgccttatat	1667
ataaaaggga cacaataatt gaggtccacc ttttaggaaa tcctaggact cgtttatttg	1727
ggacatggtg ggaataaagg tcacatattg gaaaaaaaaaaa aaa	1770

<210> 29
 <211> 2958
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (72)..(2678)

<400> 29
 cgggcggggtg tggccagggg tgtgggtctg tgagggaccg gtcggaaggg cgtcgcgcgg 60
 cctcgggtga c atg cgg ggg gcg gcg agc gcg agt gtc cgc gag ccg acg 110
 Met Arg Gly Ala Ala Ser Ala Ser Val Arg Glu Pro Thr
 1 5 10
 ccg ctc ccg ggt aga ggc gcc ccc cgc aca aag ccc cgg gcg ggc cga 158
 Pro Leu Pro Gly Arg Gly Ala Pro Arg Thr Lys Pro Arg Ala Gly Arg
 14 19 24 29
 ggc ccg act gta ggg act cca gcc acc ttg gcc ctc cct gcc cgg gga 206
 Gly Pro Thr Val Gly Thr Pro Ala Thr Leu Ala Leu Pro Ala Arg Gly
 30 35 40 45
 agg ccg cgc tca agg aat ggc ctc gca tcc aaa ggc cag cga gga gcg 254
 Arg Pro Arg Ser Arg Asn Gly Leu Ala Ser Lys Gly Gln Arg Gly Ala
 46 51 56 61
 gcc cct acg ggg cct ggg cac aga gct ctg cct tcc agg gac act gct 302
 Ala Pro Thr Gly Pro Gly His Arg Ala Leu Pro Ser Arg Asp Thr Ala
 62 67 72 77
 ctt ccc cag gag aga aac aag aag ctg gag gct gtg ggg aca gga att 350
 Leu Pro Gln Glu Arg Asn Lys Lys Leu Glu Ala Val Gly Thr Gly Ile
 78 83 88 93
 gaa cct aaa gcc atg tcc cag ggc ttg gtg aca ttt ggg gat gtg gct 398
 Glu Pro Lys Ala Met Ser Gln Gly Leu Val Thr Phe Gly Asp Val Ala
 94 99 104 109
 gta gat ttc tcc caa gag gag tgg gag tgg ctg aac ccc att cag agg 446
 Val Asp Phe Ser Gln Glu Glu Trp Glu Trp Leu Asn Pro Ile Gln Arg
 110 115 120 125
 aac ttg tac agg aag gtg atg ttg gag aac tac agg aac ctg gca tcg 494
 Asn Leu Tyr Arg Lys Val Met Leu Glu Asn Tyr Arg Asn Leu Ala Ser
 126 131 136 141
 ctg gga ctt tgt gtt tct aag ccc gat gtg atc tcc tcg ttg gaa caa 542
 Leu Gly Leu Cys Val Ser Lys Pro Asp Val Ile Ser Ser Leu Glu Gln
 142 147 152 157
 gga aaa gag cct tgg aca gtg aag cga aag atg aca aga gcc tgg tgc 590
 Gly Lys Glu Pro Trp Thr Val Lys Arg Lys Met Thr Arg Ala Trp Cys

158	163	168	173	
cca gac ttg aag gct	gtg tgg aag atc aag	gag tta cct ctc aag aag		638
Pro Asp Leu Lys Ala	Val Trp Lys Ile Lys	Glu Leu Pro Leu Lys Lys		
174	179	184	189	
gac ttc tgc gaa gga	aag cta tcc cag gca	gtg ata aca gag aga ctc		686
Asp Phe Cys Glu Gly	Lys Leu Ser Gln Ala	Val Ile Thr Glu Arg Leu		
190	195	200	205	
aca agc tat aat ctg	gag tac tct ctg tta	ggg gaa cac tgg gat tat		734
Thr Ser Tyr Asn Leu	Glu Tyr Ser Leu Leu	Gly Glu His Trp Asp Tyr		
206	211	216	221	
gat gct ctg ttt gag	aca cag ccg ggc ttg	gtg act atc aaa aac ctg		782
Asp Ala Leu Phe Glu	Thr Gln Pro Gly Leu	Val Thr Ile Lys Asn Leu		
222	227	232	237	
gct gtt gac ttc cgc	cag cag cta cac cca	gct cag aag aat ttc tgt		830
Ala Val Asp Phe Arg	Gln Gln Leu His Pro	Ala Gln Lys Asn Phe Cys		
238	243	248	253	
aag aat ggg ata tgg	gag aac aac agt gac	ctg gga tca gca gga cat		878
Lys Asn Gly Ile Trp	Glu Asn Asn Ser Asp	Leu Gly Ser Ala Gly His		
254	259	264	269	
tgt gtg gct aag cca	gat tta gtc tct tta	cta gag caa gag aag gag		926
Cys Val Ala Lys Pro	Asp Leu Val Ser Leu	Leu Glu Gln Glu Lys Glu		
270	275	280	285	
ccc tgg atg gtg aag	cga gag ctg aca gga	agc ctg ttc tca ggc cag		974
Pro Trp Met Val Lys	Arg Glu Leu Thr Gly	Ser Leu Phe Ser Gly Gln		
286	291	296	301	
cga tct gta cat gag	acc cag gaa tta ttt	cca aag caa gat tca tat		1022
Arg Ser Val His Glu	Thr Gln Glu Leu Phe	Pro Lys Gln Asp Ser Tyr		
302	307	312	317	
gct gaa ggg gta aca	gac aga acc tca aac	act aaa ctt gat tgt tcc		1070
Ala Glu Gly Val Thr	Asp Arg Thr Ser Asn	Thr Lys Leu Asp Cys Ser		
318	323	328	333	
agt ttc aga gaa aat	tgg gat tct gac tat	gtg ttc gga agg aag ctt		1118
Ser Phe Arg Glu Asn	Trp Asp Ser Asp Tyr	Val Phe Gly Arg Lys Leu		
334	339	344	349	
gca gta ggt caa gag	aca caa ttc agg caa	gag cca att act cat aac		1166
Ala Val Gly Gln Glu	Thr Gln Phe Arg Gln	Glu Pro Ile Thr His Asn		
350	355	360	365	
aaa acc ctc tct aag	gaa aga gaa cgt aca	tat aac aaa tct gga aga		1214
Lys Thr Leu Ser Lys	Glu Arg Glu Arg Thr	Tyr Asn Lys Ser Gly Arg		
366	371	376	381	
tgg tcc tat ttg gac	gat tca gaa gag aaa	gtt cat aat cgt gat tca		1262
Trp Ser Tyr Leu Asp	Asp Ser Glu Glu Lys	Val His Asn Arg Asp Ser		
382	387	392	397	

att Ile 398	aaa Lys	aat Asn	ttt Phe	caa Gln	aaa Lys 403	agt Ser	tca Ser	gtg Val	gta Val	ata Ile 408	aaa Lys	caa Gln	aca Thr	ggc Gly	atc Ile 413	1310
tat Tyr 414	gca Ala	gga Gly	aaa Lys	aag Lys	ctt Leu 419	ttc Phe	aag Lys	tgt Cys	aat Asn	gaa Glu 424	tgt Cys	aag Lys	aaa Lys	act Thr	ttt Phe 429	1358
acc Thr 430	cag Gln	agc Ser	tca Ser	tct Ser	ctt Leu 435	act Thr	gtt Val	cat His	cag Gln	aga Arg 440	att Ile	cac His	act Thr	gga Gly	gag Glu 445	1406
aaa Lys 446	cct Pro	tat Tyr	aaa Lys	tgt Cys	aat Asn 451	gaa Glu	tgt Cys	ggg Gly	aag Lys	gcc Ala 456	ttt Phe	agt Ser	gac Asp	ggc Gly	tca Ser 461	1454
tcc Ser 462	ttt Phe	gcc Ala	cga Arg	cac His	cag Gln 467	aga Arg	tgt Cys	cac His	act Thr	ggc Gly 472	aag Lys	aag Lys	ccc Pro	tat Tyr	gag Glu 477	1502
tgc Cys 478	att Ile	gag Glu	tgt Cys	ggg Gly	aaa Lys 483	gct Ala	ttc Phe	ata Ile	cag Gln	aac Asn 488	aca Thr	tcc Ser	ctt Leu	atc Ile	cgt Arg 493	1550
cac His 494	tgg Trp	aga Arg	tac Tyr	tat Tyr	cat His 499	act Thr	ggg Gly	gag Glu	aaa Lys	ccc Pro 504	ttt Phe	gat Asp	tgc Cys	atc Ile	gat Asp 509	1598
tgt Cys 510	ggg Gly	aaa Lys	gcc Ala	ttc Phe	agt Ser 515	gac Asp	cac His	ata Ile	ggg Gly	ctt Leu 520	aat Asn	caa Gln	cac His	agg Arg	aga Arg 525	1646
att Ile 526	cat His	act Thr	gga Gly	gag Glu	aaa Lys 531	cct Pro	tac Tyr	aaa Lys	tgt Cys	gat Asp 536	gta Val	tgt Cys	cac His	aaa Lys	tcc Ser 541	1694
ttc Phe 542	agg Arg	tat Tyr	ggg Gly	tcc Ser	tcc Ser 547	ctt Leu	act Thr	gta Val	cat His	caa Gln 552	agg Arg	att Ile	cat His	acc Thr	gga Gly 557	1742
gaa Glu 558	aaa Lys	cca Pro	tat Tyr	gaa Glu	tgt Cys 563	gat Asp	gtt Val	tgc Cys	aga Arg	aaa Lys 568	gcc Ala	ttc Phe	agc Ser	cat His	cat His 573	1790
gca Ala 574	tca Ser	ctc Leu	act Thr	caa Gln	cat His 579	caa Gln	aga Arg	gta Val	cat His	tct Ser 584	gga Gly	gaa Glu	aag Lys	cct Pro	ttt Phe 589	1838
aag Lys 590	tgt Cys	aaa Lys	gag Glu	tgc Cys	gga Gly 595	aaa Lys	gct Ala	ttt Phe	agg Arg	cag Gln 600	aat Asn	ata Ile	cac His	ctt Leu	gcc Ala 605	1886
agt Ser 606	cat His	tta Leu	agg Arg	att Ile	cat His 611	act Thr	ggg Gly	gag Glu	aag Lys	cct Pro 616	ttt Phe	gaa Glu	tgt Cys	gcg Ala	gag Glu 621	1934

tgt gga aaa tcc ttc agc atc agt tct cag ctt gcc act cat cag aga Cys Gly Lys Ser Phe Ser Ile Ser Ser Gln Leu Ala Thr His Gln Arg 622 627 632 637	1982
atc cat act gga gag aag ccc tat gaa tgt aag gtt tgt agt aaa gcg Ile His Thr Gly Glu Lys Pro Tyr Glu Cys Lys Val Cys Ser Lys Ala 638 643 648 653	2030
ttc acc cag aag gct cac ctt gca cag cat cag aaa acc cat aca gga Phe Thr Gln Lys Ala His Leu Ala Gln His Gln Lys Thr His Thr Gly 654 659 664 669	2078
gag aaa cca tat gag tgc aag gaa tgc ggt aaa gcc ttc agc cag acc Glu Lys Pro Tyr Glu Cys Lys Glu Cys Gly Lys Ala Phe Ser Gln Thr 670 675 680 685	2126
aca cac ctc att caa cat cag aga gtt cac act ggt gag aaa ccc tat Thr His Leu Ile Gln His Gln Arg Val His Thr Gly Glu Lys Pro Tyr 686 691 696 701	2174
aaa tgt atg gaa tgt ggg aag gcc ttt ggt gat aac tca tcc tgt act Lys Cys Met Glu Cys Gly Lys Ala Phe Gly Asp Asn Ser Ser Cys Thr 702 707 712 717	2222
caa cat caa aga ctg cac act ggc caa aga cct tat gaa tgt att gag Gln His Gln Arg Leu His Thr Gly Gln Arg Pro Tyr Glu Cys Ile Glu 718 723 728 733	2270
tgt gga aag gca ttc aag aca aaa tcc tcc ctt att tgt cat cgc aga Cys Gly Lys Ala Phe Lys Thr Lys Ser Ser Leu Ile Cys His Arg Arg 734 739 744 749	2318
agt cat act gga gaa aaa cct tat gaa tgc agt gtg tgt ggc aaa gcc Ser His Thr Gly Glu Lys Pro Tyr Glu Cys Ser Val Cys Gly Lys Ala 750 755 760 765	2366
ttt agt cat cgt caa tcc ctt agt gta cat cag aga atc cat tct gga Phe Ser His Arg Gln Ser Leu Ser Val His Gln Arg Ile His Ser Gly 766 771 776 781	2414
aag aaa cca tat gaa tgt aag gaa tgt agg aaa acc ttc atc caa att Lys Lys Pro Tyr Glu Cys Lys Glu Cys Arg Lys Thr Phe Ile Gln Ile 782 787 792 797	2462
gga cac ctt aat caa cat aag aga gtt cat act gga gag aga tct tat Gly His Leu Asn Gln His Lys Arg Val His Thr Gly Glu Arg Ser Tyr 798 803 808 813	2510
aac tat aag aaa agc aga aaa gtc ttc agg caa act gct cac tta gct Asn Tyr Lys Lys Ser Arg Lys Val Phe Arg Gln Thr Ala His Leu Ala 814 819 824 829	2558
cat cat cag cga att cat act gga gag tcg tca aca tgc ccc tct tta His His Gln Arg Ile His Thr Gly Glu Ser Ser Thr Cys Pro Ser Leu 830 835 840 845	2606
cct tcc acg tca aat cct gtg gat ctg ttt ccc aaa ttt ctc tgg aat	2654

cat aaa ctc cat gtt ctg atc aat aat gca ggt tgc atg gtc aat aaa	457
His Lys Leu His Val Leu Ile Asn Asn Ala Gly Cys Met Val Asn Lys	
94 99 104 109	
aga gag ctc aca gaa gat gga ctt gaa aaa aac ttt gct gcc aat act	505
Arg Glu Leu Thr Glu Asp Gly Leu Glu Lys Asn Phe Ala Ala Asn Thr	
110 115 120 125	
ctg ggt gtg tac att ctc acg acc ggc ctg atc cct gtg ctg gag aaa	553
Leu Gly Val Tyr Ile Leu Thr Thr Gly Leu Ile Pro Val Leu Glu Lys	
126 131 136 141	
gaa cac gac ccc cga gtg ata acc gtc tcc tca gga gga atg ttg gtt	601
Glu His Asp Pro Arg Val Ile Thr Val Ser Ser Gly Gly Met Leu Val	
142 147 152 157	
cag aaa ctg aac acc aat gat ctc cag tcc gaa aga aca cca ttt gat	649
Gln Lys Leu Asn Thr Asn Asp Leu Gln Ser Glu Arg Thr Pro Phe Asp	
158 163 168 173	
gga act atg gtc tat gca caa aac aag agg cag caa gtg gtt ctg acg	697
Gly Thr Met Val Tyr Ala Gln Asn Lys Arg Gln Gln Val Val Leu Thr	
174 179 184 189	
gag cgg tgg gcc caa ggg cac ccg gcc atc cat ttt tct tcc atg cat	745
Glu Arg Trp Ala Gln Gly His Pro Ala Ile His Phe Ser Ser Met His	
190 195 200 205	
cct ggc tgg gcc gac acc cca ggt gtg agg cag gcg atg ccg ggg ttc	793
Pro Gly Trp Ala Asp Thr Pro Gly Val Arg Gln Ala Met Pro Gly Phe	
206 211 216 221	
cac gcc agg ttc agg gac cgc ctg cgc tcc gag gcc cag ggc gcg gac	841
His Ala Arg Phe Arg Asp Arg Leu Arg Ser Glu Ala Gln Gly Ala Asp	
222 227 232 237	
acc atg ctg tgg ctg gcc ctc tcc tct gcc gca gcc gca cag ccc agc	889
Thr Met Leu Trp Leu Ala Leu Ser Ser Ala Ala Ala Ala Gln Pro Ser	
238 243 248 253	
ggc cgc tct aga gta tcc ctc gag ggg ccc aag ctt acg cgt acc cag	937
Gly Arg Ser Arg Val Ser Leu Glu Gly Pro Lys Leu Thr Arg Thr Gln	
254 259 264 269	
ctt tct tgt aca aag tgg tcc cta tag tgagt cgtatatgag ctaggcacac	989
Leu Ser Cys Thr Lys Trp Ser Leu *	
270 275	
agggcaatcc	999

<210> 31
 <211> 1687
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (129)..(725)

<400> 31

gtgcggtact cacaccacca gatcttcgtc ttcacgcgtg agtgtcccgc cggcgcaggg 60

cggggcgggc gtcctccagg ccctcaccgg gcgcccgcgc ccctgtgccc gcagtggacc 120

tgctgcag atg ctg gag atg aac atg gcc atc gcc ttc ccc gca gcg ccc 170
Met Leu Glu Met Asn Met Ala Ile Ala Phe Pro Ala Ala Pro
1 5 10

ctg ctg acc gtc atc ctg gcc ctc gtc ggg atg gag gcc atc atg tcg 218
Leu Leu Thr Val Ile Leu Ala Leu Val Gly Met Glu Ala Ile Met Ser
15 20 25 30

gag ttc ttc aac gac acc acc acc gcc ttc tac atc atc ctc atc gtg 266
Glu Phe Phe Asn Asp Thr Thr Thr Ala Phe Tyr Ile Ile Leu Ile Val
31 36 41 46

tgg ctc gcg gac cag tat gac gcc atc tgc tgc cac acc agc acc agc 314
Trp Leu Ala Asp Gln Tyr Asp Ala Ile Cys Cys His Thr Ser Thr Ser
47 52 57 62

aag cgg cat tgg ctg cgg ttc ttc tat ctc tac cac ttc gcc ttc tat 362
Lys Arg His Trp Leu Arg Phe Phe Tyr Leu Tyr His Phe Ala Phe Tyr
63 68 73 78

gcc tat cac tac cgc ttc aat ggg cag tat agc agc ctg gcc ctg gtc 410
Ala Tyr His Tyr Arg Phe Asn Gly Gln Tyr Ser Ser Leu Ala Leu Val
79 84 89 94

acc tcc tgg ctc ttc atc cag cat tcc atg atc tac ttc ttc cac cac 458
Thr Ser Trp Leu Phe Ile Gln His Ser Met Ile Tyr Phe Phe His His
95 100 105 110

tac gag ctg cct gcc atc ctg cag cag gtc cgc atc cag gag atg ctg 506
Tyr Glu Leu Pro Ala Ile Leu Gln Gln Val Arg Ile Gln Glu Met Leu
111 116 121 126

ctt cag gcg ccg aca ctg ggc ccc ggg acc ccc acg gcg ctg ccc gat 554
Leu Gln Ala Pro Thr Leu Gly Pro Gly Thr Pro Thr Ala Leu Pro Asp
127 132 137 142

gac atg aac aac aac tcg ggc gcc ccg gct aca gcc cct gac tct gcc 602
Asp Met Asn Asn Asn Ser Gly Ala Pro Ala Thr Ala Pro Asp Ser Ala
143 148 153 158

ggc cag ccc ccc gcc ctg ggc ccc gtc tcg cct ggg ggc cag cgg gag 650
Gly Gln Pro Pro Ala Leu Gly Pro Val Ser Pro Gly Gly Gln Arg Glu
159 164 169 174

tcc cgg gcc tgt ggc agc ggc gcc cag ctc cct ggt ggc cgc ggc agc 698
Ser Arg Ala Cys Gly Ser Gly Ala Gln Leu Pro Gly Gly Arg Gly Ser

175	180	185	190	
ctc agt ggc agc agc tgc cgg tgg tga cctgg gttggatggc agagaccgct				750
Leu Ser Gly Ser Ser Cys Arg Trp *				
191	196			
gccatcatca cagacgcctc cttcctgtcc ggccctgagcg cctccctcct ggagcggcgt				810
ccagccagcc cgctggggccc tgctggggggc ctccccacg cccccagga cagtgtcccc				870
ccgagtgact ccgcagcttc tgacacaact cccctggggg ctgcggtagg cgggcctagc				930
ccggcctcca tggccccaac ggaggcgccc tcggaggtgg ggtcctgagc cgcacagctg				990
agccgcctct gacccctgct ggctgggcct gaccttcccg agcccgtagg ggtgggggag				1050
gccagccacc tccttctctt gggactgccc agcctgtgtc gggggctttc agggtttctg				1110
ggggtttgcc cggaaggcgg ctttctctcc cctggtgtga ggtcgcgccc gaggcttgta				1170
cccgctagtg aggtgtttga gctggtcagc aaggagaggg ggtgggggttc cgcggaaggt				1230
tctggagggg tcttggtagg tctgcagtga accgtcctga ggatggagtg ggggtcccatg				1290
gtgcaggtct ctgagcaagg cggaggtgtg gaggagaggg cggcttgggg tggggcctcg				1350
cgcctagtgc ccggccggcc tcagcccggc tctgcctggt gctccctgca gtgccttctc				1410
catggccccg ccctccccgc gtgtgcgcca ggcttggggg ccccgggaga gcagagcttg				1470
cgcctcgggc atagggacgt ggggtgcagg cgccaacatc agtggcagca gccagggccg				1530
tgggtccagtc ccactcgggg atggagtggg ccggcgccca aaccagtcac tcggggagga				1590
atgcggagga gcgctcattc cattctatct aattgcagtg tacaaaattg tgtttgtata				1650
tagaataaac tgtctgttga cagcgaaaaa aaaaaaa				1687

<210> 32
 <211> 5079
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (428) .. (4795)

<400> 32	
agctgggtctc ctgcttgaca ccataaagag gccagcattg caggggtctat gtctttgtct	60
tgacttccag tttgatactg tgggttaaaga cagacccaca attttgagca agcttttact	120
cttgcacttt cttaagcagg atattcctgc tctgagctgg gagttctttg tcaatagatt	180

tgagacgctt tctttggaag cccagctaca tttggattgt aacaaggaat ttccttttcc	240
tacaaccatc actgctgtga ggaccaatgt tgctaacctc agcgatgcag ccttatggaa	300
gatcaagaga gtcgctttg caagaaaccg ccagaagagt gtacgttccc tgagggacag	360
cgtgaaaggg cctgtggaat ccaagagggc gctctccctc cctgagaccc tgacctccaa	420
aattcct atg agg ttg acc agg cat gag cag tct gct cca gct ctc ggt	469
Met Arg Leu Thr Arg His Glu Gln Ser Ala Pro Ala Leu Gly	
1 5 10	
ggg aca ccc gaa cag acg cca gga caa caa tct cct gag aat gac aac	517
Gly Thr Pro Glu Gln Thr Pro Gly Gln Gln Ser Pro Glu Asn Asp Asn	
15 20 25 30	
acc atc aag gac ctg ctc cca gaa gac gct ggg atc gac cac cag aca	565
Thr Ile Lys Asp Leu Leu Pro Glu Asp Ala Gly Ile Asp His Gln Thr	
31 36 41 46	
ggt cac cag ctg att aca gtg ctc atg aag ttc atg gcc aag gat gaa	613
Val His Gln Leu Ile Thr Val Leu Met Lys Phe Met Ala Lys Asp Glu	
47 52 57 62	
agc agc gct gag tca gac atc agc agt gca aag gcc ttc aac acg gtc	661
Ser Ser Ala Glu Ser Asp Ile Ser Ser Ala Lys Ala Phe Asn Thr Val	
63 68 73 78	
aag cga cac ctg tac gtc tta ctc ggc tat gac cag cag gaa ggt tgc	709
Lys Arg His Leu Tyr Val Leu Leu Gly Tyr Asp Gln Gln Glu Gly Cys	
79 84 89 94	
ttc atg att gca cct caa aaa atg cgc ctg tca act tgc ttt aat gca	757
Phe Met Ile Ala Pro Gln Lys Met Arg Leu Ser Thr Cys Phe Asn Ala	
95 100 105 110	
ttc att gca gga att gcc caa gtt atg gac tat aac att aac ttg gga	805
Phe Ile Ala Gly Ile Ala Gln Val Met Asp Tyr Asn Ile Asn Leu Gly	
111 116 121 126	
aaa cac ctt ctc ccc tta gtg gtt cag gtg ctc aaa tac tgc tct tgt	853
Lys His Leu Leu Pro Leu Val Val Gln Val Leu Lys Tyr Cys Ser Cys	
127 132 137 142	
cct caa ctc cgg cat tat ttc caa cag ccg cct cgt tgc tcc ctc tgg	901
Pro Gln Leu Arg His Tyr Phe Gln Gln Pro Pro Arg Cys Ser Leu Trp	
143 148 153 158	
tcc cta aag cct cac atc cgg cag atg tgg ttg aag gcc ttg ctt gtc	949
Ser Leu Lys Pro His Ile Arg Gln Met Trp Leu Lys Ala Leu Leu Val	
159 164 169 174	
atc ctt tac aag tat cca tac cga gac tgt gat atc agc aag atc ctg	997
Ile Leu Tyr Lys Tyr Pro Tyr Arg Asp Cys Asp Ile Ser Lys Ile Leu	
175 180 185 190	
ctg cat ctg att cac ata aca gtc aat aca ctc aat gcg cag tat cat	1045

415		420		425		430	
tcc tca gat tca acc tcg ggg cct gaa aaa cac tct ata ctc tca acc	1765						
Ser Ser Asp Ser Thr Ser Gly Pro Glu Lys His Ser Ile Leu Ser Thr							
431		436		441		446	
tcc gac agc gac tct ctt gta ttt gag cct ctt ccc cct ctc aga ata	1813						
Ser Asp Ser Asp Ser Leu Val Phe Glu Pro Leu Pro Pro Leu Arg Ile							
447		452		457		462	
gtc gag agt gac gaa gaa gag gag acg atg aac caa ggc gat gac ggc	1861						
Val Glu Ser Asp Glu Glu Glu Glu Thr Met Asn Gln Gly Asp Asp Gly							
463		468		473		478	
ccc tcc ggt aaa aat gct gcc tct tct ccc tcc atc ccc agc cat ccc	1909						
Pro Ser Gly Lys Asn Ala Ala Ser Ser Pro Ser Ile Pro Ser His Pro							
479		484		489		494	
tcc gtc ctc agc ctg agc aca gct ccg ctt gta caa gta agt gtg gag	1957						
Ser Val Leu Ser Leu Ser Thr Ala Pro Leu Val Gln Val Ser Val Glu							
495		500		505		510	
gat tgt tcc aaa gac ttt tct tct aag gac tca gga aat aat cag tca	2005						
Asp Cys Ser Lys Asp Phe Ser Ser Lys Asp Ser Gly Asn Asn Gln Ser							
511		516		521		526	
gca ggg aac act gac tct gcc ctc atc act ctg gaa gac cct atg gac	2053						
Ala Gly Asn Thr Asp Ser Ala Leu Ile Thr Leu Glu Asp Pro Met Asp							
527		532		537		542	
gcc gaa gga tcc tca aag cca gag gag ctg cca gag ttc tcc tgc ggt	2101						
Ala Glu Gly Ser Ser Lys Pro Glu Glu Leu Pro Glu Phe Ser Cys Gly							
543		548		553		558	
agc cca ctg acg ctg aag caa aaa cga gac ctc ctt cag aag tcg ttt	2149						
Ser Pro Leu Thr Leu Lys Gln Lys Arg Asp Leu Leu Gln Lys Ser Phe							
559		564		569		574	
gct ctc ccc gag atg tcg ctg gat gat cac cct gac ccg ggc act gag	2197						
Ala Leu Pro Glu Met Ser Leu Asp Asp His Pro Asp Pro Gly Thr Glu							
575		580		585		590	
ggg gag aag cct ggg gag ctg atg cca agt tca ggg gca aaa acc gtc	2245						
Gly Glu Lys Pro Gly Glu Leu Met Pro Ser Ser Gly Ala Lys Thr Val							
591		596		601		606	
ctc ctc aaa gtt ccc gaa gat gca gag aac ccc aca gaa agt gag aag	2293						
Leu Leu Lys Val Pro Glu Asp Ala Glu Asn Pro Thr Glu Ser Glu Lys							
607		612		617		622	
cct gat acc agt gca gaa tct gat aca gaa cag aat cct gaa agg aag	2341						
Pro Asp Thr Ser Ala Glu Ser Asp Thr Glu Gln Asn Pro Glu Arg Lys							
623		628		633		638	
gtg gaa gag gat gga gct gag gaa tcc gaa ttt aag att cag att gtt	2389						
Val Glu Glu Asp Gly Ala Glu Glu Ser Glu Phe Lys Ile Gln Ile Val							
639		644		649		654	

ccc agg cag agg aag cag agg aag att gct gtc agt gct atc cag aga	2437
Pro Arg Gln Arg Lys Gln Arg Lys Ile Ala Val Ser Ala Ile Gln Arg	
655 660 665 670	
gag tac ctc gac atc tcc ttc aac att ctg gac aaa ctg gga gaa cag	2485
Glu Tyr Leu Asp Ile Ser Phe Asn Ile Leu Asp Lys Leu Gly Glu Gln	
671 676 681 686	
aaa gat cca gat cct tct act aaa gga ctt tca act ttg gaa atg cca	2533
Lys Asp Pro Asp Pro Ser Thr Lys Gly Leu Ser Thr Leu Glu Met Pro	
687 692 697 702	
cga gaa tct tca tct gcc cct acg tta gat gca ggt gtg ccg gaa aca	2581
Arg Glu Ser Ser Ser Ala Pro Thr Leu Asp Ala Gly Val Pro Glu Thr	
703 708 713 718	
agt agc cat tcc tca ata tca act cag tat agg cag atg aaa agg gga	2629
Ser Ser His Ser Ser Ile Ser Thr Gln Tyr Arg Gln Met Lys Arg Gly	
719 724 729 734	
tcc ctg gga gtt ctg aca atg agc cag tta atg aag cgg cag ctg gag	2677
Ser Leu Gly Val Leu Thr Met Ser Gln Leu Met Lys Arg Gln Leu Glu	
735 740 745 750	
cat cag tct agc gcc ccc cat aac atc agc aac tgg gac act gaa cag	2725
His Gln Ser Ser Ala Pro His Asn Ile Ser Asn Trp Asp Thr Glu Gln	
751 756 761 766	
ata cag cct ggg aaa cgc cag tgt aac gtg cca aca tgc cta aac cct	2773
Ile Gln Pro Gly Lys Arg Gln Cys Asn Val Pro Thr Cys Leu Asn Pro	
767 772 777 782	
gac ctg gag gga cag cca ttg agg atg aga ggt gcc acc aaa tcc agc	2821
Asp Leu Glu Gly Gln Pro Leu Arg Met Arg Gly Ala Thr Lys Ser Ser	
783 788 793 798	
ctg cta tca gca cca agc ata gtc agt atg ttt gtg cct gca cct gaa	2869
Leu Leu Ser Ala Pro Ser Ile Val Ser Met Phe Val Pro Ala Pro Glu	
799 804 809 814	
gag ttc act gac gag cag ccg acg gtg atg acg gac aaa tgc cat gac	2917
Glu Phe Thr Asp Glu Gln Pro Thr Val Met Thr Asp Lys Cys His Asp	
815 820 825 830	
tgt ggg gcc att ctt gaa gaa tac gat gaa gag aca ctt ggg cta gcc	2965
Cys Gly Ala Ile Leu Glu Glu Tyr Asp Glu Glu Thr Leu Gly Leu Ala	
831 836 841 846	
atc gtg gtc ctc tcc aca ttc att cac tta agc cca gac ctg gca gcc	3013
Ile Val Val Leu Ser Thr Phe Ile His Leu Ser Pro Asp Leu Ala Ala	
847 852 857 862	
ccg ctg ctg ctg gat atc atg cag tct gtg gga aga ttg gca tcc agt	3061
Pro Leu Leu Leu Asp Ile Met Gln Ser Val Gly Arg Leu Ala Ser Ser	
863 868 873 878	

act Thr 879	acc Thr	ttt Phe	tct Ser	aat Asn	caa Gln 884	gca Ala	gaa Glu	agc Ser	atg Met	atg Met 889	gtt Val	ccc Pro	ggc Gly	aat Asn	gcg Ala 894	3109
gcg Ala 895	ggg Gly	gtg Val	gcc Ala	aag Lys	cag Gln 900	ttc Phe	ctg Leu	cgc Arg	tgc Cys	atc Ile 905	ttc Phe	cat His	cag Gln	ttg Leu	gcc Ala 910	3157
ccc Pro 911	aac Asn	ggc Gly	atc Ile	ttc Phe	ccg Pro 916	cag Gln	ctg Leu	ttc Phe	caa Gln	agc Ser 921	acg Thr	atc Ile	aaa Lys	gat Asp	ggg Gly 926	3205
act Thr 927	ttt Phe	tta Leu	cgg Arg	acc Thr	tta Leu 932	gcc Ala	tcg Ser	tct Ser	ctg Leu	atg Met 937	gac Asp	ttc Phe	aat Asn	gag Glu	ctg Leu 942	3253
agc Ser 943	tcc Ser	atc Ile	gca Ala	gct Ala	ctc Leu 948	agt Ser	cag Gln	ctc Leu	cta Leu	gag Glu 953	ggg Gly	cta Leu	aat Asn	aac Asn	aaa Lys 958	3301
aag Lys 959	aat Asn	tta Leu	cca Pro	gca Ala	ggg Gly 964	ggg Gly	gct Ala	atg Met	att Ile	cgc Arg 969	tgt Cys	ttg Leu	gaa Glu	aac Asn	att Ile 974	3349
gca Ala 975	acc Thr	ttc Phe	atg Met	gaa Glu	gct Ala 980	ttg Leu	cct Pro	atg Met	gat Asp	tct Ser 985	cct Pro	agt Ser	agc Ser	ctc Leu	tgg Trp 990	3397
acc Thr 991	aca Thr	att Ile	agc Ser	aac Asn	cag Gln 996	ttt Phe	cag Gln	aca Thr	ttt Phe	ttt Phe 1001	gcc Ala	aag Lys	ctg Leu	cct Pro	tgt Cys 1006	3445
gtt Val 1007	tta Leu	cct Pro	ctg Leu	aag Lys	tgt Cys 1012	tct Ser	tta Leu	gat Asp	tcc Ser	agt Ser 1017	tta Leu	aga Arg	att Ile	atg Met	att Ile 1022	3493
tgc Cys 1023	ctc Leu	ttg Leu	aag Lys	atc Ile	cct Pro 1028	tct Ser	acc Thr	aat Asn	gct Ala	aca Thr 1033	agg Arg	agt Ser	ttg Leu	ttg Leu	gaa Glu 1038	3541
cca Pro 1039	ttt Phe	tca Ser	aaa Lys	ctg Leu	ctc Leu 1044	agc Ser	ttt Phe	gta Val	att Ile	cag Gln 1049	aat Asn	gcc Ala	gtc Val	ttc Phe	act Thr 1054	3589
ctg Leu 1055	gcc Ala	tac Tyr	ctg Leu	gtg Val	gag Glu 1060	ctg Leu	tgt Cys	ggc Gly	tta Leu	tgt Cys 1065	tac Tyr	cga Arg	gct Ala	ttc Phe	act Thr 1070	3637
aag Lys 1071	gaa Glu	cga Arg	gat Asp	aaa Lys	ttc Phe 1076	tac Tyr	ttg Leu	tct Ser	cgt Arg	agt Ser 1081	gtt Val	gtt Val	cta Leu	gaa Glu	ctt Leu 1086	3685
ctg Leu 1087	cag Gln	gcc Ala	cta Leu	aag Lys	ctc Leu 1092	aaa Lys	tct Ser	cct Pro	tta Leu	cca Pro 1097	gat Asp	aca Thr	aac Asn	ctt Leu	ctt Leu 1102	3733
ctg 1107	ctt 1108	gtt 1109	cag 1110	ttt 1111	att 1112	tgt 1113	gca 1114	gat 1115	gct 1116	gga 1117	acc 1118	aaa 1119	cta 1120	gct 1121	gag 1122	3781

Leu Leu Val Gln Phe Ile Cys Ala Asp Ala Gly Thr Lys Leu Ala Glu	
1103 1108 1113 1118	
tca aca atc ctg agc aag cag atg ata gcc tct gta cct gga tgt ggg	3829
Ser Thr Ile Leu Ser Lys Gln Met Ile Ala Ser Val Pro Gly Cys Gly	
1119 1124 1129 1134	
act gca gcg atg gag tgt gtg agg cag tac atc aac gaa gtg ctg gat	3877
Thr Ala Ala Met Glu Cys Val Arg Gln Tyr Ile Asn Glu Val Leu Asp	
1135 1140 1145 1150	
ttc atg gca gac atg cac acg ctg acc aaa ctg aag agc cac atg aag	3925
Phe Met Ala Asp Met His Thr Leu Thr Lys Leu Lys Ser His Met Lys	
1151 1156 1161 1166	
aca tgt tcc cag cct ctg cat gaa gat acc ttt ggg gga cat ctc aaa	3973
Thr Cys Ser Gln Pro Leu His Glu Asp Thr Phe Gly Gly His Leu Lys	
1167 1172 1177 1182	
gtg ggg ctg gcc cag att gca gcc atg gac atc tca cgg ggc aac cac	4021
Val Gly Leu Ala Gln Ile Ala Ala Met Asp Ile Ser Arg Gly Asn His	
1183 1188 1193 1198	
aga gat aac aaa gct gtg atc cgc tat ctg cct tgg ctt tat cat ccc	4069
Arg Asp Asn Lys Ala Val Ile Arg Tyr Leu Pro Trp Leu Tyr His Pro	
1199 1204 1209 1214	
ccc tct gca atg cag caa gga cct aaa gaa ttc att gag tgt gtc tcc	4117
Pro Ser Ala Met Gln Gln Gly Pro Lys Glu Phe Ile Glu Cys Val Ser	
1215 1220 1225 1230	
cat atc cga ctg ttg tcc tgg ctg ctg ctg ggt tcc ctc act cac aat	4165
His Ile Arg Leu Leu Ser Trp Leu Leu Leu Gly Ser Leu Thr His Asn	
1231 1236 1241 1246	
gca gtg tgc cca aat gcc tcc tct ccc tgc ctg ccc att cct ctg gat	4213
Ala Val Cys Pro Asn Ala Ser Ser Pro Cys Leu Pro Ile Pro Leu Asp	
1247 1252 1257 1262	
gca ggc tcc cac gtt gca gac cat ctt att gtt atc ctg att gga ttt	4261
Ala Gly Ser His Val Ala Asp His Leu Ile Val Ile Leu Ile Gly Phe	
1263 1268 1273 1278	
cca gag caa tca aag acc tcc gtg ctg cac atg tgc tcc ctc ttc cac	4309
Pro Glu Gln Ser Lys Thr Ser Val Leu His Met Cys Ser Leu Phe His	
1279 1284 1289 1294	
gcg ttc atc ttt gct cag ctg tgg aca gtt tat tgc gag caa agt gcc	4357
Ala Phe Ile Phe Ala Gln Leu Trp Thr Val Tyr Cys Glu Gln Ser Ala	
1295 1300 1305 1310	
gtc gct aca aat ctc caa aat cag aat gaa ttc agc ttc acg gcg ata	4405
Val Ala Thr Asn Leu Gln Asn Gln Asn Glu Phe Ser Phe Thr Ala Ile	
1311 1316 1321 1326	
ctg aca gca cta gaa ttt tgg agt agg gtg aca ccc agc atc ctt cag	4453
Leu Thr Ala Leu Glu Phe Trp Ser Arg Val Thr Pro Ser Ile Leu Gln	

1327	1332	1337	1342	
cta atg gcc cat aac aaa gtg atg gta gaa atg gtg tgt ctc cat gtg				4501
Leu Met Ala His Asn Lys Val Met Val Glu Met Val Cys Leu His Val				
1343	1348	1353	1358	
att agt tta atg gag gca ttg cag gaa tgc aat tcg acc att ttt gtc				4549
Ile Ser Leu Met Glu Ala Leu Gln Glu Cys Asn Ser Thr Ile Phe Val				
1359	1364	1369	1374	
aag ctg ata cct atg tgg ttg cca atg att cag tca aat atc aag cac				4597
Lys Leu Ile Pro Met Trp Leu Pro Met Ile Gln Ser Asn Ile Lys His				
1375	1380	1385	1390	
tta tct gcg gga ctc cag ctt cgc ctc cag gct att cag aac cac gtg				4645
Leu Ser Ala Gly Leu Gln Leu Arg Leu Gln Ala Ile Gln Asn His Val				
1391	1396	1401	1406	
aac cac cac agc cta agg acg ctg ccg ggc tcg ggc cag agc agt gct				4693
Asn His His Ser Leu Arg Thr Leu Pro Gly Ser Gly Gln Ser Ser Ala				
1407	1412	1417	1422	
ggc ctg gca gcc ctc cga aag tgg ttg cag tgc act cag ttc aaa atg				4741
Gly Leu Ala Ala Leu Arg Lys Trp Leu Gln Cys Thr Gln Phe Lys Met				
1423	1428	1433	1438	
gcc cag gtg gag atc cag tcc tcg gaa gca gcc tct caa ttt tat cct				4789
Ala Gln Val Glu Ile Gln Ser Ser Glu Ala Ala Ser Gln Phe Tyr Pro				
1439	1444	1449	1454	
cta tga gtggactcct cggcgctcag tgtcaacact ctggttttagc aataatgggt				4845
Leu *				
1455				
ttaaaaacaa acaatttgat ccaagcaggt tggggaacat attggtactg tacattctct				4905
ttctagttta gtaaaagatg tgcaaaggcc agagagggcc gaaaatgaag ctttcttgct				4965
acacatattt ctgatgactc cttgggctat ctgattaagt gtttcottac attatattttt				5025
aaaaacaaaa tcatttttct ttaactaact tctatattttt ttaagaaaaa aaaa				5079

<210> 33
 <211> 1568
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (167) .. (1444)

<400> 33
 atttggccct cgaggccaag aattcggcac gaggtcga aagagtggcg cagggtcgcg 60

cgccccgcc	tccttccccg	cccagcgaag	ctctctgacc	acccctcttt	tctagagttc	120
tgccctcgctt	cccggcgcg	tcgcagccct	cagcccactt	aggata	atg gcg aca	175
					Met Ala Thr	
					1	
gct gag gta	ctg aac att	ggt aaa aaa	tta tat	gag ggt	aaa aca aaa	223
Ala Glu Val	Leu Asn Ile	Gly Lys Lys	Leu Tyr	Glu Gly Lys	Thr Lys	
4	9		14		19	
gaa gtc tac	gaa ttg tta	gac agt cca	gga aaa	gtc ctc	ctg cag tcc	271
Glu Val Tyr	Glu Leu Leu	Asp Ser Pro	Gly Lys Val	Leu Leu	Gln Ser	
20	25		30		35	
aag gac cag	att aca gca	gga aat gca	gct aga	aaa aac	cac ctg gaa	319
Lys Asp Gln	Ile Thr Ala	Gly Asn Ala	Ala Arg	Lys Asn	His Leu Glu	
36	41		46		51	
gga aaa gct	gca atc tca	aat aaa atc	acc agt	tgt att	ttt cag tta	367
Gly Lys Ala	Ala Ile Ser	Asn Lys Ile	Thr Ser	Cys Ile	Phe Gln Leu	
52	57		62		67	
tta cag gaa	gca ggt att	aaa act gcc	ttc acc	aga aaa	tgt ggg gag	415
Leu Gln Glu	Ala Gly Ile	Lys Thr Ala	Phe Thr	Arg Lys	Cys Gly Glu	
68	73		78		83	
aca gct ttc	att gca ccg	cag tgt gaa	atg att	cca att	gaa tgg gtt	463
Thr Ala Phe	Ile Ala Pro	Gln Cys Glu	Met Ile	Pro Ile	Glu Trp Val	
84	89		94		99	
tgc aga aga	ata gca act	ggt tct ttt	ctc aaa	aga aat	cct ggt gtc	511
Cys Arg Arg	Ile Ala Thr	Gly Ser Phe	Leu Lys	Arg Asn	Pro Gly Val	
100	105		110		115	
aag gaa gga	tat aag ttt	tac cca cct	aaa gtg	gag ttg	ttt ttc aag	559
Lys Glu Gly	Tyr Lys Phe	Tyr Pro Pro	Lys Val	Glu Leu	Phe Phe Lys	
116	121		126		131	
gat gat gcc	aat aat gac	cca cag tgg	tct gag	gaa cag	ctg att gct	607
Asp Asp Ala	Asn Asn Asp	Pro Gln Trp	Ser Glu	Glu Gln	Leu Ile Ala	
132	137		142		147	
gca aaa ttt	tgc ttt gct	gga ctt ctt	ata ggc	cag act	gaa gtg gat	655
Ala Lys Phe	Cys Phe Ala	Gly Leu Leu	Ile Gly	Gln Thr	Glu Val Asp	
148	153		158		163	
atc atg agt	cat gct aca	cag gct ata	ttt gaa	ata ctg	gag aaa tcc	703
Ile Met Ser	His Ala Thr	Gln Ala Ile	Phe Glu	Ile Leu	Glu Lys Ser	
164	169		174		179	
tgg ttg ccc	cag aat tgt	aca ctg gtt	gat atg	aag att	gaa ttt ggt	751
Trp Leu Pro	Gln Asn Cys	Thr Leu Val	Asp Met	Lys Ile	Glu Phe Gly	
180	185		190		195	
gtt gat gta	acc acc aaa	gaa att gtt	ctt gct	gat gtt	att gac aat	799
Val Asp Val	Thr Thr Lys	Glu Ile Val	Leu Ala	Asp Val	Ile Asp Asn	
196	201		206		211	

gat tcc tgg aga ctc tgg cca tca gga gat cga agc caa cag aaa gac	847
Asp Ser Trp Arg Leu Trp Pro Ser Gly Asp Arg Ser Gln Gln Lys Asp	
212 217 222 227	
aaa cag tct tat cgg gac ctc aaa gaa gta act cct gaa ggg ctc caa	895
Lys Gln Ser Tyr Arg Asp Leu Lys Glu Val Thr Pro Glu Gly Leu Gln	
228 233 238 243	
atg gta aag aaa aac ttt gag tgg gtt gca gag aga gta gag ttg ctt	943
Met Val Lys Lys Asn Phe Glu Trp Val Ala Glu Arg Val Glu Leu Leu	
244 249 254 259	
ttg aaa tca gaa agt cag tgc agg gtt gta gtg ttg atg ggc tct act	991
Leu Lys Ser Glu Ser Gln Cys Arg Val Val Val Leu Met Gly Ser Thr	
260 265 270 275	
tct gat ctt ggt cac tgt gaa aaa atc aag aag gcc tgt gga aat ttt	1039
Ser Asp Leu Gly His Cys Glu Lys Ile Lys Lys Ala Cys Gly Asn Phe	
276 281 286 291	
ggc att cca tgt gaa ctt cga gta aca tct gcg cat aaa gga cca gat	1087
Gly Ile Pro Cys Glu Leu Arg Val Thr Ser Ala His Lys Gly Pro Asp	
292 297 302 307	
gaa act ctg agg att aaa gct gag tat gaa ggg gat ggc att cct act	1135
Glu Thr Leu Arg Ile Lys Ala Glu Tyr Glu Gly Asp Gly Ile Pro Thr	
308 313 318 323	
gta ttt gtg gca gtg gca ggc aga agt aat ggt ttg gga cca gtg atg	1183
Val Phe Val Ala Val Ala Gly Arg Ser Asn Gly Leu Gly Pro Val Met	
324 329 334 339	
tct ggg aac act gca tat cca gtt atc agc tgt cct ccc ctc aca cca	1231
Ser Gly Asn Thr Ala Tyr Pro Val Ile Ser Cys Pro Pro Leu Thr Pro	
340 345 350 355	
gac tgg gga gtt cag gat gtg tgg tct tct ctt cga cta ccc agt ggt	1279
Asp Trp Gly Val Gln Asp Val Trp Ser Ser Leu Arg Leu Pro Ser Gly	
356 361 366 371	
ctt ggc tgt tca acc gta ctt tct cca gaa gga tca gct caa ttt gct	1327
Leu Gly Cys Ser Thr Val Leu Ser Pro Glu Gly Ser Ala Gln Phe Ala	
372 377 382 387	
gct cag ata ttt ggg tta agc aac cat ttg gta tgg agc aaa ctg cga	1375
Ala Gln Ile Phe Gly Leu Ser Asn His Leu Val Trp Ser Lys Leu Arg	
388 393 398 403	
gca agc att ttg aac aca tgg att tcc ttg aag cag gct gac aag aaa	1423
Ala Ser Ile Leu Asn Thr Trp Ile Ser Leu Lys Gln Ala Asp Lys Lys	
404 409 414 419	
atc aga gaa tgt aat tta taa ga aagaatgccca ttgaattttt taggggaaaa	1476
Ile Arg Glu Cys Asn Leu *	
420 425	

actacaaatt tctaatttag ctgaaggaaa atcaagcaag atgaaaaggt aatttttaaatt 1536
tagagaacac aaataaaatg tattagtga ca 1568

<210> 34
<211> 1686
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (230) .. (1330)

<400> 34
cacgaggggg aatgggcctc agctccccga gtcccagaga gcttggctga gccctgggtgt 60
tcccacctcc tcagagccat gaggcaggaa tgttctcctt atgtgactag gcacagggttc 120
caaatgggga ggggactggc tcagcatccg gagccaaaac aggaatagaa ctggaagctg 180
agcctggagc ggttctgggc ttttggttct ctgcatcaac acagccagc atg cct 235
Met Pro
1

atg att tct gtg ctg ggc aaa atg ttt ctg tgg cag cgt gaa ggg cct 283
Met Ile Ser Val Leu Gly Lys Met Phe Leu Trp Gln Arg Glu Gly Pro
3 8 13 18

gga gga cga tgg act tgt cag aca agt cgc aga gtg tcc tcg gac ccc 331
Gly Gly Arg Trp Thr Cys Gln Thr Ser Arg Arg Val Ser Ser Asp Pro
19 24 29 34

gct tgg gct gtg gag tgg atc gaa ctt cct cgg ggt ctc tct cta tcc 379
Ala Trp Ala Val Glu Trp Ile Glu Leu Pro Arg Gly Leu Ser Leu Ser
35 40 45 50

tct ttg gga tct gct cga acc ctc cga ggc tgg agc agg tcc tcc cgc 427
Ser Leu Gly Ser Ala Arg Thr Leu Arg Gly Trp Ser Arg Ser Ser Arg
51 56 61 66

cct tcc tcg gtg gac agt cag gac ttg cca gag gtg aat gtt gga gac 475
Pro Ser Ser Val Asp Ser Gln Asp Leu Pro Glu Val Asn Val Gly Asp
67 72 77 82

aca gtc gcg atg ctg ccc aag tcc cgg cga gcc cta act atc cag gag 523
Thr Val Ala Met Leu Pro Lys Ser Arg Arg Ala Leu Thr Ile Gln Glu
83 88 93 98

atc gct gcg ctg gcc agg tcc tcc ctg cat ggt att tcc cag gtg gtg 571
Ile Ala Ala Leu Ala Arg Ser Ser Leu His Gly Ile Ser Gln Val Val
99 104 109 114

aag gac cac gtg acc aag cct acc gcc atg gcc cag ggc cga gtg gct 619
Lys Asp His Val Thr Lys Pro Thr Ala Met Ala Gln Gly Arg Val Ala

tcc tta gat gag gat gag gca gag cca gag gaa cag tga cccacatcat 1340
 Ser Leu Asp Glu Asp Glu Ala Glu Pro Glu Glu Gln *
 355 360 365

gcctggcagt ggcatgcatc ccccggctgc tgccaggggc agagccttct gtgcccagt 1400
 gtgggctcaa ggctcccagc agagctccac agcctagagg gctcctggga gcgctcgctt 1460
 ctccgttgtg tgttttgcat gaaagtgttt ggagaggagg caggggctgg gctgggggag 1520
 catgtcctgc cccactccc ggggcttgcc ggggggttgcc cgggggcctc tggggcatgg 1580
 ctacagctgt ggcagacagt gatgttcatg ttcttaaaat gccacacaca catttcctcc 1640
 tcggataatg tgaaccacta aggggggttg gactgggctg tgtgag 1686

<210> 35
 <211> 3065
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (72) .. (1958)

<400> 35
 gccccagca ggctctccag tcccaggatg cgctgagccg ccgggggggct gaggccgcgc 60
 caactacatg c atg tcc ccc ggg ggc aag ttc gac ttt gac gac ggg ggc 110
 Met Ser Pro Gly Gly Lys Phe Asp Phe Asp Asp Gly Gly
 1 5 10
 tgc tac gtg ggg ggc tgg gag gcg ggg cgg gca cat ggc tac ggc gtg 158
 Cys Tyr Val Gly Gly Trp Glu Ala Gly Arg Ala His Gly Tyr Gly Val
 14 19 24 29
 tgc acg ggc ccc ggc gcc cag ggc gag tac agc ggc tgc tgg gca cac 206
 Cys Thr Gly Pro Gly Ala Gln Gly Glu Tyr Ser Gly Cys Trp Ala His
 30 35 40 45
 ggc ttc gag tca ctg ggc gtc ttc acg ggg ccc ggc gga cac agc tac 254
 Gly Phe Glu Ser Leu Gly Val Phe Thr Gly Pro Gly Gly His Ser Tyr
 46 51 56 61
 cag ggc cac tgg cag cag ggc aag cgc gaa ggg ctg ggc gtg gag cgc 302
 Gln Gly His Trp Gln Gln Gly Lys Arg Glu Gly Leu Gly Val Glu Arg
 62 67 72 77
 aag agc cgc tgg acg tac cgc ggc gag tgg ctg ggc ggg ctg aag ggg 350
 Lys Ser Arg Trp Thr Tyr Arg Gly Glu Trp Leu Gly Gly Leu Lys Gly
 78 83 88 93
 cgc agc ggc gtg tgg gaa agc gtg tcc ggc ctg cgc tac gcc ggg ctc 398

Arg	Ser	Gly	Val	Trp	Glu	Ser	Val	Ser	Gly	Leu	Arg	Tyr	Ala	Gly	Leu	
94					99					104					109	
tgg	aag	gac	ggt	ttc	cag	gac	ggc	tac	ggc	act	gag	acc	tac	tcc	gac	446
Trp	Lys	Asp	Gly	Phe	Gln	Asp	Gly	Tyr	Gly	Thr	Glu	Thr	Tyr	Ser	Asp	
110					115					120					125	
gga	ggc	acc	tac	cag	ggc	cag	tgg	cag	gcc	ggg	aag	cgc	cac	ggc	tac	494
Gly	Gly	Thr	Tyr	Gln	Gly	Gln	Trp	Gln	Ala	Gly	Lys	Arg	His	Gly	Tyr	
126					131					136					141	
ggg	gta	cgc	cag	agt	gtg	ccc	tac	cat	cag	gcg	gcg	ctg	ctg	cgc	tcg	542
Gly	Val	Arg	Gln	Ser	Val	Pro	Tyr	His	Gln	Ala	Ala	Leu	Leu	Arg	Ser	
142					147					152					157	
ccc	cgc	cgc	acc	tcc	ctg	gat	tcc	ggc	cac	agc	gac	ccc	ccg	acg	cca	590
Pro	Arg	Arg	Thr	Ser	Leu	Asp	Ser	Gly	His	Ser	Asp	Pro	Pro	Thr	Pro	
158					163					168					173	
ccc	ccg	ccc	ctg	ccc	ttg	ccg	ggc	gac	gag	gga	ggc	agc	ccc	gcc	tcg	638
Pro	Pro	Pro	Leu	Pro	Leu	Pro	Gly	Asp	Glu	Gly	Gly	Ser	Pro	Ala	Ser	
174					179					184					189	
ggc	tcc	cgg	ggc	ggc	ttc	gtg	ctg	gcc	ggg	ccc	ggg	gac	gcc	gac	ggc	686
Gly	Ser	Arg	Gly	Gly	Phe	Val	Leu	Ala	Gly	Pro	Gly	Asp	Ala	Asp	Gly	
190					195					200					205	
gcg	tcg	tcc	cga	aag	cgc	act	ccg	gcg	gcc	ggc	gga	ttc	ttt	cgc	cgt	734
Ala	Ser	Ser	Arg	Lys	Arg	Thr	Pro	Ala	Ala	Gly	Gly	Phe	Phe	Arg	Arg	
206					211					216					221	
tcg	ctg	ctg	ctc	agc	ggg	ctc	cga	gcg	ggc	gga	cgt	cgc	agc	tcc	ctg	782
Ser	Leu	Leu	Leu	Ser	Gly	Leu	Arg	Ala	Gly	Gly	Arg	Arg	Ser	Ser	Leu	
222					227					232					237	
ggc	agc	aag	cga	ggc	tcc	ctg	cgc	agc	gag	gtg	agc	agc	gag	gtg	ggc	830
Gly	Ser	Lys	Arg	Gly	Ser	Leu	Arg	Ser	Glu	Val	Ser	Ser	Glu	Val	Gly	
238					243					248					253	
agc	acc	gga	ccg	ccc	ggc	tcg	gag	gcc	agc	ggg	ccc	ccg	gcc	gca	gcg	878
Ser	Thr	Gly	Pro	Pro	Gly	Ser	Glu	Ala	Ser	Gly	Pro	Pro	Ala	Ala	Ala	
254					259					264					269	
ccg	ccc	gcc	ctc	atc	gag	ggc	tcg	gcc	aca	gag	gtg	tac	gcg	ggc	gag	926
Pro	Pro	Ala	Leu	Ile	Glu	Gly	Ser	Ala	Thr	Glu	Val	Tyr	Ala	Gly	Glu	
270					275					280					285	
tgg	cgc	gca	gat	cgg	cgc	agc	ggc	ttc	ggc	gtc	agc	cag	cgc	tcc	aac	974
Trp	Arg	Ala	Asp	Arg	Arg	Ser	Gly	Phe	Gly	Val	Ser	Gln	Arg	Ser	Asn	
286					291					296					301	
ggg	ctg	cgc	tac	gag	ggc	gag	tgg	ctg	ggc	aac	cgg	cgg	cac	ggc	tac	1022
Gly	Leu	Arg	Tyr	Glu	Gly	Glu	Trp	Leu	Gly	Asn	Arg	Arg	His	Gly	Tyr	
302					307					312					317	
ggg	cgc	acc	acc	cgc	ccc	gac	ggc	tcc	cgc	gag	gag	ggc	aag	tac	aag	1070
Gly	Arg	Thr	Thr	Arg	Pro	Asp	Gly	Ser	Arg	Glu	Glu	Gly	Lys	Tyr	Lys	

318		323		328		333	
cgc aac cgg ctg gtg cac ggc ggg cgc gtc cgc agt ctc ctg cct ctg	1118						
Arg Asn Arg Leu Val His Gly Gly Arg Val Arg Ser Leu Leu Pro Leu							
334		339		344		349	
gcc ctt cgg cgg ggc aag gtt aag gag aag gtg gac agg gct gtc gag	1166						
Ala Leu Arg Arg Gly Lys Val Lys Glu Lys Val Asp Arg Ala Val Glu							
350		355		360		365	
ggc gcc cgt cga gcc gtg agt gct gcc cgt cag cgc cag gag atc gcc	1214						
Gly Ala Arg Arg Ala Val Ser Ala Ala Arg Gln Arg Gln Glu Ile Ala							
366		371		376		381	
gct gcc agg gca gca gac gcc ctc cta aag gca gtg gca gcc agc agt	1262						
Ala Ala Arg Ala Ala Asp Ala Leu Leu Lys Ala Val Ala Ala Ser Ser							
382		387		392		397	
gtc gct gag aag gcc gtg gag gca gct cga atg gcc aaa ctg ata gcc	1310						
Val Ala Glu Lys Ala Val Glu Ala Ala Arg Met Ala Lys Leu Ile Ala							
398		403		408		413	
cag gac ctg cag ccc atg cta gag gcc cca ggc cgc aga ccc agg cag	1358						
Gln Asp Leu Gln Pro Met Leu Glu Ala Pro Gly Arg Arg Pro Arg Gln							
414		419		424		429	
gac tca gaa ggt tcc gac acg gag ccc ctg gat gag gac agc cct ggg	1406						
Asp Ser Glu Gly Ser Asp Thr Glu Pro Leu Asp Glu Asp Ser Pro Gly							
430		435		440		445	
gta tat gag aac gga ctg acc ccc tca gag gga tcc cct gaa ctg ccc	1454						
Val Tyr Glu Asn Gly Leu Thr Pro Ser Glu Gly Ser Pro Glu Leu Pro							
446		451		456		461	
agc agt cct gcc tcc tcc cgc caa ccc tgg cga ccc cct gcc tgc cgg	1502						
Ser Ser Pro Ala Ser Ser Arg Gln Pro Trp Arg Pro Pro Ala Cys Arg							
462		467		472		477	
agc cca ctg cct cct gga ggg gac cag ggt ccc ttc tcc agc ccc aaa	1550						
Ser Pro Leu Pro Pro Gly Gly Asp Gln Gly Pro Phe Ser Ser Pro Lys							
478		483		488		493	
gct tgg cct gag gag tgg ggg ggg gca ggc gca cag gca gag gaa cta	1598						
Ala Trp Pro Glu Glu Trp Gly Gly Ala Gly Ala Gln Ala Glu Glu Leu							
494		499		504		509	
gct ggc tat gag gct gag gat gag gct ggg atg caa ggg cca ggg ccc	1646						
Ala Gly Tyr Glu Ala Glu Asp Glu Ala Gly Met Gln Gly Pro Gly Pro							
510		515		520		525	
aga gac ggt tcc cca ctc ctc gga ggc tgc agc gac agt tca gga agt	1694						
Arg Asp Gly Ser Pro Leu Leu Gly Gly Cys Ser Asp Ser Ser Gly Ser							
526		531		536		541	
ctt cga gag gag gag ggg gag gat gaa gag ccc ctg ccc ccg ctg agg	1742						
Leu Arg Glu Glu Glu Gly Glu Asp Glu Glu Pro Leu Pro Pro Leu Arg							
542		547		552		557	

gcc cca gca ggc acg gag cct gag ccc atc gcc atg ctg gtc ctg agg	1790
Ala Pro Ala Gly Thr Glu Pro Glu Pro Ile Ala Met Leu Val Leu Arg	
558 563 568 573	
ggc tcg tcc tcg agg ggt cct gat gct ggg tgc ctg aca gaa gag ctc	1838
Gly Ser Ser Ser Arg Gly Pro Asp Ala Gly Cys Leu Thr Glu Glu Leu	
574 579 584 589	
ggg gag ccc gct gca acc gag agg cct gcc cag ccg gga gct gcc aac	1886
Gly Glu Pro Ala Ala Thr Glu Arg Pro Ala Gln Pro Gly Ala Ala Asn	
590 595 600 605	
ccc ctg gtg gtg gga gcc gtg gcc ctc ctg gac ctc agc ctg gca ttc	1934
Pro Leu Val Val Gly Ala Val Ala Leu Leu Asp Leu Ser Leu Ala Phe	
606 611 616 621	
ctg ttc tcc cag ctc ctc acc tga ggctacttcc tggcctgggt ctggctttgg	1988
Leu Phe Ser Gln Leu Leu Thr *	
622 627	
ttgcgtgcct cttcaccctt ttgacctgcc ttttttctct tctcctcttc ctggctgtgt	2048
tttctcctat ctttctttct cttcttctct tcttttctgt gctcctttgt ttttttctct	2108
cgctttttct ttccctgtct tctttcagat tatctcattt cttctggatc tgtctctgta	2168
ttcctcactc ctttcccat cccaaccct tctttctcta gattgtttac atatgaaggg	2228
cttttctctc tcagagttgc tgtcttctct gagacacaca aatctaagtc agaccattgc	2288
tccacgcct cccacctttt ctttagacct caacttcgct gcgggtgggg gtttgggtgc	2348
ctaaggagac tcctggaagc tgaatggaga ggaggaagaa aatgaagaag gagtgattga	2408
atgtcgggca aggcactggc tgagctgctg tggctcccta gcctaagggg cctgctgtcc	2468
ctctgaggcc tagtgaaaaa gctgcaggag gtgcacctc cacctctaatt cttggaggct	2528
attatcttac ctccaagcac tgagctgggt tactgcccac ttccatcctt ccctgaagga	2588
gagaagggaa gtgaaaagta gagtaactcc ccagcatttc cctctttttc tcctcatcgg	2648
ccagcccctc ctccagcccc ctctggtggc atgccatgcc aagagcaacg tgtaaaggaa	2708
cagagaatat ccaatgcagt caagtccacc ctgccagac tttgccactg acttctccca	2768
cccttctgtc tccccataa tagtttattt ggttgggtctg gactcacttg tggcctttga	2828
ttaaattcct aaggggcctg aagaagacat ttctactgca gaggggttaga ggcacttgag	2888
caaggccccc acatcccaac tctgggagtt gtgggtgggag gaggcacttc tgggggatag	2948
gaccagacaa gataacagga gctcacatgg aagcagaagc tgtgacaagt ttagtagtcc	3008
caaaatgggt tatatccctt cccctcgtg ccgaattctt ggctcagag gccaaat	3065

<210> 36
 <211> 4253
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (62)..(3421)

<400> 36

```

gaggggggcgc ccgcgcccgc atattccctc ccgccggccg gctccgcggc gcgcagccac      60

c   atg agc acc gcc gcc ttc cac atc tcc agc ctc ctg gag aag atg      106
    Met Ser Thr Ala Ala Phe His Ile Ser Ser Leu Leu Glu Lys Met
      1             5             10

acg tcc agc gac aag gac ttc agg ttc atg gcc acc agc gac ctg atg      154
Thr Ser Ser Asp Lys Asp Phe Arg Phe Met Ala Thr Ser Asp Leu Met
  16             21             26             31

tcg gag ttg cag aag gac tcc atc cag ctg gac gag gac agc gag cgc      202
Ser Glu Leu Gln Lys Asp Ser Ile Gln Leu Asp Glu Asp Ser Glu Arg
  32             37             42             47

aag gtg gtg aag atg ctg ctc cgg ctc ctg gag gac aag aac ggt gag      250
Lys Val Val Lys Met Leu Leu Arg Leu Leu Glu Asp Lys Asn Gly Glu
  48             53             58             63

gtg cag aac ctg gct gtc aag tgg ctg ggt gtc ccg ctg ggc gcc ttc      298
Val Gln Asn Leu Ala Val Lys Trp Leu Gly Val Pro Leu Gly Ala Phe
  64             69             74             79

cac gcc agc ctc ctg cac tgt ctg ctg cca cag ctg agc agc ccg cgc      346
His Ala Ser Leu Leu His Cys Leu Leu Pro Gln Leu Ser Ser Pro Arg
  80             85             90             95

ctg gcg gtg cgc aag cgg gcg gtc gga gcg ctt ggc cac ctg gcg gcc      394
Leu Ala Val Arg Lys Arg Ala Val Gly Ala Leu Gly His Leu Ala Ala
  96             101            106            111

gcc tgc agc acc gac ctc ttc gtc gag ctc gct gac cac cta ctg gac      442
Ala Cys Ser Thr Asp Leu Phe Val Glu Leu Ala Asp His Leu Leu Asp
  112            117            122            127

cgg ctg ccc ggc ccg cgg gtg ccc acc agc ccg act gcc atc cgc acc      490
Arg Leu Pro Gly Pro Arg Val Pro Thr Ser Pro Thr Ala Ile Arg Thr
  128            133            138            143

ctg atc caa tgt ttg ggc agc gtc ggc cgc cag gcc ggc cac cgc ctc      538
Leu Ile Gln Cys Leu Gly Ser Val Gly Arg Gln Ala Gly His Arg Leu
  144            149            154            159

ggg gct cac ctg gac cgc ctg gtg ccc ctg gtg gag gat ttc tgc aac      586
Gly Ala His Leu Asp Arg Leu Val Pro Leu Val Glu Asp Phe Cys Asn

```

160	165	170	175	
ctg gat gat gat gag	ctc cgg gag tcc tgc	ctc cag gct ttt gag gcc		634
Leu Asp Asp Asp Glu	Leu Arg Glu Ser Cys	Leu Gln Ala Phe Glu Ala		
176	181	186	191	
ttc ttg agg aag tgc	ccc aag gaa atg ggt	cct cac gtg ccc aac gtg		682
Phe Leu Arg Lys Cys	Pro Lys Glu Met Gly	Pro His Val Pro Asn Val		
192	197	202	207	
acc agc ctc tgc ctc	caa tac ata aaa cac	gac ccc aac tac aac tac		730
Thr Ser Leu Cys Leu	Gln Tyr Ile Lys His	Asp Pro Asn Tyr Asn Tyr		
208	213	218	223	
gac agt gat gag gat	gag gag cag atg gag	aca gag gat agt gaa ttc		778
Asp Ser Asp Glu Asp	Glu Glu Gln Met Glu	Thr Glu Asp Ser Glu Phe		
224	229	234	239	
agt gag caa gag agt	gaa gac gag tac agc	gat gac gat gac atg agc		826
Ser Glu Gln Glu Ser	Glu Asp Glu Tyr Ser	Asp Asp Asp Asp Met Ser		
240	245	250	255	
tgg aag gtg cgc cgg	gca gct gcc aag tgc	atc gca gcc ttg atc agc		874
Trp Lys Val Arg Arg	Ala Ala Ala Lys Cys	Ile Ala Ala Leu Ile Ser		
256	261	266	271	
tcg cgg cct gac ctg	ctg ccc gat ttc cac	tgc acc ctg gca cct gtg		922
Ser Arg Pro Asp Leu	Leu Pro Asp Phe His	Cys Thr Leu Ala Pro Val		
272	277	282	287	
ctc atc cgc cgc ttc	aaa gaa cgc gag gag	aac gtc aag gct gac gtc		970
Leu Ile Arg Arg Phe	Lys Glu Arg Glu Glu	Asn Val Lys Ala Asp Val		
288	293	298	303	
ttc act gct tac atc	gtg ctg ctg cgg caa	aca cgg ccc ccg aag gga		1018
Phe Thr Ala Tyr Ile	Val Leu Leu Arg Gln	Thr Arg Pro Pro Lys Gly		
304	309	314	319	
tgg ctg gag gcc atg	gag gaa ccc acc cag	acc ggc agc aac ctc cat		1066
Trp Leu Glu Ala Met	Glu Glu Pro Thr Gln	Thr Gly Ser Asn Leu His		
320	325	330	335	
atg cta cgt gga cag	gtg ccc ctt gtg gtc	aag gcc ctg cag cgg cag		1114
Met Leu Arg Gly Gln	Val Pro Leu Val Val	Lys Ala Leu Gln Arg Gln		
336	341	346	351	
ctt aaa gat cgg agc	gtc aga gcc cgc cag	gga tgc ttc agc ctc ctc		1162
Leu Lys Asp Arg Ser	Val Arg Ala Arg Gln	Gly Cys Phe Ser Leu Leu		
352	357	362	367	
acc gag ctg gcg ggt	gtc ctc cca ggc agc	ctg gcc gag cat atg cct		1210
Thr Glu Leu Ala Gly	Val Leu Pro Gly Ser	Leu Ala Glu His Met Pro		
368	373	378	383	
gtg ctg gta tca ggc	atc atc ttc tcg ctg	gcc gac cgc tcc agc tcc		1258
Val Leu Val Ser Gly	Ile Ile Phe Ser Leu	Ala Asp Arg Ser Ser Ser		
384	389	394	399	

tcc acc atc cgg atg gat gcc ctg gcc ttc ttg cag ggg ctg ctg ggc	1306
Ser Thr Ile Arg Met Asp Ala Leu Ala Phe Leu Gln Gly Leu Leu Gly	
400 405 410 415	
acc gaa cca gct gag gcc ttc cac cca cac ttg cct atc ctc ctg cca	1354
Thr Glu Pro Ala Glu Ala Phe His Pro His Leu Pro Ile Leu Leu Pro	
416 421 426 431	
cct gtg atg gcc tgt gtg gct gac tct ttc tac aag att gca gcc gag	1402
Pro Val Met Ala Cys Val Ala Asp Ser Phe Tyr Lys Ile Ala Ala Glu	
432 437 442 447	
gcc ctg gtg gtg ctg cag gag ctg gtg cgg gcc ctg tgg ccg ctg cac	1450
Ala Leu Val Val Leu Gln Glu Leu Val Arg Ala Leu Trp Pro Leu His	
448 453 458 463	
agg cct cgg atg ctg gat cct gag cca tat gtt gga gag atg tct gct	1498
Arg Pro Arg Met Leu Asp Pro Glu Pro Tyr Val Gly Glu Met Ser Ala	
464 469 474 479	
gtc acc ctg gcg cga ctt cgt gcc act gac ctg gac cag gag gtg aag	1546
Val Thr Leu Ala Arg Leu Arg Ala Thr Asp Leu Asp Gln Glu Val Lys	
480 485 490 495	
gag cgg gcc att tcc tgc atg ggc cac ctt gta ggc cac ctg ggt gac	1594
Glu Arg Ala Ile Ser Cys Met Gly His Leu Val Gly His Leu Gly Asp	
496 501 506 511	
cgg ctt ggg gat gac ctg gag ccc acg tta ctg ctc ctc ctg gac cgc	1642
Arg Leu Gly Asp Asp Leu Glu Pro Thr Leu Leu Leu Leu Asp Arg	
512 517 522 527	
ctg cgg aat gag atc acc cgg ctg ccc gcc atc aag gcg ctt acg ctg	1690
Leu Arg Asn Glu Ile Thr Arg Leu Pro Ala Ile Lys Ala Leu Thr Leu	
528 533 538 543	
gtg gcc gta tcc cca cta cag ctt gac cta cag ccc atc ctg gcc gag	1738
Val Ala Val Ser Pro Leu Gln Leu Asp Leu Gln Pro Ile Leu Ala Glu	
544 549 554 559	
gca ctg cac att ctg gcc tca ttc ctg cgg aag aac cag cgg gct ttg	1786
Ala Leu His Ile Leu Ala Ser Phe Leu Arg Lys Asn Gln Arg Ala Leu	
560 565 570 575	
cga ctg gcc aca ctg gca gcc ctg gac gcc ctg gcc cag agc cag ggc	1834
Arg Leu Ala Thr Leu Ala Ala Leu Asp Ala Leu Ala Gln Ser Gln Gly	
576 581 586 591	
ctc agc ctc cca ccg tct gcc gtg cag gcc gtg ctg gct gag ctg cct	1882
Leu Ser Leu Pro Pro Ser Ala Val Gln Ala Val Leu Ala Glu Leu Pro	
592 597 602 607	
gcc ctg gtc aac gag agc gac atg cat gtg gcc cag ctg gct gtg gac	1930
Ala Leu Val Asn Glu Ser Asp Met His Val Ala Gln Leu Ala Val Asp	
608 613 618 623	

ttc ctt gcc aca gtg acc cag gcc cag cca gcc tct ttg gtg gag gtc Phe Leu Ala Thr Val Thr Gln Ala Gln Pro Ala Ser Leu Val Glu Val 624 629 634 639	1978
agt ggc cct gtg ctc tca gag ctg ctg cgg ctg ctg cgt tcg ccc ctg Ser Gly Pro Val Leu Ser Glu Leu Leu Arg Leu Leu Arg Ser Pro Leu 640 645 650 655	2026
ttg cca gcc gga gtt ctg gca gct gct gaa ggc ttc ctg cag gcc ctg Leu Pro Ala Gly Val Leu Ala Ala Ala Glu Gly Phe Leu Gln Ala Leu 656 661 666 671	2074
gta ggg acc cgt ccc ccg tgt gtg gac tat gcc aaa ctc atc agc ctg Val Gly Thr Arg Pro Pro Cys Val Asp Tyr Ala Lys Leu Ile Ser Leu 672 677 682 687	2122
ctc act gcg cct gtt tat gag cag gct gtg gat ggt ggg cct ggc ctg Leu Thr Ala Pro Val Tyr Glu Gln Ala Val Asp Gly Gly Pro Gly Leu 688 693 698 703	2170
cac aag cag gtg ttc cac tca ttg gcc cgg tgt gtg gca gcc ctc tca His Lys Gln Val Phe His Ser Leu Ala Arg Cys Val Ala Ala Leu Ser 704 709 714 719	2218
gct gcc tgt ccc caa gag gcg gca agc aca gcc agt cgc ctg gtc tgc Ala Ala Cys Pro Gln Glu Ala Ala Ser Thr Ala Ser Arg Leu Val Cys 720 725 730 735	2266
gat gcc agg tcg ccc cac tcc agc acg ggg gtc aag gtc ctg gca ttc Asp Ala Arg Ser Pro His Ser Ser Thr Gly Val Lys Val Leu Ala Phe 736 741 746 751	2314
ttg tcg ctg gct gag gtg ggt cag gtg gct ggg cca ggc ccc cag cgg Leu Ser Leu Ala Glu Val Gly Gln Val Ala Gly Pro Gly Pro Gln Arg 752 757 762 767	2362
gag ctg aag gcg gtg ctc ctg gaa gct ttg ggg tca ccc agt gag gat Glu Leu Lys Ala Val Leu Leu Glu Ala Leu Gly Ser Pro Ser Glu Asp 768 773 778 783	2410
gtg agg gct gca gcc tcg tat gca ctg ggc cgt gtg ggt gct ggc agc Val Arg Ala Ala Ala Ser Tyr Ala Leu Gly Arg Val Gly Ala Gly Ser 784 789 794 799	2458
ctg ccc gac ttc ctg ccc ttc ctg ctg gag cag atc gag gct gag ccc Leu Pro Asp Phe Leu Pro Phe Leu Leu Glu Gln Ile Glu Ala Glu Pro 800 805 810 815	2506
cga cga cag tac ctg ctg ctg cac tca ctc agg gag gcc ctg ggg gcc Arg Arg Gln Tyr Leu Leu Leu His Ser Leu Arg Glu Ala Leu Gly Ala 816 821 826 831	2554
gcc cag cct gac agc ctg aag ccc tac gcc gag gac atc tgg gcc ttg Ala Gln Pro Asp Ser Leu Lys Pro Tyr Ala Glu Asp Ile Trp Ala Leu 832 837 842 847	2602
ctg ttc cag cgc tgc gag ggt gct gag gag ggc acc cgg ggg gtg gtg	2650

Leu Phe Gln Arg Cys Glu Gly Ala Glu Glu Gly Thr Arg Gly Val Val	
848 853 858 863	
gcc gag tgc att ggg aag ctg gtc ctt gtg aac cct tcg ttc ctt ctg	2698
Ala Glu Cys Ile Gly Lys Leu Val Leu Val Asn Pro Ser Phe Leu Leu	
864 869 874 879	
ccc cgc ttg cgg aag cag ctt gct gca ggt cgg cca cac acc cgg agc	2746
Pro Arg Leu Arg Lys Gln Leu Ala Ala Gly Arg Pro His Thr Arg Ser	
880 885 890 895	
acc gtc atc aca gcg gtc aag ttc ctt atc tcg gac cag ccc cat ccc	2794
Thr Val Ile Thr Ala Val Lys Phe Leu Ile Ser Asp Gln Pro His Pro	
896 901 906 911	
att gac ccc ctc ctg aag agc ttc atc gct gtg cac aac aag ccc tcg	2842
Ile Asp Pro Leu Leu Lys Ser Phe Ile Ala Val His Asn Lys Pro Ser	
912 917 922 927	
cta gtc cgg gac ctg ctg gat gac atc ctg ccc ctc ctc tac cag gag	2890
Leu Val Arg Asp Leu Leu Asp Asp Ile Leu Pro Leu Leu Tyr Gln Glu	
928 933 938 943	
aca aag atc cgg cgg gac ctc atc cga gag gtg gag atg ggg ccc ttt	2938
Thr Lys Ile Arg Arg Asp Leu Ile Arg Glu Val Glu Met Gly Pro Phe	
944 949 954 959	
aaa cat aca gtg gac gat ggg ctg gac gtg cgg aag gcg gcc ttt gaa	2986
Lys His Thr Val Asp Asp Gly Leu Asp Val Arg Lys Ala Ala Phe Glu	
960 965 970 975	
tgc atg tat tca ctg ctt gag agc tgc ctg ggc cag ctg gat atc tgt	3034
Cys Met Tyr Ser Leu Leu Glu Ser Cys Leu Gly Gln Leu Asp Ile Cys	
976 981 986 991	
gag ttc ctg aac cat gtg gag gac ggg ctg aag gac cac tac gac atc	3082
Glu Phe Leu Asn His Val Glu Asp Gly Leu Lys Asp His Tyr Asp Ile	
992 997 1002 1007	
cgg atg ctg acc ttc atc atg gtt gcc cgg ctg gcc acc ctg tgt cct	3130
Arg Met Leu Thr Phe Ile Met Val Ala Arg Leu Ala Thr Leu Cys Pro	
1008 1013 1018 1023	
gca cct gtc ctg cag agg gtg gac cga ctc att gag cca cta agg gcc	3178
Ala Pro Val Leu Gln Arg Val Asp Arg Leu Ile Glu Pro Leu Arg Ala	
1024 1029 1034 1039	
acc tgc act gcc aag gtc aaa gct ggt tct gtg aag cag gag ttt gaa	3226
Thr Cys Thr Ala Lys Val Lys Ala Gly Ser Val Lys Gln Glu Phe Glu	
1040 1045 1050 1055	
aag caa gat gaa ctg aag cgc tct gca atg agg gca gtg gct gcc ctg	3274
Lys Gln Asp Glu Leu Lys Arg Ser Ala Met Arg Ala Val Ala Ala Leu	
1056 1061 1066 1071	
ctg acc atc ccc gag gtg ggg aaa agc ccc atc atg gcc gac ttc tct	3322
Leu Thr Ile Pro Glu Val Gly Lys Ser Pro Ile Met Ala Asp Phe Ser	

1072	1077	1082	1087	
tcc caa atc aga tcc aac cct gaa ctt gct gcc ctc ttt gaa agc atc				3370
Ser Gln Ile Arg Ser Asn Pro Glu Leu Ala Ala Leu Phe Glu Ser Ile				
1088	1093	1098	1103	
cag aag gat tcc act tca gcc ccc agc aca gac tca atg gag ctc agc				3418
Gln Lys Asp Ser Thr Ser Ala Pro Ser Thr Asp Ser Met Glu Leu Ser				
1104	1109	1114	1119	
tag tccc ctcagcacca aggtgggccc tcgcttaaga gaaaggagcc cacccaagtc				3475
*				
1120				
cgaggcctcc ccatcccacc atcgcaggtc tctacttttg cccttccacc atctcactgg				3535
gggccctgtc gtccttggtc agggcttaca gtgcctttctc cagggaccca actcaaaggc				3595
ccccagccca agctgtgagg ctgccaacag ttggggccct tccttaactc aggacagtca				3655
tccaaagaaa tagggtgagg aagttttcca gtgacttcac actgtacccc tccatagtct				3715
gtctggttcc ttcagagggg gtctctgcct cacaaactag tagtatttag aaataggctg				3775
tgctgtcagc tgtaaaagat caggaggcag cagacaccac tctgctttct tcaactgcatt				3835
cagcaatgcc tgaagttagt gctcaggccg ggcatctcaa aagaaaagat acttgagtta				3895
ttcacatttt aaaattcaaa acggttcatt tttaagtggc agtgatgaat cagaaatttg				3955
gaagatgata cgggtttctt ttttccaggg aggaggaatg ggttgggtag ggaactggac				4015
aggcttggac ctcatgtttc atttctaatt tcaaaatact tattagcaaa ttgggcaaca				4075
atgggcatct tccatgccac caccagggca taaccagttg gtttggttcc ttctgaggaa				4135
ggtttcaaat gtgtctagtg ttcagtattg aggacaaaga aatacaagtg gcaggcccaa				4195
gtattttctg tgatatccca ggttaataaa gattagattc taagttaaaa aaaaaaaaa				4253

<210> 37
 <211> 4325
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (62) .. (3493)

<400> 37	
gaggggggcgc ccgcgcgcgc atattccctc ccgcgcgcgc gctccgcgc gcgcagccac	60
c atg agc acc gcc gcc ttc cac atc tcc agc ctc ctg gag aag atg	106
Met Ser Thr Ala Ala Phe His Ile Ser Ser Leu Leu Glu Lys Met	

1	5	10	
acg tcc agc gac aag gac ttc agg ttc atg gcc acc agc gac ctg atg Thr Ser Ser Asp Lys Asp Phe Arg Phe Met Ala Thr Ser Asp Leu Met 16 21 26 31			154
tcg gag ttg cag aag gac tcc atc cag ctg gac gag gac agc gag cgc Ser Glu Leu Gln Lys Asp Ser Ile Gln Leu Asp Glu Asp Ser Glu Arg 32 37 42 47			202
aag gtg gtg aag atg ctg ctc cgg ctc ctg gag gac aag aac ggt gag Lys Val Val Lys Met Leu Leu Arg Leu Leu Glu Asp Lys Asn Gly Glu 48 53 58 63			250
gtg cag aac ctg gct gtc aag tgg ctg ggt gtc ccg ctg ggc gcc ttc Val Gln Asn Leu Ala Val Lys Trp Leu Gly Val Pro Leu Gly Ala Phe 64 69 74 79			298
cac gcc agc ctc ctg cac tgt ctg ctg cca cag ctg agc agc ccg cgc His Ala Ser Leu Leu His Cys Leu Leu Pro Gln Leu Ser Ser Pro Arg 80 85 90 95			346
ctg gcg gtg cgc aag cgg gcg gtc gga gcg ctt ggc cac ctg gcg gcc Leu Ala Val Arg Lys Arg Ala Val Gly Ala Leu Gly His Leu Ala Ala 96 101 106 111			394
gcc tgc agc acc gac ctc ttc gtc gag ctc gct gac cac cta ctg gac Ala Cys Ser Thr Asp Leu Phe Val Glu Leu Ala Asp His Leu Leu Asp 112 117 122 127			442
cgg ctg ccc ggc ccg cgg gtg ccc acc agc ccg act gcc atc cgc acc Arg Leu Pro Gly Pro Arg Val Pro Thr Ser Pro Thr Ala Ile Arg Thr 128 133 138 143			490
ctg atc caa tgt ttg ggc agc gtc ggc cgc cag gcc ggc cac cgc ctc Leu Ile Gln Cys Leu Gly Ser Val Gly Arg Gln Ala Gly His Arg Leu 144 149 154 159			538
ggg gct cac ctg gac cgc ctg gtg ccc ctg gtg gag gat ttc tgc aac Gly Ala His Leu Asp Arg Leu Val Pro Leu Val Glu Asp Phe Cys Asn 160 165 170 175			586
ctg gat gat gat gag ctc cgg gag tcc tgc ctc cag gct ttt gag gcc Leu Asp Asp Asp Glu Leu Arg Glu Ser Cys Leu Gln Ala Phe Glu Ala 176 181 186 191			634
ttc ttg agg aag tgc ccc aag gaa atg ggt cct cac gtg ccc aac gtg Phe Leu Arg Lys Cys Pro Lys Glu Met Gly Pro His Val Pro Asn Val 192 197 202 207			682
acc agc ctc tgc ctc caa tac ata aaa cac gac ccc aac tac aac tac Thr Ser Leu Cys Leu Gln Tyr Ile Lys His Asp Pro Asn Tyr Asn Tyr 208 213 218 223			730
gac agt gat gag gat gag gag cag atg gag aca gag gat agt gaa ttc Asp Ser Asp Glu Asp Glu Glu Gln Met Glu Thr Glu Asp Ser Glu Phe 224 229 234 239			778

agt gag caa gag agt gaa gac gag tac agc gat gac gat gac atg agc	826
Ser Glu Gln Glu Ser Glu Asp Glu Tyr Ser Asp Asp Asp Asp Met Ser	
240 245 250 255	
tgg aag gtg cgc cgg gca gct gcc aag tgc atc gca gcc ttg atc agc	874
Trp Lys Val Arg Arg Ala Ala Ala Lys Cys Ile Ala Ala Leu Ile Ser	
256 261 266 271	
tcg cgg cct gac ctg ctg ccc gat ttc cac tgc acc ctg gca cct gtg	922
Ser Arg Pro Asp Leu Leu Pro Asp Phe His Cys Thr Leu Ala Pro Val	
272 277 282 287	
ctc atc cgc cgc ttc aaa gaa cgc gag gag aac gtc aag gct gac gtc	970
Leu Ile Arg Arg Phe Lys Glu Arg Glu Glu Asn Val Lys Ala Asp Val	
288 293 298 303	
ttc act gct tac atc gtg ctg ctg cgg caa aca cgg ccc ccg aag gga	1018
Phe Thr Ala Tyr Ile Val Leu Leu Arg Gln Thr Arg Pro Pro Lys Gly	
304 309 314 319	
tgg ctg gag gcc atg gag gaa ccc acc cag acc ggc agc aac ctc cat	1066
Trp Leu Glu Ala Met Glu Glu Pro Thr Gln Thr Gly Ser Asn Leu His	
320 325 330 335	
atg cta cgt gga cag gtg ccc ctt gtg gtc aag gcc ctg cag cgg cag	1114
Met Leu Arg Gly Gln Val Pro Leu Val Val Lys Ala Leu Gln Arg Gln	
336 341 346 351	
ctt aaa gat cgg agc gtc aga gcc cgc cag gga tgc ttc agc ctc ctc	1162
Leu Lys Asp Arg Ser Val Arg Ala Arg Gln Gly Cys Phe Ser Leu Leu	
352 357 362 367	
acc gag ctg gcg ggt gtc ctc cca ggc agc ctg gcc gag cat atg cct	1210
Thr Glu Leu Ala Gly Val Leu Pro Gly Ser Leu Ala Glu His Met Pro	
368 373 378 383	
gtg ctg gta tca ggc atc atc ttc tcg ctg gcc gac cgc tcc agc tcc	1258
Val Leu Val Ser Gly Ile Ile Phe Ser Leu Ala Asp Arg Ser Ser Ser	
384 389 394 399	
tcc acc atc cgg atg gat gcc ctg gcc ttc ttg cag ggg ctg ctg ggc	1306
Ser Thr Ile Arg Met Asp Ala Leu Ala Phe Leu Gln Gly Leu Leu Gly	
400 405 410 415	
acc gaa cca gct gag gcc ttc cac cca cac ttg cct atc ctc ctg cca	1354
Thr Glu Pro Ala Glu Ala Phe His Pro His Leu Pro Ile Leu Leu Pro	
416 421 426 431	
cct gtg atg gcc tgt gtg gct gac tct ttc tac aag att gca gcc gag	1402
Pro Val Met Ala Cys Val Ala Asp Ser Phe Tyr Lys Ile Ala Ala Glu	
432 437 442 447	
gcc ctg gtg gtg ctg cag gag ctg gtg cgg gcc ctg tgg ccg ctg cac	1450
Ala Leu Val Val Leu Gln Glu Leu Val Arg Ala Leu Trp Pro Leu His	
448 453 458 463	

agg cct cgg atg ctg gat cct gag cca tat gtt gga gag atg tct gct	1498
Arg Pro Arg Met Leu Asp Pro Glu Pro Tyr Val Gly Glu Met Ser Ala	
464 469 474 479	
gtc acc ctg gcg cga ctt cgt gcc act gac ctg gac cag gag gtg aag	1546
Val Thr Leu Ala Arg Leu Arg Ala Thr Asp Leu Asp Gln Glu Val Lys	
480 485 490 495	
gag cgg gcc att tcc tgc atg ggc cac ctt gta ggc cac ctg ggt gac	1594
Glu Arg Ala Ile Ser Cys Met Gly His Leu Val Gly His Leu Gly Asp	
496 501 506 511	
cgg ctt ggg gat gac ctg gag ccc acg tta ctg ctc ctc ctg gac cgc	1642
Arg Leu Gly Asp Asp Leu Glu Pro Thr Leu Leu Leu Leu Asp Arg	
512 517 522 527	
ctg cgg aat gag atc acc cgg ctg ccc gcc atc aag gcg ctt acg ctg	1690
Leu Arg Asn Glu Ile Thr Arg Leu Pro Ala Ile Lys Ala Leu Thr Leu	
528 533 538 543	
gtg gcc gta tcc cca cta cag ctt gac cta cag ccc atc ctg gcc gag	1738
Val Ala Val Ser Pro Leu Gln Leu Asp Leu Gln Pro Ile Leu Ala Glu	
544 549 554 559	
gca ctg cac att ctg gcc tca ttc ctg cgg aag aac cag cgg gct ttg	1786
Ala Leu His Ile Leu Ala Ser Phe Leu Arg Lys Asn Gln Arg Ala Leu	
560 565 570 575	
cga ctg gcc aca ctg gca gcc ctg gac gcc ctg gcc cag agc cag gcc	1834
Arg Leu Ala Thr Leu Ala Ala Leu Asp Ala Leu Ala Gln Ser Gln Gly	
576 581 586 591	
ctc agc ctc cca ccg tct gcc gtg cag gcc gtg ctg gct gag ctg cct	1882
Leu Ser Leu Pro Pro Ser Ala Val Gln Ala Val Leu Ala Glu Leu Pro	
592 597 602 607	
gcc ctg gtc aac gag agc gac atg cat gtg gcc cag ctg gct gtg gac	1930
Ala Leu Val Asn Glu Ser Asp Met His Val Ala Gln Leu Ala Val Asp	
608 613 618 623	
ttc ctt gcc aca gtg acc cag gcc cag cca gcc tct ttg gtg gag gtc	1978
Phe Leu Ala Thr Val Thr Gln Ala Gln Pro Ala Ser Leu Val Glu Val	
624 629 634 639	
agt ggc cct gtg ctc tca gag ctg ctg cgg ctg ctg cgt tcg ccc ctg	2026
Ser Gly Pro Val Leu Ser Glu Leu Leu Arg Leu Leu Arg Ser Pro Leu	
640 645 650 655	
ttg cca gcc gga gtt ctg gca gct gct gaa ggc ttc ctg cag gcc ctg	2074
Leu Pro Ala Gly Val Leu Ala Ala Ala Glu Gly Phe Leu Gln Ala Leu	
656 661 666 671	
gta ggg acc cgt ccc ccg tgt gtg gac tat gcc aaa ctc atc agc ctg	2122
Val Gly Thr Arg Pro Pro Cys Val Asp Tyr Ala Lys Leu Ile Ser Leu	
672 677 682 687	
ctc act gcg cct gtt tat gag cag gct gtg gat ggt ggg cct ggc ctg	2170

Leu Thr Ala Pro Val Tyr Glu Gln Ala Val Asp Gly Gly Pro Gly Leu 688 693 698 703	
cac aag cag gtg ttc cac tca ttg gcc cgg tgt gtg gca gcc ctc tca His Lys Gln Val Phe His Ser Leu Ala Arg Cys Val Ala Ala Leu Ser 704 709 714 719	2218
gct gcc tgt ccc caa gag gcg gca agc aca gcc agt cgc ctg gtc tgc Ala Ala Cys Pro Gln Glu Ala Ala Ser Thr Ala Ser Arg Leu Val Cys 720 725 730 735	2266
gat gcc agg tcg ccc cac tcc agc acg ggg gtc aag gtc ctg gca ttc Asp Ala Arg Ser Pro His Ser Ser Thr Gly Val Lys Val Leu Ala Phe 736 741 746 751	2314
ttg tcg ctg gct gag gtg ggt cag gtg gct ggg cca ggc ccc cag cgg Leu Ser Leu Ala Glu Val Gly Gln Val Ala Gly Pro Gly Pro Gln Arg 752 757 762 767	2362
gag ctg aag gcg gtg ctc ctg gaa gct ttg ggg tca ccc agt gag gat Glu Leu Lys Ala Val Leu Leu Glu Ala Leu Gly Ser Pro Ser Glu Asp 768 773 778 783	2410
gtg agg gct gca gcc tcg tat gca ctg ggc cgt gtg ggt gct ggc agc Val Arg Ala Ala Ala Ser Tyr Ala Leu Gly Arg Val Gly Ala Gly Ser 784 789 794 799	2458
ctg ccc gac ttc ctg ccc ttc ctg ctg gag cag atc gag gct gag ccc Leu Pro Asp Phe Leu Pro Phe Leu Leu Glu Gln Ile Glu Ala Glu Pro 800 805 810 815	2506
cga cga cag tac ctg ctg ctg cac tca ctc agg gag gcc ctg ggg gcc Arg Arg Gln Tyr Leu Leu Leu His Ser Leu Arg Glu Ala Leu Gly Ala 816 821 826 831	2554
gcc cag cct gac agc ctg aag ccc tac gcc gag gac atc tgg gcc ttg Ala Gln Pro Asp Ser Leu Lys Pro Tyr Ala Glu Asp Ile Trp Ala Leu 832 837 842 847	2602
ctg ttc cag cgc tgc gag ggt gct gag gag ggc acc cgg ggg gtg gtg Leu Phe Gln Arg Cys Glu Gly Ala Glu Glu Gly Thr Arg Gly Val Val 848 853 858 863	2650
gcc gag tgc att ggg aag ctg gtc ctt gtg aac cct tcg ttc ctt ctg Ala Glu Cys Ile Gly Lys Leu Val Leu Val Asn Pro Ser Phe Leu Leu 864 869 874 879	2698
ccc cgc ttg cgg aag cag ctt gct gca ggt cgg cca cac acc cgg agc Pro Arg Leu Arg Lys Gln Leu Ala Ala Gly Arg Pro His Thr Arg Ser 880 885 890 895	2746
acc gtc atc aca gcg gtc aag ttc ctt atc tcg gac cag ccc cat ccc Thr Val Ile Thr Ala Val Lys Phe Leu Ile Ser Asp Gln Pro His Pro 896 901 906 911	2794
att gac ccc ctc ctg aag agc ttc atc gga gag ttc atg gag agc ctg Ile Asp Pro Leu Leu Lys Ser Phe Ile Gly Glu Phe Met Glu Ser Leu	2842

912	917	922	927	
cag gac cca gac ctg aac gtg cgc cgt gcg act ctg gct ttc ttc aac				2890
Gln Asp Pro Asp Leu Asn Val Arg Arg Ala Thr Leu Ala Phe Phe Asn				
928	933	938	943	
tca gct gtg cac aac aag ccc tcg cta gtc cgg gac ctg ctg gat gac				2938
Ser Ala Val His Asn Lys Pro Ser Leu Val Arg Asp Leu Leu Asp Asp				
944	949	954	959	
atc ctg ccc ctc ctc tac cag gag aca aag atc cgg cgg gac ctc atc				2986
Ile Leu Pro Leu Leu Tyr Gln Glu Thr Lys Ile Arg Arg Asp Leu Ile				
960	965	970	975	
cga gag gtg gag atg ggg ccc ttt aaa cat aca gtg gac gat ggg ctg				3034
Arg Glu Val Glu Met Gly Pro Phe Lys His Thr Val Asp Asp Gly Leu				
976	981	986	991	
gac gtg cgg aag gcg gcc ttt gaa tgc atg tat tca ctg ctt gag agc				3082
Asp Val Arg Lys Ala Ala Phe Glu Cys Met Tyr Ser Leu Leu Glu Ser				
992	997	1002	1007	
tgc ctg ggc cag ctg gat atc tgt gag ttc ctg aac cat gtg gag gac				3130
Cys Leu Gly Gln Leu Asp Ile Cys Glu Phe Leu Asn His Val Glu Asp				
1008	1013	1018	1023	
ggg ctg aag gac cac tac gac atc cgg atg ctg acc ttc atc atg gtt				3178
Gly Leu Lys Asp His Tyr Asp Ile Arg Met Leu Thr Phe Ile Met Val				
1024	1029	1034	1039	
gcc cgg ctg gcc acc ctg tgt cct gca cct gtc ctg cag agg gtg gac				3226
Ala Arg Leu Ala Thr Leu Cys Pro Ala Pro Val Leu Gln Arg Val Asp				
1040	1045	1050	1055	
cga ctc att gag cca cta agg gcc acc tgc act gcc aag gtc aaa gct				3274
Arg Leu Ile Glu Pro Leu Arg Ala Thr Cys Thr Ala Lys Val Lys Ala				
1056	1061	1066	1071	
ggt tct gtg aag cag gag ttt gaa aag caa gat gaa ctg aag cgc tct				3322
Gly Ser Val Lys Gln Glu Phe Glu Lys Gln Asp Glu Leu Lys Arg Ser				
1072	1077	1082	1087	
gca atg agg gca gtg gct gcc ctg ctg acc atc ccc gag gtg ggg aaa				3370
Ala Met Arg Ala Val Ala Ala Leu Leu Thr Ile Pro Glu Val Gly Lys				
1088	1093	1098	1103	
agc ccc atc atg gcc gac ttc tct tcc caa atc aga tcc aac cct gaa				3418
Ser Pro Ile Met Ala Asp Phe Ser Ser Gln Ile Arg Ser Asn Pro Glu				
1104	1109	1114	1119	
ctt gct gcc ctc ttt gaa agc atc cag aag gat tcc act tca gcc ccc				3466
Leu Ala Ala Leu Phe Glu Ser Ile Gln Lys Asp Ser Thr Ser Ala Pro				
1120	1125	1130	1135	
agc aca gac tca atg gag ctc agc tag tcccc tcagcaccaa ggtgggacct				3518
Ser Thr Asp Ser Met Glu Leu Ser *				
1136	1141			

cgcttaagag aaaggagccc acccaagtcc gaggcctccc catcccacca tcgcaggtct 3578
ctacttttgc ccttccacca tctcactggg ggccctgtcg ctcttggtca gggcttacag 3638
tgcctttctc agggacccaa ctcaaaggcc cccagcccaa gctgtgaggc tgccaacagt 3698
tggggcccctt ccttaactca ggacagtcac ccaaagaaat agggtgagga agttttccag 3758
tgacttcaca ctgtaccctt ccatagtctg tctggttcct tcagaggggtg tctctgcctc 3818
acaaactagt agtatttaga aataggctgt gctgtcagct gtaaaagatc aggaggcagc 3878
agacaccact ctgctttctt cactgcattc agcaatgcct gaagttagtg ctcaggccgg 3938
gcatctcaaa agaaaagata cttgagttat tcacatttta aaattcaaaa cggttcattt 3998
ttaagtggca gtgatgaatc agaaatttgg aagatgatac gggtttcttt tttccagga 4058
ggaggaatgg gttgggtagg gaactggaca ggcttggacc tcatgtttca tttctaattt 4118
caaaatactt attagcaaat tgggcaacaa tgggcatctt ccatgccacc acccaggcat 4178
aaccagttgg tttgtttcct tctgaggaag gtttcaaagtg tgtctagtgt tcagtattga 4238
ggacaaagaa atacaagtgg caggcccaag tattttctgt gatatcccag gtaataaag 4298
attagattct aagttaaaaa aaaaaaa 4325

<210> 38
<211> 1409
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> (190)..(1368)

<400> 38
attgaaatcg atagcgtgta ggaccggccc ggaattcccg gttccacggg aggcaggagg 60
ggaagtccca acggtgctag aatggtgctg cagttgcaga agacggctca caagtgaagt 120
ctggaagagc aacaggggaag acatccatca tttgctccaa agtgtgcaag tcaaatactg 180
gggagaatc atg ata acc ctg atc act gag cag cta cag aag cag act 228
Met Ile Thr Leu Ile Thr Glu Gln Leu Gln Lys Gln Thr
1 5 10
ctg gat gag ctg aaa tgc aca cgc ttc agc atc agt ctg cct ttg cct 276
Leu Asp Glu Leu Lys Cys Thr Arg Phe Ser Ile Ser Leu Pro Leu Pro
14 19 24 29
gat cat gca gac atc tcc aac tgt ggg aac tct ttc cag ctt gtg tct 324

Asp	His	Ala	Asp	Ile	Ser	Asn	Cys	Gly	Asn	Ser	Phe	Gln	Leu	Val	Ser		
30					35					40					45		
372																	
gaa	ggg	gct	tcc	tgg	agg	ggc	ctg	ccc	cac	tgt	tcc	tgt	gct	gag	ttc		
Glu	Gly	Ala	Ser	Trp	Arg	Gly	Leu	Pro	His	Cys	Ser	Cys	Ala	Glu	Phe		
46					51					56					61		
420																	
cag	gac	agc	ctc	aac	ttc	agc	tac	cat	ccc	tca	ggc	ctg	agc	ctg	cac		
Gln	Asp	Ser	Leu	Asn	Phe	Ser	Tyr	His	Pro	Ser	Gly	Leu	Ser	Leu	His		
62					67					72					77		
468																	
ctc	aga	cca	ccc	agt	cgg	gga	aac	tcc	ccc	aag	gag	cag	ccc	ttc	ttc		
Leu	Arg	Pro	Pro	Ser	Arg	Gly	Asn	Ser	Pro	Lys	Glu	Gln	Pro	Phe	Ser		
78					83					88					93		
516																	
caa	gtc	cta	aga	cct	gag	ccc	cca	gat	cca	gag	aag	ctt	cct	gtg	ccc		
Gln	Val	Leu	Arg	Pro	Glu	Pro	Pro	Asp	Pro	Glu	Lys	Leu	Pro	Val	Pro		
94					99					104					109		
564																	
cct	gcc	cct	cca	tcc	aag	agg	cac	tgc	cgc	tca	ctc	tca	gtg	ccc	gtg		
Pro	Ala	Pro	Pro	Ser	Lys	Arg	His	Cys	Arg	Ser	Leu	Ser	Val	Pro	Val		
110					115					120					125		
612																	
gac	ctg	tct	cgc	tgg	cag	ccg	gtg	tgg	cgg	ccc	gcc	ccc	tcc	aag	ctg		
Asp	Leu	Ser	Arg	Trp	Gln	Pro	Val	Trp	Arg	Pro	Ala	Pro	Ser	Lys	Leu		
126					131					136					141		
660																	
tgg	act	ccc	ata	aag	cac	cgg	ggc	agt	ggg	gga	ggg	ggg	ggg	ccg	cag		
Trp	Thr	Pro	Ile	Lys	His	Arg	Gly	Ser	Gly	Gly	Gly	Gly	Gly	Pro	Gln		
142					147					152					157		
708																	
gtg	cct	cac	cag	agc	ccc	cca	aag	cgg	gtc	tcc	agc	ctc	agg	ttc	ctc		
Val	Pro	His	Gln	Ser	Pro	Pro	Lys	Arg	Val	Ser	Ser	Leu	Arg	Phe	Leu		
158					163					168					173		
756																	
caa	gct	ccc	agt	gcc	tct	tct	caa	tgt	gcc	cca	gct	cac	aga	ccc	tac		
Gln	Ala	Pro	Ser	Ala	Ser	Ser	Gln	Cys	Ala	Pro	Ala	His	Arg	Pro	Tyr		
174					179					184					189		
804																	
agc	cct	cct	ttc	ttc	agc	ctg	gcc	ctg	gcc	caa	gat	tcc	tct	cga	ccc		
Ser	Pro	Pro	Phe	Phe	Ser	Leu	Ala	Leu	Ala	Gln	Asp	Ser	Ser	Arg	Pro		
190					195					200					205		
852																	
tgc	gcc	gcc	tcc	cct	caa	agt	ggc	tcc	tgg	gag	agt	gat	gct	gag	tcc		
Cys	Ala	Ala	Ser	Pro	Gln	Ser	Gly	Ser	Trp	Glu	Ser	Asp	Ala	Glu	Ser		
206					211					216					221		
900																	
ttg	tca	cct	tgc	cca	cct	cag	cgc	cgc	ttc	tcc	ctg	tca	ccc	agt	ctg		
Leu	Ser	Pro	Cys	Pro	Pro	Gln	Arg	Arg	Phe	Ser	Leu	Ser	Pro	Ser	Leu		
222					227					232					237		
948																	
ggc	ccg	cag	gca	agc	cgc	ttc	ttg	ccc	tct	gcc	cgg	agc	tct	ccc	gca		
Gly	Pro	Gln	Ala	Ser	Arg	Phe	Leu	Pro	Ser	Ala	Arg	Ser	Ser	Pro	Ala		
238					243					248					253		
996																	
tcc	tcc	cca	gag	ctg	ccc	tgg	cga	cct	cga	ggg	ctc	cgc	aac	ctt	ccc		
Ser	Ser	Pro	Glu	Leu	Pro	Trp	Arg	Pro	Arg	Gly	Leu	Arg	Asn	Leu	Pro		

254	259	264	269	
cga agc cgc tca cag cct tgt gat ctg gat gcc cgc aaa act ggg gtc				1044
Arg Ser Arg Ser Gln Pro Cys Asp Leu Asp Ala Arg Lys Thr Gly Val				
270	275	280	285	
aag cgg cgc cac gag gaa gac ccc cgg cgt ctg cgg cct tcg ttg gac				1092
Lys Arg Arg His Glu Glu Asp Pro Arg Arg Leu Arg Pro Ser Leu Asp				
286	291	296	301	
ttt gac aag atg aat cag aaa cca tac tca gga ggt ctt tgt ctc caa				1140
Phe Asp Lys Met Asn Gln Lys Pro Tyr Ser Gly Gly Leu Cys Leu Gln				
302	307	312	317	
gaa aca gcc cgg gaa ggc agc agc atc tct cca cca tgg ttc atg gcc				1188
Glu Thr Ala Arg Glu Gly Ser Ser Ile Ser Pro Pro Trp Phe Met Ala				
318	323	328	333	
tgt agc ccc cca ccc ctc tct gct tcc tgc agc ccc act ggg ggt tcc				1236
Cys Ser Pro Pro Pro Leu Ser Ala Ser Cys Ser Pro Thr Gly Gly Ser				
334	339	344	349	
tcc cag gtg ctg agt gaa agc gaa gag gag gag gag ggg gct gtg cgg				1284
Ser Gln Val Leu Ser Glu Ser Glu Glu Glu Glu Glu Gly Ala Val Arg				
350	355	360	365	
tgg ggt cgg cag gcg ctg agc aag cgg aca ctg tgc cag cgg gac ttt				1332
Trp Gly Arg Gln Ala Leu Ser Lys Arg Thr Leu Cys Gln Arg Asp Phe				
366	371	376	381	
ggg gac ctg gac ttg aat ttg att gag gaa aac taa aact gagaggctac				1382
Gly Asp Leu Asp Leu Asn Leu Ile Glu Glu Asn *				
382	387	392		
ttcctgggaa aaaaaaaaaa aaaaaaa				1409

<210> 39
 <211> 4344
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (140)..(1768)

<400> 39	
ctgccggcggg cccggggcggg ctggcagcta gagtgggtgc gatagccgcc tccgcctctg	60
cccgcctccg ccgtcgcttc ctccgcccg gccgttcgct gctgcgcggg gagagcgagg	120
cggggcccggc ggggcccggc atg gag ccc gac tcg gtg att gag gac aag acc	172
Met Glu Pro Asp Ser Val Ile Glu Asp Lys Thr	
1 5	

atc gag ctc atg tgt tct gtg cca agg tct ttg tgg cta ggc tgc gcc Ile Glu Leu Met Cys Ser Val Pro Arg Ser Leu Trp Leu Gly Cys Ala 12 17 22 27	220
aac ctg gta gag agc atg tgc gca ctg agt tgc ctg cag agc atg ccc Asn Leu Val Glu Ser Met Cys Ala Leu Ser Cys Leu Gln Ser Met Pro 28 33 38 43	268
agt gtc aga tgt ctc cag ata agt aat gga aca tca tct gtg atc gtc Ser Val Arg Cys Leu Gln Ile Ser Asn Gly Thr Ser Ser Val Ile Val 44 49 54 59	316
tcc aga aag agg cca tca gaa gga aac tat caa aaa gaa aaa gac ttg Ser Arg Lys Arg Pro Ser Glu Gly Asn Tyr Gln Lys Glu Lys Asp Leu 60 65 70 75	364
tgt att aaa tat ttt gac cag tgg tct gaa tca gat caa gtg gaa ttt Cys Ile Lys Tyr Phe Asp Gln Trp Ser Glu Ser Asp Gln Val Glu Phe 76 81 86 91	412
gtg gaa cat ctt att tca cga atg tgt cat tat cag cat gga cat att Val Glu His Leu Ile Ser Arg Met Cys His Tyr Gln His Gly His Ile 92 97 102 107	460
aac tct tac ctg aag ccc atg ttg cag cgg gac ttt att acc gct tta Asn Ser Tyr Leu Lys Pro Met Leu Gln Arg Asp Phe Ile Thr Ala Leu 108 113 118 123	508
cca gag caa ggc tta gat cac ata gca gaa aac att ctt tcg tac ctg Pro Glu Gln Gly Leu Asp His Ile Ala Glu Asn Ile Leu Ser Tyr Leu 124 129 134 139	556
gat gcc agg tct ctg tgt gca gca gag ctg gta tgt aaa gaa tgg cag Asp Ala Arg Ser Leu Cys Ala Ala Glu Leu Val Cys Lys Glu Trp Gln 140 145 150 155	604
cga gtg atc tca gaa gga atg ctt tgg aag aag ctg att gaa cga atg Arg Val Ile Ser Glu Gly Met Leu Trp Lys Lys Leu Ile Glu Arg Met 156 161 166 171	652
gta cgc act gat ccc cta tgg aaa gga ctt tca gaa aga aga ggg tgg Val Arg Thr Asp Pro Leu Trp Lys Gly Leu Ser Glu Arg Arg Gly Trp 172 177 182 187	700
gat cag tac ctg ttt aaa aac aga ccc aca gat ggc cct cca aat tca Asp Gln Tyr Leu Phe Lys Asn Arg Pro Thr Asp Gly Pro Pro Asn Ser 188 193 198 203	748
ttt tat agg tca tta tac cca aag att atc cag gat ata gag act ata Phe Tyr Arg Ser Leu Tyr Pro Lys Ile Ile Gln Asp Ile Glu Thr Ile 204 209 214 219	796
gaa tct aac tgg cgg tgt gga cga cac aac ttg cag agg att cag tgc Glu Ser Asn Trp Arg Cys Gly Arg His Asn Leu Gln Arg Ile Gln Cys 220 225 230 235	844
cgc tct gaa aat agt aaa ggt gtc tac tgt tta cag tac gat gat gaa	892

Arg 236	Ser	Glu	Asn	Ser	Lys 241	Gly	Val	Tyr	Cys	Leu 246	Gln	Tyr	Asp	Asp	Glu 251	
aaa 252	att	atc	agt	ggc	cta	cga	gat	aat	tct	att	aag	ata	tgg	gat	aaa	940
Lys 252	Ile	Ile	Ser	Gly	Leu 257	Arg	Asp	Asn	Ser	Ile 262	Lys	Ile	Trp	Asp	Lys 267	
acc 268	agc	ctg	gaa	tgt	ttg	aaa	gtg	tta	aca	gga	cac	aca	ggc	tct	gtc	988
Thr 268	Ser	Leu	Glu	Cys	Leu 273	Lys	Val	Leu	Thr	Gly 278	His	Thr	Gly	Ser	Val 283	
ctc 284	tgt	ctg	cag	tat	gat	gag	cgt	gtc	att	gta	act	ggc	tct	tca	gat	1036
Leu 284	Cys	Leu	Gln	Tyr	Asp 289	Glu	Arg	Val	Ile	Val 294	Thr	Gly	Ser	Ser	Asp 299	
tct 300	acg	gtg	aga	gtg	tgg	gat	gtg	aac	acg	ggc	gaa	gtt	ctt	aac	aca	1084
Ser 300	Thr	Val	Arg	Val	Trp 305	Asp	Val	Asn	Thr	Gly 310	Glu	Val	Leu	Asn	Thr 315	
ttg 316	atc	cac	cac	aat	gag	gct	gta	ttg	cac	tta	cgc	ttc	agc	aat	gga	1132
Leu 316	Ile	His	His	Asn	Glu 321	Ala	Val	Leu	His	Leu 326	Arg	Phe	Ser	Asn	Gly 331	
ctg 332	atg	gtg	acc	tgt	tcc	aag	gac	cgc	tcc	att	gct	gtg	tgg	gac	atg	1180
Leu 332	Met	Val	Thr	Cys	Ser 337	Lys	Asp	Arg	Ser	Ile 342	Ala	Val	Trp	Asp	Met 347	
gct 348	tct	gcg	acc	gac	atc	act	tta	cgc	cgt	gtc	ctg	gtt	ggc	cac	cgg	1228
Ala 348	Ser	Ala	Thr	Asp	Ile 353	Thr	Leu	Arg	Arg	Val 358	Leu	Val	Gly	His	Arg 363	
gct 364	gcc	gtc	aat	gta	gta	gac	ttt	gac	gac	aag	tac	atc	gtg	tct	gcc	1276
Ala 364	Ala	Val	Asn	Val	Val 369	Asp	Phe	Asp	Asp	Lys 374	Tyr	Ile	Val	Ser	Ala 379	
tct 380	ggc	gac	agg	acc	atc	aaa	gtc	tgg	agc	acg	agc	acc	tgt	gaa	ttt	1324
Ser 380	Gly	Asp	Arg	Thr	Ile 385	Lys	Val	Trp	Ser	Thr 390	Ser	Thr	Cys	Glu	Phe 395	
gtt 396	cgt	act	ctc	aat	ggg	cac	aag	cgg	ggc	att	gcc	tgt	ctc	cag	tac	1372
Val 396	Arg	Thr	Leu	Asn	Gly 401	His	Lys	Arg	Gly	Ile 406	Ala	Cys	Leu	Gln	Tyr 411	
agg 412	gat	cgc	ctg	gtt	gtt	agt	gga	tca	tca	gat	aat	acc	att	agg	ctc	1420
Arg 412	Asp	Arg	Leu	Val	Val 417	Ser	Gly	Ser	Ser	Asp 422	Asn	Thr	Ile	Arg	Leu 427	
tgg 428	gat	att	gaa	tgt	ggc	tgt	tta	aga	gtc	cta	gag	gga	cat	gaa		1468
Trp 428	Asp	Ile	Glu	Cys	Gly 433	Ala	Cys	Leu	Arg	Val 438	Leu	Glu	Gly	His	Glu 443	
gaa 444	ttg	gtc	cga	tgc	atc	cgg	ttt	gat	aac	aag	agg	att	gtc	agt	ggg	1516
Glu 444	Leu	Val	Arg	Cys	Ile 449	Arg	Phe	Asp	Asn	Lys 454	Arg	Ile	Val	Ser	Gly 459	
gcc 1564	tat	gat	ggg	aaa	att	aaa	gtt	tgg	gac	ttg	caa	gct	gct	ctt	gac	
Ala	Tyr	Asp	Gly	Lys	Ile	Lys	Val	Trp	Asp	Leu	Gln	Ala	Ala	Leu	Asp	

460	465	470	475	
cct cga gcc cca gca agc aca ttg tgt ttg cgc aca ttg gtg gaa cat				1612
Pro Arg Ala Pro Ala Ser Thr Leu Cys Leu Arg Thr Leu Val Glu His				
476	481	486	491	
tct gga cgt gtg ttt cgg ctc cag ttt gat gag ttt cag atc atc agc				1660
Ser Gly Arg Val Phe Arg Leu Gln Phe Asp Glu Phe Gln Ile Ile Ser				
492	497	502	507	
agc tcc cat gat gac act att ttg att tgg gat ttc tta aat gtg cct				1708
Ser Ser His Asp Asp Thr Ile Leu Ile Trp Asp Phe Leu Asn Val Pro				
508	513	518	523	
ccc agt gcc cag aat gag acc cgt tct ccc tcc aga aca tac act tac				1756
Pro Ser Ala Gln Asn Glu Thr Arg Ser Pro Ser Arg Thr Tyr Thr Tyr				
524	529	534	539	
atc tct aga taa cag tctgcacttt caccggtttc aggggttttct agtcttgaac				1811
Ile Ser Arg *				
540				
tactggctac gtggctacca aatgcctaag ggagttcgtt cacagctgag ttatgaagct				1871
ggaattgggtt ctagacgctg ggtagatgca aagcagccta actcttcaag taccgacatt				1931
tctcacctct gattccgggt ctcctttgag aaggagacct tagcttcccc ggcttcaagt				1991
agaacagaag cccgtttcct tccctcatca gtgaaaaaat ctaatgtttc aaatgtaa				2051
tgttcataga aaaggaacat agaatctgtt ttacagaagt aaatcgaccg tcaagagaag				2111
acttggcctc taatttatat tgctttgcac tttggtttga tattaagaaa cagcattctt				2171
cttcagtga attttgggtg ccaaacacct acccagaatg tccagggctt tcattttcaa				2231
aagttagcat tctccttttg accgtccaag tcattatgaa ttctgacttg ttgtattagg				2291
aacatggttg acagtggaaa attttctctg gattgtttta gtaatatatt tgggattata				2351
cttcctttct gtaccaatth cttttaatth aaagaactat aagtcagtta tattatctac				2411
caacaggtaa tatagctctt tcttttatta actgttctct gtcccccaac catctcctga				2471
tatttggtag agtaacacct ttatacgtgt gcttgctcc taatttaaaa tactgtattc				2531
gcatgtagat ataatgtaca taacagttta acctcaaagt tgctggagtc agggccccct				2591
gtgcttgaga cactaatata gagtgtgttc gcacttagcc atgggctggg ctcaagaacc				2651
tgatacctgg gttgatgtgg attacctaga acccttctct cagtattcat acagtgtttt				2711
tattttgttg ttgtcattgc gtgtgtgtgg tttgtgtgtg tttttaatga gaatcttgtt				2771
ttaaaatgta atttctaagg tttaacacca aaatgtttta tttgttgtgg agtatatatt				2831
atacaataga gaggtacctt aaacattttt tgttcttatt ctttttctca taagtactcc				2891

tgagtacaag	tggtcacctc	ccatagttatt	cattttggctt	cgctgtcaaa	aatcattatt	2951
ctgtgcagtc	gtggcccttg	gaaggggaaa	taagaaggcc	ctgttgacgg	gctgtcttgg	3011
ctctggaatt	catgcatcct	ggccttgcca	aggttctggc	agggcctgct	ggtgtgttgg	3071
agcctgcagg	gcaggtcagg	ctgggttcaga	ggcccatgct	gaggggtggg	tgctctgaag	3131
tggagtgaag	cctcaagccc	atgaatgcca	ccccagtcac	ctctgggtgtc	agctgctgct	3191
gtggccccag	caggtttctca	aagctcccaa	gtcctcccta	cgacacagcc	caaagtgtga	3251
aatggcactg	ttgccctgac	agtgcattga	aaggacgttg	gcacccaatt	ggcactcctt	3311
ctcccttatt	caatattagg	tttgatttgc	ccttcgccat	tgtttccaaa	gatcaaggaa	3371
tgtcaataac	attttaaagg	accaataaac	agcctcctat	aaagtaaacc	tcttcccggtg	3431
gaagcacact	ctactactaa	aggggaaggcc	cctgggctct	gattttgtcct	ttgcattgag	3491
aacgggtgtg	ggatcagtgt	gtgtgtatgt	gattttgttta	ttgagttggc	tttgcttttt	3551
tagtttttct	tttaaaaata	aaatccttcc	ttcccatgtt	actaaattaa	tttatgtttt	3611
tgagagggtt	agtctcaaag	tgtaaacaat	aaacctccat	tcataagggtg	gatgttgtaa	3671
gcttgatggt	ggttggtgaa	gtgatttagc	tttgaccact	tttcatccta	cagcttcaat	3731
atcaaactgg	ttaggaaagc	ccaggggggaa	gggagggggc	aggggaggag	gcaattctga	3791
atgaatgaat	ggattttttg	ttgtttttgc	atgtttaata	tagaagttcc	cctcgttcct	3851
tgggagatga	tggcctttga	atatgcagac	aacctttgaa	ttgtgcctac	taaattatag	3911
caggggactt	tggcacccaa	ggagttctga	ctttctggga	ttataatagt	aattcccagc	3971
catactctgg	actttatttt	gctaaccata	actgagcaaa	tgtaaattac	tgctatatta	4031
atgttttaaa	gcactgggat	agtctaattc	taacttgtaa	ttaattatgt	ttgccaatta	4091
tctgtttgaa	ataaatttgt	gtctgaacag	ctattgaaac	tgtaaattg	tacagatatt	4151
attcatgaca	gctttgtact	gtggaatgtg	cttaataaaa	aacaaaaaag	tttgactttt	4211
gtccagtaaa	ttgctaagta	atgtcaataa	atcgagtatg	ggtattatgc	agtgcaccta	4271
atctggcttc	atgcaattgt	tacttcagct	actgattcaa	agccaatact	cttaataaag	4331
tgttgcaata	ctc					4344

<210> 40
 <211> 2907
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (76) .. (2907)

<400> 40

cctgtaagcc gtacgcctgc ggtaccggtc cggaattccc gggtcgacga tttcgtatct	60
ggcagcccat ggagg atg gat ggg agc acg gag agg ctg gag gca agg aga	111
Met Asp Gly Ser Thr Glu Arg Leu Glu Ala Arg Arg	
1 5 10	
cca gcc ggg agg ctg ccg tgg tca tcc agg caa gaa atg acg agg cgt	159
Pro Ala Gly Arg Leu Pro Trp Ser Ser Arg Gln Glu Met Thr Arg Arg	
13 18 23 28	
ccc tcc ctg atg gcg ggc aga cag cac gga tgg agc gcc cag cag agt	207
Pro Ser Leu Met Ala Gly Arg Gln His Gly Trp Ser Ala Gln Gln Ser	
29 34 39 44	
gcc acc gtg gcc aac cca gtg cct ggt gcc aac ccg gac ctg ctt ccc	255
Ala Thr Val Ala Asn Pro Val Pro Gly Ala Asn Pro Asp Leu Leu Pro	
45 50 55 60	
cac ttc ctg gtg gag ccc gag gat gtg tac atc gtc aag aac aag cca	303
His Phe Leu Val Glu Pro Glu Asp Val Tyr Ile Val Lys Asn Lys Pro	
61 66 71 76	
gtg ctg ctt gtg tgc aag gcc gtg ccc gcc acg cag atc ttc ttc aag	351
Val Leu Leu Val Cys Lys Ala Val Pro Ala Thr Gln Ile Phe Phe Lys	
77 82 87 92	
tgc aac ggg gag tgg gtg cgc cag gtg gac cac gtg atc gag cgc agc	399
Cys Asn Gly Glu Trp Val Arg Gln Val Asp His Val Ile Glu Arg Ser	
93 98 103 108	
aca gac ggg agc agt ggg ctg ccc acc atg gag gtc cgc att aat gtc	447
Thr Asp Gly Ser Ser Gly Leu Pro Thr Met Glu Val Arg Ile Asn Val	
109 114 119 124	
tca agg cag cag gtc gag aag gtg ttc ggg ctg gag gaa tac tgg tgc	495
Ser Arg Gln Gln Val Glu Lys Val Phe Gly Leu Glu Glu Tyr Trp Cys	
125 130 135 140	
cag tgc gtg gca tgg agc tcc tcg ggc acc acc aag agt cag aag gcc	543
Gln Cys Val Ala Trp Ser Ser Ser Gly Thr Thr Lys Ser Gln Lys Ala	
141 146 151 156	
tac atc cgc ata gcc tat ttg cgc aag aac ttc gag cag gag ccg ctg	591
Tyr Ile Arg Ile Ala Tyr Leu Arg Lys Asn Phe Glu Gln Glu Pro Leu	
157 162 167 172	
gcc aag gag gtg tcc ctg gag cag ggc atc gtg ctg ccc tgc cgt cca	639
Ala Lys Glu Val Ser Leu Glu Gln Gly Ile Val Leu Pro Cys Arg Pro	
173 178 183 188	

ccg gag ggc atc cct cca gcc gag gtg gag tgg ctc cgg aac gag gac	687
Pro Glu Gly Ile Pro Pro Ala Glu Val Glu Trp Leu Arg Asn Glu Asp	
189 194 199 204	
ctg gtg gac ccg tcc ctg gac ccc aat gta tac atc acg cgg gag cac	735
Leu Val Asp Pro Ser Leu Asp Pro Asn Val Tyr Ile Thr Arg Glu His	
205 210 215 220	
agc ctg gtg gtg cga cag gcc cgc ctt gct gac acg gcc aac tac acc	783
Ser Leu Val Val Arg Gln Ala Arg Leu Ala Asp Thr Ala Asn Tyr Thr	
221 226 231 236	
tgc gtg gcc aag aac atc gtg gca cgt cgc cgc agc gcc tcc gct gct	831
Cys Val Ala Lys Asn Ile Val Ala Arg Arg Arg Ser Ala Ser Ala Ala	
237 242 247 252	
gtc atc gtc tac ggt ggg ccc cgg gac tcc ctg gtc aca ggg aga ggc	879
Val Ile Val Tyr Gly Gly Pro Arg Asp Ser Leu Val Thr Gly Arg Gly	
253 258 263 268	
act gcg gtg ccc ctg ggc agt gac atg tgg ctg tcc ttc tct gtc cgg	927
Thr Ala Val Pro Leu Gly Ser Asp Met Trp Leu Ser Phe Ser Val Arg	
269 274 279 284	
cca gtg aac ggt ggg tgg tcg acg tgg acc gag tgg tcc gtc tgc agc	975
Pro Val Asn Gly Gly Trp Ser Thr Trp Thr Glu Trp Ser Val Cys Ser	
285 290 295 300	
gcc agc tgt ggg cgc ggc tgg cag aaa cgg agc cgg agc tgc acc aac	1023
Ala Ser Cys Gly Arg Gly Trp Gln Lys Arg Ser Arg Ser Cys Thr Asn	
301 306 311 316	
ccg gcg cct ctc aac ggg ggc gct ttc tgt gag ggg cag aat gtc cag	1071
Pro Ala Pro Leu Asn Gly Gly Ala Phe Cys Glu Gly Gln Asn Val Gln	
317 322 327 332	
aaa aca gcc tgc gcc acc ctg tgc cca gtg gac ggc agc tgg agc ccg	1119
Lys Thr Ala Cys Ala Thr Leu Cys Pro Val Asp Gly Ser Trp Ser Pro	
333 338 343 348	
tgg agc aag tgg tcg gcc tgt ggg ctg gac tgc acc cac tgg cgg agc	1167
Trp Ser Lys Trp Ser Ala Cys Gly Leu Asp Cys Thr His Trp Arg Ser	
349 354 359 364	
cgt gag tgc tct gac cca gca ccc cgc aac gga ggg gag gag tgc cag	1215
Arg Glu Cys Ser Asp Pro Ala Pro Arg Asn Gly Gly Glu Glu Cys Gln	
365 370 375 380	
ggc act gac ctg gac acc cgc aac tgt acc agt gac ctc tgt gta cac	1263
Gly Thr Asp Leu Asp Thr Arg Asn Cys Thr Ser Asp Leu Cys Val His	
381 386 391 396	
aac tcc tac acc cct gcc ccc acc aag gcc atg ctg tct ccc gca gct	1311
Asn Ser Tyr Thr Pro Ala Pro Thr Lys Ala Met Leu Ser Pro Ala Ala	
397 402 407 412	
gct tct ggc cct gag gac gtg gcc ctc tat gtg ggc ctc atc gcc gtg	1359

Ala Ser Gly Pro Glu Asp Val Ala Leu Tyr Val Gly Leu Ile Ala Val	
413 418 423 428	
gcc gtc tgc ctg gtc ctg ctg ctg ctt gtc ctc atc ctc gtt tat tgc	1407
Ala Val Cys Leu Val Leu Leu Leu Leu Val Leu Ile Leu Val Tyr Cys	
429 434 439 444	
cgg aag aag gag ggg ctg gac tca gat gtg gct gac tcg tcc att ctc	1455
Arg Lys Lys Glu Gly Leu Asp Ser Asp Val Ala Asp Ser Ser Ile Leu	
445 450 455 460	
acc tca ggc ttc cag ccc gtc agc atc aag ccc agc aaa gca gac aac	1503
Thr Ser Gly Phe Gln Pro Val Ser Ile Lys Pro Ser Lys Ala Asp Asn	
461 466 471 476	
ccc cat ctg ctc acc atc cag ccg gac ctc agc acc acc acc acc acc	1551
Pro His Leu Leu Thr Ile Gln Pro Asp Leu Ser Thr Thr Thr Thr Thr	
477 482 487 492	
tac cag ggc agt ctc tgt ccc cgg cag gat ggg ccc agc ccc aag ttc	1599
Tyr Gln Gly Ser Leu Cys Pro Arg Gln Asp Gly Pro Ser Pro Lys Phe	
493 498 503 508	
cag ctc acc aat ggg cac ctg ctc agc ccc ctg ggt ggc ggc cgc cac	1647
Gln Leu Thr Asn Gly His Leu Leu Ser Pro Leu Gly Gly Gly Arg His	
509 514 519 524	
aca ctg cac cac agc tct ccc acc tct gag gcc gag gag ttc gtc tcc	1695
Thr Leu His His Ser Ser Pro Thr Ser Glu Ala Glu Glu Phe Val Ser	
525 530 535 540	
cgc ctc tcc acc cag aac tac ttc cgc tcc ctg ccc cga ggc acc agc	1743
Arg Leu Ser Thr Gln Asn Tyr Phe Arg Ser Leu Pro Arg Gly Thr Ser	
541 546 551 556	
aac atg acc tat ggg acc ttc aac ttc ctc ggg ggc cgg ctg atg atc	1791
Asn Met Thr Tyr Gly Thr Phe Asn Phe Leu Gly Gly Arg Leu Met Ile	
557 562 567 572	
cct aat aca gga atc agc ctc ctc atc ccc cca gat gcc ata ccc cga	1839
Pro Asn Thr Gly Ile Ser Leu Leu Ile Pro Pro Asp Ala Ile Pro Arg	
573 578 583 588	
ggg aag atc tat gag atc tac ctc acg ctg cac aag ccg gaa gac gtg	1887
Gly Lys Ile Tyr Glu Ile Tyr Leu Thr Leu His Lys Pro Glu Asp Val	
589 594 599 604	
agc tgt gga ccc cct ggc gtc ctg ctc acc cgg cca gtc atc ctg gct	1935
Ser Cys Gly Pro Pro Gly Val Leu Leu Thr Arg Pro Val Ile Leu Ala	
605 610 615 620	
atg gac cac tgt ggg gag ccc agc cct gac agc tgg agc ctg cgc ctc	1983
Met Asp His Cys Gly Glu Pro Ser Pro Asp Ser Trp Ser Leu Arg Leu	
621 626 631 636	
aaa aag cag tcg tgc gag ggc agc tgg gag gat gtg ctg cac ctg ggc	2031
Lys Lys Gln Ser Cys Glu Gly Ser Trp Glu Asp Val Leu His Leu Gly	

637	642	647	652	
gag gag gcg ccc tcc cac ctc tac tac tgc	cag ctg gag gcc agt gcc	2079		
Glu Glu Ala Pro Ser His Leu Tyr Tyr Cys	Gln Leu Glu Ala Ser Ala			
653	658	663	668	
tgc tac gtc ttc acc gag cag ctg ggc cgc	ttt gcc ctg gtg gga gag	2127		
Cys Tyr Val Phe Thr Glu Gln Leu Gly Arg	Phe Ala Leu Val Gly Glu			
669	674	679	684	
gcc ctc agc gtg gct gcc gcc aag cgc ctc	aag ctg ctt ctg ttt gcg	2175		
Ala Leu Ser Val Ala Ala Ala Lys Arg Leu	Lys Leu Leu Leu Phe Ala			
685	690	695	700	
ccg gtg gcc tgc acc tcc ctc gag tac aac	atc cgg gtc tac tgc ctg	2223		
Pro Val Ala Cys Thr Ser Leu Glu Tyr Asn	Ile Arg Val Tyr Cys Leu			
701	706	711	716	
cat gac acc cac gat gca ctc aag gag gtg	gtg cag ctg gag aag cag	2271		
His Asp Thr His Asp Ala Leu Lys Glu Val	Val Gln Leu Glu Lys Gln			
717	722	727	732	
ctg ggg gga cag ctg atc cag gag cca cgg	gtc ctg cac ttc aag gac	2319		
Leu Gly Gly Gln Leu Ile Gln Glu Pro Arg	Val Leu His Phe Lys Asp			
733	738	743	748	
agt tac cac aac ctg cgc cta tcc atc cac	gat gtg ccc agc tcc ctg	2367		
Ser Tyr His Asn Leu Arg Leu Ser Ile His	Asp Val Pro Ser Ser Leu			
749	754	759	764	
tgg aag agt aag ctc ctt gtc agc tac cag	gag atc ccc ttt tat cac	2415		
Trp Lys Ser Lys Leu Leu Val Ser Tyr Gln	Glu Ile Pro Phe Tyr His			
765	770	775	780	
atc tgg aat ggc acg cag cgg tac ttg cac	tgc acc ttc acc ctg gag	2463		
Ile Trp Asn Gly Thr Gln Arg Tyr Leu His	Cys Thr Phe Thr Leu Glu			
781	786	791	796	
cgt gtc agc ccc agc act agt gac ctg gcc	tgc aag ctg tgg gtg tgg	2511		
Arg Val Ser Pro Ser Thr Ser Asp Leu Ala	Cys Lys Leu Trp Val Trp			
797	802	807	812	
cag gtg gag ggc gac ggg cag agc ttc agc	atc aac ttc aac atc acc	2559		
Gln Val Glu Gly Asp Gly Gln Ser Phe Ser	Ile Asn Phe Asn Ile Thr			
813	818	823	828	
aag gac aca agg ttt gct gag ctg ctg gct	ctg gag agt gaa gcg ggg	2607		
Lys Asp Thr Arg Phe Ala Glu Leu Leu Ala	Leu Glu Ser Glu Ala Gly			
829	834	839	844	
gtc cca gcc ctg gtg ggc ccc agt gcc ttc	aag atc ccc ttc ctc att	2655		
Val Pro Ala Leu Val Gly Pro Ser Ala Phe	Lys Ile Pro Phe Leu Ile			
845	850	855	860	
cgg cag aag ata att tcc agc ctg gac cca	ccc tgt agg cgg ggt gcc	2703		
Arg Gln Lys Ile Ile Ser Ser Leu Asp Pro	Pro Cys Arg Arg Gly Ala			
861	866	871	876	

gac tgg cgg act ctg gcc cag aaa ctc cac ctg gac agc cat ctc agc	2751
Asp Trp Arg Thr Leu Ala Gln Lys Leu His Leu Asp Ser His Leu Ser	
877 882 887 892	
ttc ttt gcc tcc aag ccc agc ccc aca gcc atg atc ctc aac ctg tgg	2799
Phe Phe Ala Ser Lys Pro Ser Pro Thr Ala Met Ile Leu Asn Leu Trp	
893 898 903 908	
gag gcg cgg cac ttc ccc aac ggc aac ctc agc cag ctg gct gca gca	2847
Glu Ala Arg His Phe Pro Asn Gly Asn Leu Ser Gln Leu Ala Ala Ala	
909 914 919 924	
gtg gct gga ctg ggc cag cca gac gct ggc ctc ttc aca gtg tcg gag	2895
Val Ala Gly Leu Gly Gln Pro Asp Ala Gly Leu Phe Thr Val Ser Glu	
925 930 935 940	
gct gag tgc tga	2907
Ala Glu Cys *	
941	

<210> 41
 <211> 3218
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (187)..(3198)

<400> 41	
taagcttgcg gccgcgcgtc ttgtcgtcgc agtatttcct gttcggatga tcttttgccg	60
gccccagct gcctccttac cctcacactc ccactcctcc gtttcgcgcg gcgaagctgc	120
cttcggcccc ggggtggtctc ccccgccccg ggacccctg tgctccct cccgggctcc	180
gagacc atg agg aaa ttc aac atc agg aag gtg ctg gac ggc ctg acc	228
Met Arg Lys Phe Asn Ile Arg Lys Val Leu Asp Gly Leu Thr	
1 5 10	
gcc ggc tcg tcc tcg gcg tcg cag cag caa cag cag cag cat ccg cct	276
Ala Gly Ser Ser Ser Ala Ser Gln Gln Gln Gln Gln Gln His Pro Pro	
15 20 25 30	
ggg aac cgg gag ccg gag atc cag gaa acg ctc cag tcc gag cac ttt	324
Gly Asn Arg Glu Pro Glu Ile Gln Glu Thr Leu Gln Ser Glu His Phe	
31 36 41 46	
cag ctc tgc aag act gtt cgc cat gga ttt ccc tat caa ccc tca gcc	372
Gln Leu Cys Lys Thr Val Arg His Gly Phe Pro Tyr Gln Pro Ser Ala	
47 52 57 62	

ctg gcc ttt gat cct gta cag aag atc ctg gca gtg gga act cag act	420
Leu Ala Phe Asp Pro Val Gln Lys Ile Leu Ala Val Gly Thr Gln Thr	
63 68 73 78	
ggg gct tta agg ctc ttt ggt cgt cca gga gta gaa tgt tat tgc cag	468
Gly Ala Leu Arg Leu Phe Gly Arg Pro Gly Val Glu Cys Tyr Cys Gln	
79 84 89 94	
cat gac agt gga gct gca gta atc cag ctc cag ttc ctg att aat gag	516
His Asp Ser Gly Ala Ala Val Ile Gln Leu Gln Phe Leu Ile Asn Glu	
95 100 105 110	
gga gcg ctt gtg agt gcc ttg gct gat gac acc tta cac tta tgg aat	564
Gly Ala Leu Val Ser Ala Leu Ala Asp Asp Thr Leu His Leu Trp Asn	
111 116 121 126	
tta cgt cag aag agg cct gcc ata cta cat tcg ctt aaa ttt tgc aga	612
Leu Arg Gln Lys Arg Pro Ala Ile Leu His Ser Leu Lys Phe Cys Arg	
127 132 137 142	
gaa agg gtt aca ttt tgc cat ctg cct ttc cag agt aag tgg ctc tat	660
Glu Arg Val Thr Phe Cys His Leu Pro Phe Gln Ser Lys Trp Leu Tyr	
143 148 153 158	
gtg ggc act gaa cga ggt aat ata cat att gtc aat gtg gag tcc ttc	708
Val Gly Thr Glu Arg Gly Asn Ile His Ile Val Asn Val Glu Ser Phe	
159 164 169 174	
aca ctc tca ggc tac gtc att atg tgg aat aaa gcc att gaa ctg tca	756
Thr Leu Ser Gly Tyr Val Ile Met Trp Asn Lys Ala Ile Glu Leu Ser	
175 180 185 190	
tct aaa tct cac cca gga cct gtg gtc cat ata agt gat aat cca atg	804
Ser Lys Ser His Pro Gly Pro Val Val His Ile Ser Asp Asn Pro Met	
191 196 201 206	
gac gag gga aag ctt ttg att ggc ttt gaa tct gga aca gta gtt cta	852
Asp Glu Gly Lys Leu Leu Ile Gly Phe Glu Ser Gly Thr Val Val Leu	
207 212 217 222	
tgg gac ctc aaa tac aag aaa gcc gac tac aga tac aca tat gat gag	900
Trp Asp Leu Lys Tyr Lys Lys Ala Asp Tyr Arg Tyr Thr Tyr Asp Glu	
223 228 233 238	
gct atc cac tct gtt gct tgg cat cat gaa gga aaa caa ttt att tgc	948
Ala Ile His Ser Val Ala Trp His His Glu Gly Lys Gln Phe Ile Cys	
239 244 249 254	
agt cat tca gat ggc acc ttg acc ata tgg aat gta agg tcc cct gct	996
Ser His Ser Asp Gly Thr Leu Thr Ile Trp Asn Val Arg Ser Pro Ala	
255 260 265 270	
aaa cca gta cag aca atc act cca cat gga aaa cag tta agg gat ggg	1044
Lys Pro Val Gln Thr Ile Thr Pro His Gly Lys Gln Leu Arg Asp Gly	
271 276 281 286	
aag aag cca gaa cca tgc aaa cct atc ctc aag gtg gaa ttc aaa acg	1092

Lys 287	Lys	Pro	Glu	Pro	Cys 292	Lys	Pro	Ile	Leu	Lys 297	Val	Glu	Phe	Lys	Thr 302	
act	aga	tct	ggg	gag	cct	ttt	att	att	tta	tca	gga	ggg	ttg	tca	tat	1140
Thr	Arg	Ser	Gly	Glu	Pro	Phe	Ile	Ile	Leu	Ser	Gly	Gly	Leu	Ser	Tyr	
303					308					313					318	
gat	act	gta	gga	aga	aga	cct	tgc	tta	aca	gtg	atg	cat	ggg	aaa	agc	1188
Asp	Thr	Val	Gly	Arg	Arg	Pro	Cys	Leu	Thr	Val	Met	His	Gly	Lys	Ser	
319					324					329					334	
act	gct	gtg	cta	gaa	atg	gac	tat	tca	att	gtc	gat	ttt	cta	acg	ctg	1236
Thr	Ala	Val	Leu	Glu	Met	Asp	Tyr	Ser	Ile	Val	Asp	Phe	Leu	Thr	Leu	
335					340					345					350	
tgt	gaa	aca	cca	tac	cca	aat	gat	ttt	caa	gaa	cca	tat	gct	gtg	gtt	1284
Cys	Glu	Thr	Pro	Tyr	Pro	Asn	Asp	Phe	Gln	Glu	Pro	Tyr	Ala	Val	Val	
351					356					361					366	
gtt	ctt	cta	gaa	aag	gat	tta	gta	ctt	ata	gac	ctt	gca	caa	aat	gga	1332
Val	Leu	Leu	Glu	Lys	Asp	Leu	Val	Leu	Ile	Asp	Leu	Ala	Gln	Asn	Gly	
367					372					377					382	
tat	cct	ata	ttt	gaa	aat	ccc	tac	cct	ttg	agt	ata	cat	gag	tcc	cct	1380
Tyr	Pro	Ile	Phe	Glu	Asn	Pro	Tyr	Pro	Leu	Ser	Ile	His	Glu	Ser	Pro	
383					388					393					398	
gtt	aca	tgt	tgc	gaa	tat	ttt	gcg	gat	tgt	cct	gtg	gac	ctt	att	cct	1428
Val	Thr	Cys	Cys	Glu	Tyr	Phe	Ala	Asp	Cys	Pro	Val	Asp	Leu	Ile	Pro	
399					404					409					414	
gca	ctt	tat	tct	gtt	gga	gct	aga	cag	aaa	cgt	caa	ggg	tac	agc	aaa	1476
Ala	Leu	Tyr	Ser	Val	Gly	Ala	Arg	Gln	Lys	Arg	Gln	Gly	Tyr	Ser	Lys	
415					420					425					430	
aag	gaa	tgg	ccc	atc	aac	gga	ggg	aat	tgg	ggc	ttg	ggg	gct	caa	agt	1524
Lys	Glu	Trp	Pro	Ile	Asn	Gly	Gly	Asn	Trp	Gly	Leu	Gly	Ala	Gln	Ser	
431					436					441					446	
tac	cca	gaa	ata	att	att	aca	ggg	cat	gct	gat	ggg	tca	gtt	aag	ttc	1572
Tyr	Pro	Glu	Ile	Ile	Ile	Thr	Gly	His	Ala	Asp	Gly	Ser	Val	Lys	Phe	
447					452					457					462	
tgg	gat	gct	tct	gca	ata	act	cta	caa	gta	tta	tat	aag	cta	aag	aca	1620
Trp	Asp	Ala	Ser	Ala	Ile	Thr	Leu	Gln	Val	Leu	Tyr	Lys	Leu	Lys	Thr	
463					468					473					478	
tct	aaa	gta	ttt	gaa	aag	tca	aga	aat	aaa	gat	gac	agg	cca	aac	aca	1668
Ser	Lys	Val	Phe	Glu	Lys	Ser	Arg	Asn	Lys	Asp	Asp	Arg	Pro	Asn	Thr	
479					484					489					494	
gac	att	gta	gat	gaa	gat	cca	tat	gcc	att	cag	atc	atc	tcc	tgg	tgt	1716
Asp	Ile	Val	Asp	Glu	Asp	Pro	Tyr	Ala	Ile	Gln	Ile	Ile	Ser	Trp	Cys	
495					500					505					510	
cca	gaa	agt	aga	atg	ctg	tgc	atc	gct	gga	gtt	tca	gct	cat	gtc	att	1764
Pro	Glu	Ser	Arg	Met	Leu	Cys	Ile	Ala	Gly	Val	Ser	Ala	His	Val	Ile	

511	516	521	526	
att tat aga ttc agc aag cag gaa gta atc aca gaa gtc att ccg atg				1812
Ile Tyr Arg Phe Ser Lys Gln Glu Val Ile Thr Glu Val Ile Pro Met				
527	532	537	542	
ctt gaa gtt cga tta tta tat gag ata aat gat gtg gaa act ccg gag				1860
Leu Glu Val Arg Leu Leu Tyr Glu Ile Asn Asp Val Glu Thr Pro Glu				
543	548	553	558	
ggt gag cag cca cca cct ttg cca aca ccc gtg gga ggg tcc aac cct				1908
Gly Glu Gln Pro Pro Pro Leu Pro Thr Pro Val Gly Gly Ser Asn Pro				
559	564	569	574	
cag ccc atc cct cct cag tct cat cca tct acc agt agc agt tca tct				1956
Gln Pro Ile Pro Pro Gln Ser His Pro Ser Thr Ser Ser Ser Ser Ser				
575	580	585	590	
gat ggg ctt cgt gat aat gta cct tgt tta aat gta gtg tgt aag gag				2004
Asp Gly Leu Arg Asp Asn Val Pro Cys Leu Asn Val Val Cys Lys Glu				
591	596	601	606	
cat gga aat cat ttt atc tta aca aga agt aaa aag ctg aac aaa ctg				2052
His Gly Asn His Phe Ile Leu Thr Arg Ser Lys Lys Leu Asn Lys Leu				
607	612	617	622	
gaa aat caa caa ctc ttc tta aag atc tgt aag aga aga ctg cct tca				2100
Glu Asn Gln Gln Leu Phe Leu Lys Ile Cys Lys Arg Arg Leu Pro Ser				
623	628	633	638	
gaa ata aca ctt tta cga gag cct aac ctg ctg ggg ttt tat cag gga				2148
Glu Ile Thr Leu Leu Arg Glu Pro Asn Leu Leu Gly Phe Tyr Gln Gly				
639	644	649	654	
cca act aac ctg aga gaa gaa aaa tca ctc cag tgg gcc caa gcc ttc				2196
Pro Thr Asn Leu Arg Glu Glu Lys Ser Leu Gln Trp Ala Gln Ala Phe				
655	660	665	670	
caa gta aag gaa gag aag tac gca act cca gcc cac ttt agc cat ctt				2244
Gln Val Lys Glu Glu Lys Tyr Ala Thr Pro Ala His Phe Ser His Leu				
671	676	681	686	
att cca cct aaa agg gag tgg gag gaa gta aaa gaa cca gtg gaa ttt				2292
Ile Pro Pro Lys Arg Glu Trp Glu Glu Val Lys Glu Pro Val Glu Phe				
687	692	697	702	
gaa ata att aat ttg aaa tta ttt gaa att tat att agc acc cca aaa				2340
Glu Ile Ile Asn Leu Lys Leu Phe Glu Ile Tyr Ile Ser Thr Pro Lys				
703	708	713	718	
aat gaa ata ctt aaa tat aaa tct aac aaa tat gta caa gat cta cac				2388
Asn Glu Ile Leu Lys Tyr Lys Ser Asn Lys Tyr Val Gln Asp Leu His				
719	724	729	734	
gaa gaa cag cac aaa act ctg cag agt gag aat att ctg tat gat att				2436
Glu Glu Gln His Lys Thr Leu Gln Ser Glu Asn Ile Leu Tyr Asp Ile				
735	740	745	750	

ata Ile 751	atg Met 751	atg Met 751	aaa Lys 751	gac Asp 751	atg Met 756	gtt Val 756	aca Thr 756	ttt Phe 756	tgc Cys 761	cat His 761	ctg Leu 761	cct Pro 761	ttc Phe 761	cag Gln 766	agt Ser 766	2484
aag Lys 767	tgg Trp 767	ctc Leu 767	tat Tyr 767	gtg Val 772	ggc Gly 772	act Thr 772	gaa Glu 772	cga Arg 772	ggt Gly 777	aat Asn 777	ata Ile 777	cat His 777	att Ile 782	gtc Val 782	aat Asn 782	2532
gtg Val 783	gag Glu 783	tcc Ser 783	ttc Phe 783	aca Thr 788	ctc Leu 788	tca Ser 788	ggc Gly 788	tac Tyr 788	gtc Val 793	att Ile 793	atg Met 793	tgg Trp 793	aat Asn 798	aaa Lys 798	gcc Ala 798	2580
att Ile 799	gaa Glu 799	ctg Leu 799	tca Ser 804	tct Ser 804	aaa Lys 804	tct Ser 809	cac His 809	cca Pro 809	gga Gly 809	cct Pro 809	gtg Val 814	gtc Val 814	cat His 814	ata Ile 814	agt Ser 814	2628
gat Asp 815	aat Asn 815	cca Pro 820	atg Met 820	gac Asp 820	gag Glu 820	gga Gly 825	aag Lys 825	ctt Leu 825	ttg Leu 825	att Ile 825	ggc Gly 830	ttt Phe 830	gaa Glu 830	tct Ser 830	gga Gly 830	2676
aca Thr 831	gta Val 831	gtt Val 836	tta Leu 836	tgg Trp 836	gac Asp 836	ctc Leu 841	aaa Lys 841	tca Ser 841	aag Lys 841	aaa Lys 841	gcc Ala 846	gac Asp 846	tac Tyr 846	aga Arg 846	tac Tyr 846	2724
aca Thr 847	tat Tyr 847	gat Asp 852	gag Glu 852	gct Ala 852	atc Ile 852	cac His 857	tct Ser 857	gtt Val 857	gct Ala 857	tgg Trp 857	cat His 862	cat His 862	gaa Glu 862	gga Gly 862	aaa Lys 862	2772
caa Gln 863	ttt Phe 863	att Ile 868	tgc Cys 868	agt Ser 868	cat His 868	tca Ser 873	gat Asp 873	ggc Gly 873	acc Thr 873	ttg Leu 873	act Thr 878	ata Ile 878	tgg Trp 878	aat Asn 878	gta Val 878	2820
agg Arg 879	tcc Ser 884	cct Pro 884	gct Ala 884	aaa Lys 884	cca Pro 884	gta Val 889	cag Gln 889	aca Thr 889	atc Ile 889	act Thr 889	cca Pro 894	cat His 894	gga Gly 894	aaa Lys 894	cag Gln 894	2868
tta Leu 895	aag Lys 895	gat Asp 900	ggg Gly 900	aag Lys 900	aag Lys 900	cca Pro 905	gaa Glu 905	cca Pro 905	tgc Cys 905	aaa Lys 905	cct Pro 910	atc Ile 910	ctc Leu 910	aag Lys 910	gtg Val 910	2916
gaa Glu 911	ttc Phe 911	aaa Lys 916	acg Thr 916	act Thr 916	aga Arg 916	tct Ser 921	ggg Gly 921	gag Glu 921	cct Pro 921	ttt Phe 921	att Ile 926	att Ile 926	tta Leu 926	tca Ser 926	gga Gly 926	2964
ggt Gly 927	ttg Leu 927	tca Ser 932	tat Tyr 932	gat Asp 932	act Thr 932	gta Val 937	gga Gly 937	aga Arg 937	aga Arg 937	cct Pro 937	tgc Cys 942	tta Leu 942	aca Thr 942	gtg Val 942	atg Met 942	3012
cat His 943	ggg Gly 943	aaa Lys 948	agc Ser 948	act Thr 948	gct Ala 948	gtg Val 953	cta Leu 953	gaa Glu 953	atg Met 953	gac Asp 953	tat Tyr 958	tca Ser 958	att Ile 958	gtt Val 958	gat Asp 958	3060
ttt Phe 959	cta Leu 959	acg Thr 964	ctg Leu 964	tgt Cys 964	gaa Glu 964	aca Thr 969	cca Pro 969	tac Tyr 969	cca Pro 969	aat Asn 969	gat Asp 974	ttt Phe 974	caa Gln 974	gaa Glu 974	cca Pro 974	3108

tat gct gtg gtt gtt ctt cta gaa aag gat tta gta ctt ata gac ctt 3156
Tyr Ala Val Val Val Leu Leu Glu Lys Asp Leu Val Leu Ile Asp Leu
975 980 985 990

gca caa aat gga tat cct ata ttt gaa atc cct acc ctt tga gtaacat 3205
Ala Gln Asn Gly Tyr Pro Ile Phe Glu Ile Pro Thr Leu *
991 996 1001

gagactgtat tag 3218

<210> 42
<211> 5355
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (53)..(5302)

<400> 42
ccgttcgga attcccgggt cgacgatttc gtctgaaaga caggtgtgcg tc atg 55
Met
1

cac ttg aag cac ctg agg acc ctg ctg agc cct cag gat gga gct gca 103
His Leu Lys His Leu Arg Thr Leu Leu Ser Pro Gln Asp Gly Ala Ala
2 7 12 17

aag gtg acc tgc atg gct tgg tcc cag aac aat gcc aaa ttt gct gtc 151
Lys Val Thr Cys Met Ala Trp Ser Gln Asn Asn Ala Lys Phe Ala Val
18 23 28 33

tgc aca gtg gac cga gtg gtc ttg ctg tat gat gaa cat gga gaa cgg 199
Cys Thr Val Asp Arg Val Val Leu Leu Tyr Asp Glu His Gly Glu Arg
34 39 44 49

aga gat aaa ttc tcc acc aaa cca gct gac atg aag tat ggc agg aag 247
Arg Asp Lys Phe Ser Thr Lys Pro Ala Asp Met Lys Tyr Gly Arg Lys
50 55 60 65

agc tat atg gtg aag ggc atg gct ttt tct cct gat tcc act aaa att 295
Ser Tyr Met Val Lys Gly Met Ala Phe Ser Pro Asp Ser Thr Lys Ile
66 71 76 81

gcc ata gga cag act gac aac atc atc tat gtc tac aag att gga gaa 343
Ala Ile Gly Gln Thr Asp Asn Ile Ile Tyr Val Tyr Lys Ile Gly Glu
82 87 92 97

gat tgg ggt gac aag aaa gtc atc tgc aac aag ttc atc cag acg agt 391
Asp Trp Gly Asp Lys Lys Val Ile Cys Asn Lys Phe Ile Gln Thr Ser
98 103 108 113

gct gtc act tgt ctg caa tgg ccg gca gaa tac atc att gtc ttt gga 439
Ala Val Thr Cys Leu Gln Trp Pro Ala Glu Tyr Ile Ile Val Phe Gly

114	119	124	129	
ctg gct gaa ggg aag gtt cgt tta gca aac acc aaa act aat aaa tca				487
Leu Ala Glu Gly Lys Val Arg Leu Ala Asn Thr Lys Thr Asn Lys Ser				
130	135	140	145	
tct acc atc tat ggg aca gag tct tac gtg gtg tcc ctg aca aca aat				535
Ser Thr Ile Tyr Gly Thr Glu Ser Tyr Val Val Ser Leu Thr Thr Asn				
146	151	156	161	
tgc tct ggg aaa gga att ctc tct ggt cat gca gat ggt acc atc gtt				583
Cys Ser Gly Lys Gly Ile Leu Ser Gly His Ala Asp Gly Thr Ile Val				
162	167	172	177	
agg tat ttc ttt gat gat gaa ggc tct gga gag tca cag gag aag ttg				631
Arg Tyr Phe Phe Asp Asp Glu Gly Ser Gly Glu Ser Gln Glu Lys Leu				
178	183	188	193	
gtt aac cac ccg tgt cca ccc tat gcc ttg gca tgg gca acc aat agc				679
Val Asn His Pro Cys Pro Pro Tyr Ala Leu Ala Trp Ala Thr Asn Ser				
194	199	204	209	
atc gtg gct gca ggc tgt gat cgg aaa att gta gcc tat gga aaa gaa				727
Ile Val Ala Ala Gly Cys Asp Arg Lys Ile Val Ala Tyr Gly Lys Glu				
210	215	220	225	
ggg cac atg cta caa act ttt gat tat agc cgt gac cct cag gag cgg				775
Gly His Met Leu Gln Thr Phe Asp Tyr Ser Arg Asp Pro Gln Glu Arg				
226	231	236	241	
gag ttc acc aca gct gta tca agt cct ggg ggc cag tct gtt gtg cta				823
Glu Phe Thr Thr Ala Val Ser Ser Pro Gly Gly Gln Ser Val Val Leu				
242	247	252	257	
gga agt tat gac agg ctt cgg gtg ttc aac tgg atc cct cga aga agc				871
Gly Ser Tyr Asp Arg Leu Arg Val Phe Asn Trp Ile Pro Arg Arg Ser				
258	263	268	273	
atc tgg gaa gag gca aag ccc aag gag att acc aat tta tac acc atc				919
Ile Trp Glu Glu Ala Lys Pro Lys Glu Ile Thr Asn Leu Tyr Thr Ile				
274	279	284	289	
act gcc ttg gcc tgg aag cgg gat ggc tca cgg ctc tgt gtg ggc aca				967
Thr Ala Leu Ala Trp Lys Arg Asp Gly Ser Arg Leu Cys Val Gly Thr				
290	295	300	305	
cta tgt ggt ggg gtg gaa cag ttt gac tgc tgc ctc cga agg agt att				1015
Leu Cys Gly Gly Val Glu Gln Phe Asp Cys Cys Leu Arg Arg Ser Ile				
306	311	316	321	
tac aag aac aag ttt gag ttg acg tat gtg gga cct agc cag gtg att				1063
Tyr Lys Asn Lys Phe Glu Leu Thr Tyr Val Gly Pro Ser Gln Val Ile				
322	327	332	337	
gtg aag aac ctg tca tca gga acc cga gtg gtg ctc aag tca cac tat				1111
Val Lys Asn Leu Ser Ser Gly Thr Arg Val Val Leu Lys Ser His Tyr				
338	343	348	353	

ggc Gly 354	tat Tyr	gag Glu	gtg Val	gaa Glu	gag Glu 359	gtg Val	aaa Lys	atc Ile	cta Leu	gga Gly 364	aag Lys	gaa Glu	cgt Arg	tac Tyr	ttg Leu 369	1159
gtg Val 370	gct Ala	cac His	aca Thr	tca Ser	gaa Glu 375	aca Thr	ctg Leu	ctg Leu	ctg Leu	ggg Gly 380	gac Asp	ctg Leu	aac Asn	act Thr	aat Asn 385	1207
cgg Arg 386	ctt Leu	agt Ser	gag Glu	ata Ile	gcc Ala 391	tgg Trp	caa Gln	gga Gly	tct Ser	ggg Gly 396	ggc Gly	aat Asn	gag Glu	aag Lys	tat Tyr 401	1255
ttc Phe 402	ttt Phe	gaa Glu	aat Asn	gag Glu	aat Asn 407	gta Val	tgc Cys	atg Met	atc Ile	ttc Phe 412	aat Asn	gcc Ala	gga Gly	gag Glu	cta Leu 417	1303
acc Thr 418	ctg Leu	gtg Val	gaa Glu	tat Tyr	ggg Gly 423	aat Asn	aat Asn	gac Asp	acc Thr	ctg Leu 428	ggg Gly	tct Ser	gta Val	cgc Arg	act Thr 433	1351
gaa Glu 434	ttc Phe	atg Met	aac Asn	ccc Pro	cac His 439	ctc Leu	atc Ile	agt Ser	gtt Val	cgt Arg 444	att Ile	aat Asn	gag Glu	agg Arg	tgt Cys 449	1399
cag Gln 450	cga Arg	gga Gly	aca Thr	gaa Glu	gat Asp 455	aat Asn	aag Lys	aaa Lys	ttg Leu	gct Ala 460	tat Tyr	ctt Leu	att Ile	gat Asp	att Ile 465	1447
aag Lys 466	act Thr	att Ile	gct Ala	ata Ile	gtg Val 471	gat Asp	ctg Leu	att Ile	ggg Gly	ggc Gly 476	tac Tyr	aac Asn	att Ile	ggc Gly	acc Thr 481	1495
gtc Val 482	agc Ser	cat His	gag Glu	agc Ser	cgt Arg 487	gtg Val	gat Asp	tgg Trp	ctg Leu	gaa Glu 492	ctt Leu	aat Asn	gag Glu	act Thr	gga Gly 497	1543
cac His 498	aag Lys	ctc Leu	ctc Leu	ttc Phe	agg Arg 503	gac Asp	cgg Arg	aaa Lys	ctt Leu	cgt Arg 508	ttg Leu	cat His	ctg Leu	tat Tyr	gat Asp 513	1591
att Ile 514	gaa Glu	agc Ser	tgc Cys	tct Ser	aag Lys 519	aca Thr	atg Met	atc Ile	ctc Leu	aac Asn 524	ttc Phe	tgc Cys	tcc Ser	tat Tyr	atg Met 529	1639
cag Gln 530	tgg Trp	gtc Val	cca Pro	gga Gly	agt Ser 535	gac Asp	gtg Val	ctg Leu	gta Val	gct Ala 540	cag Gln	aac Asn	cga Arg	aac Asn	agt Ser 545	1687
ctg Leu 546	tgt Cys	gta Val	tgg Trp	tac Tyr	aac Asn 551	att Ile	gag Glu	gca Ala	cct Pro	gag Glu 556	aga Arg	gtc Val	acc Thr	atg Met	ttc Phe 561	1735
act Thr 562	att Ile	agg Arg	ggg Gly	gat Asp	gtt Val 567	ata Ile	ggg Gly	ctg Leu	gag Glu	cgg Arg 572	ggc Gly	ggg Gly	gga Gly	aag Lys	acc Thr 577	1783

gag gtg atg gtg atg gaa ggt gtg act act gtt gcc tac aca ttg gat	1831
Glu Val Met Val Met Glu Gly Val Thr Thr Val Ala Tyr Thr Leu Asp	
578 583 588 593	
gag ggc ctc atc gag ttt gga aca gcc att gat gat ggc aac tac atc	1879
Glu Gly Leu Ile Glu Phe Gly Thr Ala Ile Asp Asp Gly Asn Tyr Ile	
594 599 604 609	
cgg gca aca gcc ttc tta gag act ctg gaa atg acc cca gaa aca gag	1927
Arg Ala Thr Ala Phe Leu Glu Thr Leu Glu Met Thr Pro Glu Thr Glu	
610 615 620 625	
gca atg tgg aaa acc ttg agt aaa ctg gca cta gag gca agg caa cta	1975
Ala Met Trp Lys Thr Leu Ser Lys Leu Ala Leu Glu Ala Arg Gln Leu	
626 631 636 641	
cac att gcg gag agg tgc ttt tct gct ttg ggc caa gta gca aaa gct	2023
His Ile Ala Glu Arg Cys Phe Ser Ala Leu Gly Gln Val Ala Lys Ala	
642 647 652 657	
cga ttc ctg cat gag acc aat gag att gca gat caa gta tcc cgg gaa	2071
Arg Phe Leu His Glu Thr Asn Glu Ile Ala Asp Gln Val Ser Arg Glu	
658 663 668 673	
tat ggc gga gaa gga aca gac ttt tat cag gtc cga gca cgt cta gcc	2119
Tyr Gly Gly Glu Gly Thr Asp Phe Tyr Gln Val Arg Ala Arg Leu Ala	
674 679 684 689	
atg ctg gaa aag aac tac aaa ctg gct gaa atg atc ttt ttg gaa cag	2167
Met Leu Glu Lys Asn Tyr Lys Leu Ala Glu Met Ile Phe Leu Glu Gln	
690 695 700 705	
aat gct gtg gag gag gcc atg ggc atg tac cag gag cta cac cgt tgg	2215
Asn Ala Val Glu Glu Ala Met Gly Met Tyr Gln Glu Leu His Arg Trp	
706 711 716 721	
gat gag tgt atc gct gtg gct gaa gcc aag ggg cac cca gcc ctg gag	2263
Asp Glu Cys Ile Ala Val Ala Glu Ala Lys Gly His Pro Ala Leu Glu	
722 727 732 737	
aag cta cgt cgt agt tac tac cag tgg ctg atg gac aca cag caa gag	2311
Lys Leu Arg Arg Ser Tyr Tyr Gln Trp Leu Met Asp Thr Gln Gln Glu	
738 743 748 753	
gag cga gca ggt gaa cta cag gag agc caa ggg gat ggg cta gca gcc	2359
Glu Arg Ala Gly Glu Leu Gln Glu Ser Gln Gly Asp Gly Leu Ala Ala	
754 759 764 769	
atc agc ctc tac ctc aaa gct ggg ctc cct gcc aaa gct gct cgg ctg	2407
Ile Ser Leu Tyr Leu Lys Ala Gly Leu Pro Ala Lys Ala Ala Arg Leu	
770 775 780 785	
gtg ctg acc cga gag gaa ctg cta gcc aac aca gag ctg gta gaa cac	2455
Val Leu Thr Arg Glu Glu Leu Leu Ala Asn Thr Glu Leu Val Glu His	
786 791 796 801	
atc act gca gcc ctt atc aag ggg gaa ctc tac gaa agg gca ggt gat	2503

Ile Thr Ala Ala Leu Ile Lys Gly Glu Leu Tyr Glu Arg Ala Gly Asp 802 807 812 817	
ctc ttt gag aag att cac aat cca cag aag gcc ctg gag tgc tac cgt Leu Phe Glu Lys Ile His Asn Pro Gln Lys Ala Leu Glu Cys Tyr Arg 818 823 828 833	2551
aaa ggc aac gca ttc atg aaa gcg gta gag ctg gct cga ttg gcc ttc Lys Gly Asn Ala Phe Met Lys Ala Val Glu Leu Ala Arg Leu Ala Phe 834 839 844 849	2599
cca gtg gag gtg gtg aaa cta gag gag gca tgg ggg gac cac ctg gtg Pro Val Glu Val Val Lys Leu Glu Glu Ala Trp Gly Asp His Leu Val 850 855 860 865	2647
cag cag aag cag ctt gat gca gcc att aat cac tac atc gaa gcc agg Gln Gln Lys Gln Leu Asp Ala Ala Ile Asn His Tyr Ile Glu Ala Arg 866 871 876 881	2695
tgc tcc att aag gca att gag gcc gcc ctg ggt gcc cgc cag tgg aag Cys Ser Ile Lys Ala Ile Glu Ala Ala Leu Gly Ala Arg Gln Trp Lys 882 887 892 897	2743
aag gca att tat ata tta gat cta cag gac cgg aac act gca tcc aaa Lys Ala Ile Tyr Ile Leu Asp Leu Gln Asp Arg Asn Thr Ala Ser Lys 898 903 908 913	2791
tac tat cct ctc gtg gcc caa cac tat gca tcc ctg cag gag tat gag Tyr Tyr Pro Leu Val Ala Gln His Tyr Ala Ser Leu Gln Glu Tyr Glu 914 919 924 929	2839
att gct gag gag ctc tat act aag gga gat cgg aca aaa gat gcc ata Ile Ala Glu Glu Leu Tyr Thr Lys Gly Asp Arg Thr Lys Asp Ala Ile 930 935 940 945	2887
gac atg tac acc cag gct ggt cgt tgg gaa caa gcc cac aag ctg gcg Asp Met Tyr Thr Gln Ala Gly Arg Trp Glu Gln Ala His Lys Leu Ala 946 951 956 961	2935
atg aaa tgc atg aga cca gaa gat gtg tca gtg cta tac atc act cag Met Lys Cys Met Arg Pro Glu Asp Val Ser Val Leu Tyr Ile Thr Gln 962 967 972 977	2983
gcc cag gaa atg gag aag cag ggc aag tac cgt gag gct gaa agg cta Ala Gln Glu Met Glu Lys Gln Gly Lys Tyr Arg Glu Ala Glu Arg Leu 978 983 988 993	3031
tat gtg aca gta caa gag cct gat ctt gcc atc acc atg tac aaa aag Tyr Val Thr Val Gln Glu Pro Asp Leu Ala Ile Thr Met Tyr Lys Lys 994 999 1004 1009	3079
cac aag ttg tat gat gac atg atc cgc ctg gta ggg aag cac cat cca His Lys Leu Tyr Asp Asp Met Ile Arg Leu Val Gly Lys His His Pro 1010 1015 1020 1025	3127
gat ctc ctc agt gat aca cac cta cat ctg ggc aag gag ctg gag gct Asp Leu Leu Ser Asp Thr His Leu His Leu Gly Lys Glu Leu Glu Ala 3175	

1026	1031	1036	1041	
gaa ggc cga cta cag gag gct gag tac cac tac ctc gag gcc cag gaa				3223
Glu Gly Arg Leu Gln Glu Ala Glu Tyr His Tyr Leu Glu Ala Gln Glu				
1042	1047	1052	1057	
tgg aag gca aca gtg aac atg tac cgg gcc agt ggg ctt tgg gaa gag				3271
Trp Lys Ala Thr Val Asn Met Tyr Arg Ala Ser Gly Leu Trp Glu Glu				
1058	1063	1068	1073	
gcc tac agg gtg gcc aga act caa gga ggg gct aat gcc cac aaa cac				3319
Ala Tyr Arg Val Ala Arg Thr Gln Gly Gly Ala Asn Ala His Lys His				
1074	1079	1084	1089	
gtg gcc tat ctg tgg gca aag agc ctg gga gga gag gct gca gtt aga				3367
Val Ala Tyr Leu Trp Ala Lys Ser Leu Gly Gly Glu Ala Ala Val Arg				
1090	1095	1100	1105	
ctg ctt aat aag ctg gga ctc ctg gaa gct gct gtt gac cac gct gca				3415
Leu Leu Asn Lys Leu Gly Leu Leu Glu Ala Ala Val Asp His Ala Ala				
1106	1111	1116	1121	
gac aat tgc tcc ttt gaa ttt gcg ttt gaa ctc tct cgg ctg gcc ctc				3463
Asp Asn Cys Ser Phe Glu Phe Ala Phe Glu Leu Ser Arg Leu Ala Leu				
1122	1127	1132	1137	
aag cac aaa acc ccc gag gtt cat ctc aaa tat gct atg ttc ctg gag				3511
Lys His Lys Thr Pro Glu Val His Leu Lys Tyr Ala Met Phe Leu Glu				
1138	1143	1148	1153	
gat gag ggt aaa ttc gaa gag gct gaa gct gaa ttc atc aga gct ggt				3559
Asp Glu Gly Lys Phe Glu Glu Ala Glu Ala Glu Phe Ile Arg Ala Gly				
1154	1159	1164	1169	
aaa ccc aag gag gca gtc ctc atg ttt gtc cat aac cag gat tgg gag				3607
Lys Pro Lys Glu Ala Val Leu Met Phe Val His Asn Gln Asp Trp Glu				
1170	1175	1180	1185	
gca gct cag cgt gtg gct gag gct cac gac cct gac agt gtc gcc gag				3655
Ala Ala Gln Arg Val Ala Glu Ala His Asp Pro Asp Ser Val Ala Glu				
1186	1191	1196	1201	
gtg ctt gtg gga cag gcc cgg ggg gcc ttg gag gag aag gac ttt cag				3703
Val Leu Val Gly Gln Ala Arg Gly Ala Leu Glu Glu Lys Asp Phe Gln				
1202	1207	1212	1217	
aaa gca gaa ggg ctg ctg ctc cgg gcc cag aga cca ggc ctg gcc ctc				3751
Lys Ala Glu Gly Leu Leu Leu Arg Ala Gln Arg Pro Gly Leu Ala Leu				
1218	1223	1228	1233	
aat tat tat aag gag gct gga tta tgg agt gac gct ctg cgc atc tgc				3799
Asn Tyr Tyr Lys Glu Ala Gly Leu Trp Ser Asp Ala Leu Arg Ile Cys				
1234	1239	1244	1249	
aag gac tat gtg ccc agc cag ctg gag gct ctg cag gaa gaa tat gag				3847
Lys Asp Tyr Val Pro Ser Gln Leu Glu Ala Leu Gln Glu Glu Tyr Glu				
1250	1255	1260	1265	

cgg gaa gct act aag aag ggg gcc agg ggt gtg gag gga ttt gtg gaa	3895
Arg Glu Ala Thr Lys Lys Gly Ala Arg Gly Val Glu Gly Phe Val Glu	
1266 1271 1276 1281	
caa gct cga cac tgg gag cag gct gga gag tac agc cgt gcc gtg gac	3943
Gln Ala Arg His Trp Glu Gln Ala Gly Glu Tyr Ser Arg Ala Val Asp	
1282 1287 1292 1297	
tgc tac ctc aaa gtg cga gac tct gga aac agc ggc ctg gcg gag aag	3991
Cys Tyr Leu Lys Val Arg Asp Ser Gly Asn Ser Gly Leu Ala Glu Lys	
1298 1303 1308 1313	
tgc tgg atg aag gca gct gaa ctc tcc atc aag ttt ctg cct ccc caa	4039
Cys Trp Met Lys Ala Ala Glu Leu Ser Ile Lys Phe Leu Pro Pro Gln	
1314 1319 1324 1329	
cgt aat atg gaa gtc gtt ctg gct gta gga ccc cag ctg att gga att	4087
Arg Asn Met Glu Val Val Leu Ala Val Gly Pro Gln Leu Ile Gly Ile	
1330 1335 1340 1345	
gga aag cac agt gca gct gca gag ctc tat ctg aat ctg gac ctt gtc	4135
Gly Lys His Ser Ala Ala Ala Glu Leu Tyr Leu Asn Leu Asp Leu Val	
1346 1351 1356 1361	
aag gaa gca atc gat gct ttc atc gag ggt gag gag tgg aac aag gcg	4183
Lys Glu Ala Ile Asp Ala Phe Ile Glu Gly Glu Glu Trp Asn Lys Ala	
1362 1367 1372 1377	
aag cgt gta gct aag gag tta gat ccc agg tat gaa gac tat gtg gac	4231
Lys Arg Val Ala Lys Glu Leu Asp Pro Arg Tyr Glu Asp Tyr Val Asp	
1378 1383 1388 1393	
cag cat tat aaa gag ttc ctc aag aat cag ggc aaa gtg gac tcg ctg	4279
Gln His Tyr Lys Glu Phe Leu Lys Asn Gln Gly Lys Val Asp Ser Leu	
1394 1399 1404 1409	
gtg ggt gtg gat gtg ata gct gct ttg gac ctg tat gtg gag cag ggc	4327
Val Gly Val Asp Val Ile Ala Ala Leu Asp Leu Tyr Val Glu Gln Gly	
1410 1415 1420 1425	
cag tgg gac aag tgc att gaa aca gct acc aag cag aac tac aag att	4375
Gln Trp Asp Lys Cys Ile Glu Thr Ala Thr Lys Gln Asn Tyr Lys Ile	
1426 1431 1436 1441	
ctg cac aag tat gtg gct ttg tat gca act cac ttg atc cgg gag ggt	4423
Leu His Lys Tyr Val Ala Leu Tyr Ala Thr His Leu Ile Arg Glu Gly	
1442 1447 1452 1457	
agc tct gcc cag gca ttg gcc ctg tat gta cag cac gga gcc cct gct	4471
Ser Ser Ala Gln Ala Leu Ala Leu Tyr Val Gln His Gly Ala Pro Ala	
1458 1463 1468 1473	
aac cca cag aac ttc aat atc tac aaa agg atc ttc act gac atg gtg	4519
Asn Pro Gln Asn Phe Asn Ile Tyr Lys Arg Ile Phe Thr Asp Met Val	
1474 1479 1484 1489	

agc tct cct gga acc aac tgt gcc gag gcc tat cat agc tgg gct gat	4567
Ser Ser Pro Gly Thr Asn Cys Ala Glu Ala Tyr His Ser Trp Ala Asp	
1490 1495 1500 1505	
ctt cga gat gtc ctc ttc aac ctg tgt gaa aac ctg gtg aag tcc agt	4615
Leu Arg Asp Val Leu Phe Asn Leu Cys Glu Asn Leu Val Lys Ser Ser	
1506 1511 1516 1521	
gag gca aac tct cca gcc cat gag gag ttc aag acg atg ctg ctg atc	4663
Glu Ala Asn Ser Pro Ala His Glu Glu Phe Lys Thr Met Leu Leu Ile	
1522 1527 1532 1537	
gct cat tac tat gcc acg cgc tct gca gcc cag agt gtc aaa cag ctg	4711
Ala His Tyr Tyr Ala Thr Arg Ser Ala Ala Gln Ser Val Lys Gln Leu	
1538 1543 1548 1553	
gaa acc gtg gct gcc agg ctt tct gtt tca ctc ttg cgt cac acc cag	4759
Glu Thr Val Ala Ala Arg Leu Ser Val Ser Leu Leu Arg His Thr Gln	
1554 1559 1564 1569	
cta cta cct gta gac aaa gcc ttc tat gaa gca ggc att gct gcc aag	4807
Leu Leu Pro Val Asp Lys Ala Phe Tyr Glu Ala Gly Ile Ala Ala Lys	
1570 1575 1580 1585	
gca gtt ggc tgg gat aac atg gca ttc atc ttc ctc aat cgc ttt ttg	4855
Ala Val Gly Trp Asp Asn Met Ala Phe Ile Phe Leu Asn Arg Phe Leu	
1586 1591 1596 1601	
gac ctg acc gat gca atc gag gaa ggg act cta gat ggc ctt gac cac	4903
Asp Leu Thr Asp Ala Ile Glu Glu Gly Thr Leu Asp Gly Leu Asp His	
1602 1607 1612 1617	
tct gat ttt cag gat aca gac att ccc ttt gag gtg cca ctc cca gct	4951
Ser Asp Phe Gln Asp Thr Asp Ile Pro Phe Glu Val Pro Leu Pro Ala	
1618 1623 1628 1633	
aag cag cat gta ccg gag gct gag aga gaa gag gtt cga gac tgg gtg	4999
Lys Gln His Val Pro Glu Ala Glu Arg Glu Glu Val Arg Asp Trp Val	
1634 1639 1644 1649	
ctt aca gtc tcc atg gac cag cgg ctg gag cag gtt ctg cct cgg gat	5047
Leu Thr Val Ser Met Asp Gln Arg Leu Glu Gln Val Leu Pro Arg Asp	
1650 1655 1660 1665	
gag cgt ggc gcc tac gag gcc tcc cta gtg gca gcg agc act ggt gtt	5095
Glu Arg Gly Ala Tyr Glu Ala Ser Leu Val Ala Ala Ser Thr Gly Val	
1666 1671 1676 1681	
cga gcc ctg ccc tgc ctt att aca gga tac ccc att ctg agg aac aaa	5143
Arg Ala Leu Pro Cys Leu Ile Thr Gly Tyr Pro Ile Leu Arg Asn Lys	
1682 1687 1692 1697	
att gaa ttt aag cgg cca ggg aag gct gct aac aag gac aac tgg aat	5191
Ile Glu Phe Lys Arg Pro Gly Lys Ala Ala Asn Lys Asp Asn Trp Asn	
1698 1703 1708 1713	
aaa ttc ctt atg gcc atc aag acc tcc cac agc cca gtg tgc cag gac	5239


```

Lys Phe Leu Met Ala Ile Lys Thr Ser His Ser Pro Val Cys Gln Asp
1714                      1719                      1724                      1729

gtg ctg aaa ttc atc agt cag tgg tgt gga ggg ctc ccc agc acc agc      5287
Val Leu Lys Phe Ile Ser Gln Trp Cys Gly Gly Leu Pro Ser Thr Ser
1730                      1735                      1740                      1745

ttt tcc ttt cag tag ttggtagagc tgaggaagag ttagggcctc tccctcatta      5342
Phe Ser Phe Gln  *
1746

aagttttata aat                                                    5355

```

```

<210> 43
<211> 2660
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (40)..(2334)

```

```

<400> 43
gagatcccc gagacctcac gctggatgcc ctgctggag      atg aat gag gcc aag      54
                                   Met Asn Glu Ala Lys
                                   1

gtg aag gag acg ctg cgg cgc tgt ggg gcc agc ggg gat gag tgt ggc      102
Val Lys Glu Thr Leu Arg Arg Cys Gly Ala Ser Gly Asp Glu Cys Gly
  6                      11                      16                      21

cgt ctg cag tat gcc ctc acc tgc ctg cgg aag gtg aca ggc ctg gga      150
Arg Leu Gln Tyr Ala Leu Thr Cys Leu Arg Lys Val Thr Gly Leu Gly
  22                      27                      32                      37

ggg gag cac aag gag gac tcc agt tgg agt tca ttg gat gcg cgg cgg      198
Gly Glu His Lys Glu Asp Ser Ser Trp Ser Ser Leu Asp Ala Arg Arg
  38                      43                      48                      53

gaa agt ggc tca ggg cct tcc acg gac acc ctc tca gca gcc agc ctg      246
Glu Ser Gly Ser Gly Pro Ser Thr Asp Thr Leu Ser Ala Ala Ser Leu
  54                      59                      64                      69

ccc tgg ccc cca ggg agc tcc cag ctg ggc aga gca ggc aac agc gcc      294
Pro Trp Pro Pro Gly Ser Ser Gln Leu Gly Arg Ala Gly Asn Ser Ala
  70                      75                      80                      85

cag ggc cca cgc tcc atc tcc gtg tca gct ctg ccc gcc tca gac tcc      342
Gln Gly Pro Arg Ser Ile Ser Val Ser Ala Leu Pro Ala Ser Asp Ser
  86                      91                      96                      101

ccc acc ccc agc ttc agt gag ggc ctc tca gac acc tgt att ccc ctg      390
Pro Thr Pro Ser Phe Ser Glu Gly Leu Ser Asp Thr Cys Ile Pro Leu
  102                      107                      112                      117

```

cac His 118	gcc Ala	agc Ser	ggc Gly	cgg Arg	ctg Leu 123	acc Thr	ccc Pro	cgt Arg	gcc Ala	ctg Leu 128	cac His	agc Ser	ttc Phe	atc Ile	acc Thr 133	438
ccg Pro 134	ccc Pro	acc Thr	aca Thr	ccc Pro	cag Gln 139	ctg Leu	cga Arg	cgg Arg	cac His	acc Thr 144	aag Lys	ctg Leu	aag Lys	cca Pro	cca Pro 149	486
cgg Arg 150	acg Thr	ccc Pro	ccc Pro	cca Pro	ccc Pro 155	agc Ser	cgc Arg	aag Lys	gtc Val	ttc Phe 160	cag Gln	ctg Leu	ctg Leu	ccc Pro	agc Ser 165	534
ttc Phe 166	ccc Pro	aca Thr	ctc Leu	acc Thr	cgg Arg 171	agc Ser	aag Lys	tcc Ser	cat His	gag Glu 176	tct Ser	cag Gln	ctg Leu	ggg Gly	aac Asn 181	582
cgc Arg 182	att Ile	gat Asp	gac Asp	gtc Val	tcc Ser 187	tcg Ser	atg Met	agg Arg	ttt Phe	gat Asp 192	ctc Leu	tcg Ser	cat His	gga Gly	tcc Ser 197	630
cca Pro 198	cag Gln	atg Met	gta Val	cgg Arg	agg Arg 203	gat Asp	atc Ile	ggg Gly	ctg Leu	tcg Ser 208	gtg Val	acg Thr	cac His	agg Arg	ttc Phe 213	678
tcc Ser 214	acc Thr	aag Lys	tcc Ser	tgg Trp	ctg Leu 219	tcg Ser	cag Gln	gtc Val	tgc Cys	cac His 224	gtg Val	tgc Cys	cag Gln	aag Lys	agc Ser 229	726
atg Met 230	ata Ile	ttt Phe	gga Gly	gtg Val	aag Lys 235	tgc Cys	aag Lys	cat His	tgc Cys	agg Arg 240	ttg Leu	aag Lys	tgt Cys	cac His	aac Asn 245	774
aaa Lys 246	tgt Cys	acc Thr	aaa Lys	gaa Glu	gcc Ala 251	cct Pro	gcc Ala	tgt Cys	aga Arg	ata Ile 256	tcc Ser	ttc Phe	ctg Leu	cca Pro	cta Leu 261	822
act Thr 262	cgg Arg	ctt Leu	cgg Arg	agg Arg	aca Thr 267	gaa Glu	tct Ser	gtc Val	ccc Pro	tcg Ser 272	gac Asp	atc Ile	aac Asn	aac Asn	ccg Pro 277	870
gtg Val 278	gac Asp	aga Arg	gca Ala	gcc Ala	gaa Glu 283	ccc Pro	cat His	ttt Phe	gga Gly	acc Thr 288	ctc Leu	ccc Pro	aaa Lys	gca Ala	ctg Leu 293	918
aca Thr 294	aag Lys	aag Lys	gag Glu	cac His	cct Pro 299	ccg Pro	gcc Ala	atg Met	aat Asn	cac His 304	ctg Leu	gac Asp	tcc Ser	agc Ser	agc Ser 309	966
aac Asn 310	cct Pro	tcc Ser	tcc Ser	acc Thr	acc Thr 315	tcc Ser	tcc Ser	aca Thr	ccc Pro	tcc Ser 320	tca Ser	ccg Pro	gcg Ala	ccc Pro	ttc Phe 325	1014
ccg Pro 326	aca Thr	tca Ser	tcc Ser	aac Asn	cca Pro 331	tcc Ser	agc Ser	gcc Ala	acc Thr	acg Thr 336	ccc Pro	ccc Pro	aac Asn	ccc Pro	tca Ser 341	1062

His Ala Lys Gly Ile Val His Lys Asp Leu Lys Ser Lys Asn Val Phe	
566	571 576 581
tat gac aac ggc aag gtg gtc atc aca gac ttc ggg ctg ttt ggg atc	1830
Tyr Asp Asn Gly Lys Val Val Ile Thr Asp Phe Gly Leu Phe Gly Ile	
582	587 592 597
tca ggc gtg gtc cga gag gga cgg cgt gag aac cag cta aag ctg tcc	1878
Ser Gly Val Val Arg Glu Gly Arg Arg Glu Asn Gln Leu Lys Leu Ser	
598	603 608 613
cac gac tgg ctg tgc tat ctg gcc cct gag att gta cgc gag atg acc	1926
His Asp Trp Leu Cys Tyr Leu Ala Pro Glu Ile Val Arg Glu Met Thr	
614	619 624 629
ccc ggg aag gac gag gat cag ctg cca ttc tcc aaa gct gct gat gtc	1974
Pro Gly Lys Asp Glu Asp Gln Leu Pro Phe Ser Lys Ala Ala Asp Val	
630	635 640 645
tat gca ttt ggg act gtt tgg tat gag ctg caa gca aga gac tgg ccc	2022
Tyr Ala Phe Gly Thr Val Trp Tyr Glu Leu Gln Ala Arg Asp Trp Pro	
646	651 656 661
ttg aag aac cag gct gca gag gca tcc atc tgg cag att gga agc ggg	2070
Leu Lys Asn Gln Ala Ala Glu Ala Ser Ile Trp Gln Ile Gly Ser Gly	
662	667 672 677
gaa gga atg aag cgt gtc ctg act tct gtc agc ttg ggg aag gaa gtc	2118
Glu Gly Met Lys Arg Val Leu Thr Ser Val Ser Leu Gly Lys Glu Val	
678	683 688 693
agt gag atc ctg tcg gcc tgc tgg gct ttc gac ctg cag gag aga ccc	2166
Ser Glu Ile Leu Ser Ala Cys Trp Ala Phe Asp Leu Gln Glu Arg Pro	
694	699 704 709
agc ttc agc ctg ctg atg gac atg ctg gag aaa ctt ccc aag ctg aac	2214
Ser Phe Ser Leu Leu Met Asp Met Leu Glu Lys Leu Pro Lys Leu Asn	
710	715 720 725
cgg cgg ctc tcc cac cct gga cac ttc tgg aag tca gct gac att aac	2262
Arg Arg Leu Ser His Pro Gly His Phe Trp Lys Ser Ala Asp Ile Asn	
726	731 736 741
agc agc aaa gtt gta ccc cgg ttt gaa agg ttt ggc ttg ggc gtc ctg	2310
Ser Ser Lys Val Val Pro Arg Phe Glu Arg Phe Gly Leu Gly Val Leu	
742	747 752 757
gag tcc agt aat cca aag atg tag ccagccatat ggtttttcgc tgctgatctc	2364
Glu Ser Ser Asn Pro Lys Met *	
758	763
ttttttttta aaatgtgttt ctgaaacatc ccaacaacca ccacgacaaa aaaacactgc	2424
ctgcccagcg ctgcaaacca ggagcacacg tcctagattc agactgttgg ccataaaccc	2484
cactcggggag atggagctgc acctgctatt tcttaaaatg acaccaccaa caaccaaacc	2544

130	135	140	145	
aag tcc caa gat gac gtc aag gat gca gct caa gca gca aga gat agt				597
Lys Ser Gln Asp Asp Val Lys Asp Ala Ala Gln Ala Ala Arg Asp Ser				
146	151	156	161	
aag ata aca tta ttt gct att ggt gtt ggt tca gaa aca gaa gat gcc				645
Lys Ile Thr Leu Phe Ala Ile Gly Val Gly Ser Glu Thr Glu Asp Ala				
162	167	172	177	
gaa ctt aga gct att gcc aac aag cct tcg tct act tat gtg ttt tat				693
Glu Leu Arg Ala Ile Ala Asn Lys Pro Ser Ser Thr Tyr Val Phe Tyr				
178	183	188	193	
gtg gaa gac tat att gca ata tcc aaa ata agg gaa gtg atg aag cag				741
Val Glu Asp Tyr Ile Ala Ile Ser Lys Ile Arg Glu Val Met Lys Gln				
194	199	204	209	
aaa ctt tgt gaa gaa tct gtc tgt cca aca cga att cca gtg gca gct				789
Lys Leu Cys Glu Glu Ser Val Cys Pro Thr Arg Ile Pro Val Ala Ala				
210	215	220	225	
cgt gat gaa agg gga ttt gat att ctt tta ggt tta gat gta aat aaa				837
Arg Asp Glu Arg Gly Phe Asp Ile Leu Leu Gly Leu Asp Val Asn Lys				
226	231	236	241	
aag gtt aag aaa aga ata cag ctt tca cca aaa aag ata aaa gga tat				885
Lys Val Lys Lys Arg Ile Gln Leu Ser Pro Lys Lys Ile Lys Gly Tyr				
242	247	252	257	
gaa gta aca tca aaa gtt gat tta tca gaa ctc aca agc aat gtt ttc				933
Glu Val Thr Ser Lys Val Asp Leu Ser Glu Leu Thr Ser Asn Val Phe				
258	263	268	273	
cca gaa ggt ctt cct cca tca tat gta ttt gtg tct act caa aga ttt				981
Pro Glu Gly Leu Pro Pro Ser Tyr Val Phe Val Ser Thr Gln Arg Phe				
274	279	284	289	
aaa gtc aag aaa att tgg gat tta tgg aga ata tta act att gat gga				1029
Lys Val Lys Lys Ile Trp Asp Leu Trp Arg Ile Leu Thr Ile Asp Gly				
290	295	300	305	
tgc cac aaa tag cag ttaccttaaa tgggtgtggac aaaatcttat tatttacaac				1084
Cys His Lys *				
306				
aaccagcgta attaatggct cacaagtggc tacctttgct aaccctcaag ttaagacgtt				1144
gtttgatgaa ggctggcacc aaattcgtct cttagtaaca gaacaagatg tgactttgta				1204
tattgatgac caacaaattg aaaacaagcc cttacatcca gtttttaggga tcttgatcaa				1264
tgggcaaacc caaattggaa aatattcttg aaaagaagaa actgttcagt ttgatgtcca				1324
aaagttgcga atctactgtg acccagaaca gaacaaccgg gagacagcat gtgagattcc				1384
tggattttgc cttaatgggc ccagtgatgt aggttcaact ccagctccct gtattttgtcc				1444

Asp Met Asn Leu Ser Ala Gln Asp His Gln Thr Phe Phe Thr Cys Asp	
129 134 139 144	
tcg gac cat ctg cgt ccc gca gat gca ata atg cag aaa gcc tgg aga	480
Ser Asp His Leu Arg Pro Ala Asp Ala Ile Met Gln Lys Ala Trp Arg	
145 150 155 160	
gag aga aac ccc caa gct agg att tct gca gct cat gaa gcc ttg gag	528
Glu Arg Asn Pro Gln Ala Arg Ile Ser Ala Ala His Glu Ala Leu Glu	
161 166 171 176	
ata aat gag acg aga cac caa tgt ctt ggt gta cat caa aag aag gct	576
Ile Asn Glu Thr Arg His Gln Cys Leu Gly Val His Gln Lys Lys Ala	
177 182 187 192	
agc aat gtg tgc cag aag act cgg gag gac cag gga agc aaa gcc ctt	624
Ser Asn Val Cys Gln Lys Thr Arg Glu Asp Gln Gly Ser Lys Ala Leu	
193 198 203 208	
ctg gaa cta caa gca tat gct gat gtt cag gca gtc tta gca aag tat	672
Leu Glu Leu Gln Ala Tyr Ala Asp Val Gln Ala Val Leu Ala Lys Tyr	
209 214 219 224	
gat gat ata agc tta cca aag tca gca aca ata tgc tac aca gct gct	720
Asp Asp Ile Ser Leu Pro Lys Ser Ala Thr Ile Cys Tyr Thr Ala Ala	
225 230 235 240	
ttg ctc aaa gca aga gct gtc tct gac aaa ttc tct cct gag gct gca	768
Leu Leu Lys Ala Arg Ala Val Ser Asp Lys Phe Ser Pro Glu Ala Ala	
241 246 251 256	
tct cgg cgg ggg ctg agc aca gca gag atg aat gca gta gag gcc att	816
Ser Arg Arg Gly Leu Ser Thr Ala Glu Met Asn Ala Val Glu Ala Ile	
257 262 267 272	
cat aga gct gtg gaa ttc aat cct cat gtg cca aaa tac cta cta gaa	864
His Arg Ala Val Glu Phe Asn Pro His Val Pro Lys Tyr Leu Leu Glu	
273 278 283 288	
atg aaa agc tta atc cta ccc cca gaa cat atc ctg aag aga gga gac	912
Met Lys Ser Leu Ile Leu Pro Pro Glu His Ile Leu Lys Arg Gly Asp	
289 294 299 304	
agt gaa gca ata gca tat gca ttc ttt cat ctt gca cac tgg aag aga	960
Ser Glu Ala Ile Ala Tyr Ala Phe Phe His Leu Ala His Trp Lys Arg	
305 310 315 320	
gtg gaa ggg gct ttg aat ctt ttg cat tgt acg tgg gaa ggc act ttt	1008
Val Glu Gly Ala Leu Asn Leu Leu His Cys Thr Trp Glu Gly Thr Phe	
321 326 331 336	
cgg atg atc cct tat ccc ttg gaa aag ggg cac cta ttt tat cct tac	1056
Arg Met Ile Pro Tyr Pro Leu Glu Lys Gly His Leu Phe Tyr Pro Tyr	
337 342 347 352	
cca atc tgt aca gaa aca gca gac cga gag ctg ctt cca tct ttc cat	1104
Pro Ile Cys Thr Glu Thr Ala Asp Arg Glu Leu Leu Pro Ser Phe His	

His Glu Phe Pro Leu Asn Gly Asn Gln Glu Asn Pro Ser Cys Cys Gly	
46 51 56 61	
atc gac ggc atc ctg gag gcc tac cac cgc agc ctg cgc act gtg cag	480
Ile Asp Gly Ile Leu Glu Ala Tyr His Arg Ser Leu Arg Thr Val Gln	
62 67 72 77	
ctg tac ggc ccc acc aac ttt gcc ccc gtg gtc acc cac gtg gcc agg	528
Leu Tyr Gly Pro Thr Asn Phe Ala Pro Val Val Thr His Val Ala Arg	
78 83 88 93	
aat gca gcg gcc gtg cag gat ggc tcc cag tac tcg gtg ctg ctc atc	576
Asn Ala Ala Ala Val Gln Asp Gly Ser Gln Tyr Ser Val Leu Leu Ile	
94 99 104 109	
att act gat ggg gtc atc tcg gac atg gcg cag acc aag gag gcc att	624
Ile Thr Asp Gly Val Ile Ser Asp Met Ala Gln Thr Lys Glu Ala Ile	
110 115 120 125	
gtc aac gct gcc aag ctc ccc atg tcc atc att atc gtc ggc gtg ggc	672
Val Asn Ala Ala Lys Leu Pro Met Ser Ile Ile Ile Val Gly Val Gly	
126 131 136 141	
cag gca gag ttc gac gcc atg gtg gag ctg gat ggc gac gac gtg cgg	720
Gln Ala Glu Phe Asp Ala Met Val Glu Leu Asp Gly Asp Asp Val Arg	
142 147 152 157	
atc tcc tcc cgg ggg aag ctg gct gaa cgc gac atc gtc cag ttt gta	768
Ile Ser Ser Arg Gly Lys Leu Ala Glu Arg Asp Ile Val Gln Phe Val	
158 163 168 173	
ccc ttc cgg gac tat gtg gac cgc aca ggc aac cac gtg ctg agc atg	816
Pro Phe Arg Asp Tyr Val Asp Arg Thr Gly Asn His Val Leu Ser Met	
174 179 184 189	
gcc cgc ctg gcc cga gac gtg ctg gca gag atc cct gac caa ctg gtg	864
Ala Arg Leu Ala Arg Asp Val Leu Ala Glu Ile Pro Asp Gln Leu Val	
190 195 200 205	
tcc tac atg aag gca cag ggc att cgc ccg cgt tcc cca ccc gca gca	912
Ser Tyr Met Lys Ala Gln Gly Ile Arg Pro Arg Ser Pro Pro Ala Ala	
206 211 216 221	
cca acc cac tcg ccc tcg cag tcc cca gcc cgc acg ccc cct gcg tgc	960
Pro Thr His Ser Pro Ser Gln Ser Pro Ala Arg Thr Pro Pro Ala Cys	
222 227 232 237	
ccc ctg cac acg cac atc tga ac ctggtctcag caggcaggtg gctggggcct	1013
Pro Leu His Thr His Ile *	
238 243	
gggagaggcc aggtgaatgg gaggccaggg cccagactc cccgaagtgt gctgcccgg	1073
cctttggggac atctgtgtgc ctgggaggct gccaggggggt ggggcttctg aagaccctc	1133
ctcaatttct tggcctcact tattgcccac acccaggggag ttaggggggt acgggtgaaa	1193

gaggggtaca cagggacca gcccttctct tcttcccaa tacctggctc taaccagcc 1253
 aggaaggtgt aaacaataag ggtgattggg gtccctgtcg cccacccccg gcaatcctat 1313
 ttgcttacct gtcaccctga agcctgggct tggcctcctc cagcccccca tctccgtccc 1373
 atcctcccat ggtgtctact cctgtccctg agccccgccc tgtgggtctat cctgtgcccc 1433
 atttccagtg aaccccatga agctgatggg tttgcaggaa ggctgaaca tgtgcaccct 1493
 cccagggaca ctggatgctc tgggagcccc ggggacccca tgggggtgctg taatcatgga 1553
 ccgtaggcca tgtgatgggc ctgaagtgga ggctgctcag cacagagccc tttctgggtgc 1613
 ctctcgaact cagtacgatg caagttctag acacacagat ggctgtgga ggctctccc 1673
 tgggtgtgggc ccacaggtac ttccatgggt gactcctggc ttcaggaatc cttcctccc 1733
 tccagaggct tcccagggcc ctcggtgccc acgcctctgc ccctctggag gcctgagtaa 1793
 ggagtggctc aacccccagt tcccacactg ctctgtctct ttgccctgta tcccatgagg 1853
 ctaggagaca ggagtccctgg gtttgagccc tgcctcccc cactgcctaa tgtgggaacc 1913
 caagcaaggc ccttctacct tttgggcctc agtttccatg tctgtacgac aagaggggtg 1973
 gaccaagatg gccccaggg gttttccttt 2003

<210> 47
 <211> 3704
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (217) .. (3495)

<400> 47
 gacgcaccgg tccggaattc ccgggccgac ccacgcgtcc ggagcagtcc gaggggaacg 60
 tgggttgaac gttgcaacta ggggtggagat caagctggaa caggagttcc gatcgacccg 120
 gtaccaagaa ggggagtgcc cgcggcaggg ttcatgaaa aaatccttag tgatattgac 180
 atgtctcaag tgacataaat tagccaatga ctcgga atg atg gat tct ccg aag 234
 Met Met Asp Ser Pro Lys
 1
 att gga aat ggt ttg cca gtg att gga cca ggg act gat ata ggg ata 282
 Ile Gly Asn Gly Leu Pro Val Ile Gly Pro Gly Thr Asp Ile Gly Ile
 7 12 17 22
 tct tca ctc cac atg gtg ggg tat ttg gga aaa aat ttt gat tca gct 330
 Ser Ser Leu His Met Val Gly Tyr Leu Gly Lys Asn Phe Asp Ser Ala

23	28	33	38	
aaa gtt cca tca gat gag tat tgc cct gct tgt aga gag aag gga aag				378
Lys Val Pro Ser Asp Glu Tyr Cys Pro Ala Cys Arg Glu Lys Gly Lys				
39	44	49	54	
tta aaa gcc tta aag act tac cga att agt ttt caa gaa tct atc ttt				426
Leu Lys Ala Leu Lys Thr Tyr Arg Ile Ser Phe Gln Glu Ser Ile Phe				
55	60	65	70	
ttg tgt gag gat ctg cag tgc atc tat cct ttg ggc tct aaa tca ctt				474
Leu Cys Glu Asp Leu Gln Cys Ile Tyr Pro Leu Gly Ser Lys Ser Leu				
71	76	81	86	
aat aac cta att tct cct gat ttg gaa gaa tgt cac act cca cat aag				522
Asn Asn Leu Ile Ser Pro Asp Leu Glu Glu Cys His Thr Pro His Lys				
87	92	97	102	
cct cag aaa agg aag agc tta gaa agc agc tat aag gat tca ctc ctt				570
Pro Gln Lys Arg Lys Ser Leu Glu Ser Ser Tyr Lys Asp Ser Leu Leu				
103	108	113	118	
tta gca aat tcc aaa aag act aga aat tat att gct att gac ggt gga				618
Leu Ala Asn Ser Lys Lys Thr Arg Asn Tyr Ile Ala Ile Asp Gly Gly				
119	124	129	134	
aaa gtt ttg aac agc aaa cat aat gga gaa gta tat gac gaa acc tcg				666
Lys Val Leu Asn Ser Lys His Asn Gly Glu Val Tyr Asp Glu Thr Ser				
135	140	145	150	
tca aac tta cct gat agt agt ggt caa cag aat cca att agg aca gct				714
Ser Asn Leu Pro Asp Ser Ser Gly Gln Gln Asn Pro Ile Arg Thr Ala				
151	156	161	166	
gat tcc ttg gag cgg aat gag att ttg gaa gct gat act gtt gac atg				762
Asp Ser Leu Glu Arg Asn Glu Ile Leu Glu Ala Asp Thr Val Asp Met				
167	172	177	182	
gct act aca aaa gat cct gct aca gtt gat gtc tct gga act ggc aga				810
Ala Thr Thr Lys Asp Pro Ala Thr Val Asp Val Ser Gly Thr Gly Arg				
183	188	193	198	
cct tcc cct caa aat gaa gga tgt aca tct aaa ctg gaa atg cca ctg				858
Pro Ser Pro Gln Asn Glu Gly Cys Thr Ser Lys Leu Glu Met Pro Leu				
199	204	209	214	
gag agc aaa tgt aca tca ttt ccc cag gct tta tgt gtc cag tgg aaa				906
Glu Ser Lys Cys Thr Ser Phe Pro Gln Ala Leu Cys Val Gln Trp Lys				
215	220	225	230	
aat gct tat gct ctc tgt tgg tta gac tgt atc ctg tca gct ttg gtg				954
Asn Ala Tyr Ala Leu Cys Trp Leu Asp Cys Ile Leu Ser Ala Leu Val				
231	236	241	246	
cac tcg gaa gag tta aag aac acc gtg act gga ctg tgc tcg aag gag				1002
His Ser Glu Glu Leu Lys Asn Thr Val Thr Gly Leu Cys Ser Lys Glu				
247	252	257	262	

gaa tct ata ttc tgg cgg ttg ctt aca aaa tat aat caa gca aat aca	1050
Glu Ser Ile Phe Trp Arg Leu Leu Thr Lys Tyr Asn Gln Ala Asn Thr	
263 268 273 278	
ctt cta tat acc agt caa ttg agt ggt gtt aaa gat gga gat tgt aaa	1098
Leu Leu Tyr Thr Ser Gln Leu Ser Gly Val Lys Asp Gly Asp Cys Lys	
279 284 289 294	
aaa ctt acc tca gaa ata ttt gca gag ata gag acc tgt ctg aat gaa	1146
Lys Leu Thr Ser Glu Ile Phe Ala Glu Ile Glu Thr Cys Leu Asn Glu	
295 300 305 310	
gtt aga gat gaa att ttt att agc ctt cag ccc cag ctt aga tgc aca	1194
Val Arg Asp Glu Ile Phe Ile Ser Leu Gln Pro Gln Leu Arg Cys Thr	
311 316 321 326	
tta ggt gat atg gaa agc cct gtg ttt gca ttt ccc ctg ctc tta aaa	1242
Leu Gly Asp Met Glu Ser Pro Val Phe Ala Phe Pro Leu Leu Leu Lys	
327 332 337 342	
cta gaa acc cac att gaa aag ctc ttc cta tat tct ttt tct tgg gac	1290
Leu Glu Thr His Ile Glu Lys Leu Phe Leu Tyr Ser Phe Ser Trp Asp	
343 348 353 358	
ttt gaa tgt tcg cag tgt gga cac caa tat caa aac agg cat atg aag	1338
Phe Glu Cys Ser Gln Cys Gly His Gln Tyr Gln Asn Arg His Met Lys	
359 364 369 374	
agt ctg gtc acc ttt aca aat gtc atc cct gag tgg cac cca ctt aat	1386
Ser Leu Val Thr Phe Thr Asn Val Ile Pro Glu Trp His Pro Leu Asn	
375 380 385 390	
gct gcc cat ttt ggc cca tgt aac aat tgc aac agt aaa tca caa ata	1434
Ala Ala His Phe Gly Pro Cys Asn Asn Cys Asn Ser Lys Ser Gln Ile	
391 396 401 406	
aga aaa atg gta tta gaa aaa gta tct ccc ata ttc atg ttg cac ttt	1482
Arg Lys Met Val Leu Glu Lys Val Ser Pro Ile Phe Met Leu His Phe	
407 412 417 422	
gta gaa ggc tta cca cag aat gac ttg cag cac tat gca ttt cat ttt	1530
Val Glu Gly Leu Pro Gln Asn Asp Leu Gln His Tyr Ala Phe His Phe	
423 428 433 438	
gaa ggc tgt ctt tat cag ata act tct gta att cag tat cga gca aat	1578
Glu Gly Cys Leu Tyr Gln Ile Thr Ser Val Ile Gln Tyr Arg Ala Asn	
439 444 449 454	
aat cat ttt ata aca tgg att tta gat gct gat gga agt tgg ctg gaa	1626
Asn His Phe Ile Thr Trp Ile Leu Asp Ala Asp Gly Ser Trp Leu Glu	
455 460 465 470	
tgt gat gac tta aaa ggc cca tgt tct gaa agg cac aag aaa ttt gaa	1674
Cys Asp Asp Leu Lys Gly Pro Cys Ser Glu Arg His Lys Lys Phe Glu	
471 476 481 486	

gtt cct gct tca gag ata cat att gtt att tgg gaa aga aaa ata tcc	1722
Val Pro Ala Ser Glu Ile His Ile Val Ile Trp Glu Arg Lys Ile Ser	
487 492 497 502	
caa gtg aca gat aaa gaa gct gcc tgc ctt cca ctt aaa aag act aat	1770
Gln Val Thr Asp Lys Glu Ala Ala Cys Leu Pro Leu Lys Lys Thr Asn	
503 508 513 518	
gac caa cac gct ctc agt aat gag aaa cca gta tct tta aca tcg tgt	1818
Asp Gln His Ala Leu Ser Asn Glu Lys Pro Val Ser Leu Thr Ser Cys	
519 524 529 534	
tct gtg ggt gat gct gcc tca gct gaa aca gcc tca gta act cac cct	1866
Ser Val Gly Asp Ala Ala Ser Ala Glu Thr Ala Ser Val Thr His Pro	
535 540 545 550	
aaa gat ata tca gtt gcc cct cgt act ctt tca cag gac aca gct gta	1914
Lys Asp Ile Ser Val Ala Pro Arg Thr Leu Ser Gln Asp Thr Ala Val	
551 556 561 566	
act cat gga gat cat tta ctt tca ggt cca aaa ggt ttg gtt gac aat	1962
Thr His Gly Asp His Leu Leu Ser Gly Pro Lys Gly Leu Val Asp Asn	
567 572 577 582	
att tta cct ctg aca ctt gaa gaa act atc cag aaa aca gcc tca gtt	2010
Ile Leu Pro Leu Thr Leu Glu Glu Thr Ile Gln Lys Thr Ala Ser Val	
583 588 593 598	
tca cag tta aat tct gaa gct ttc ctg tta gaa aat aaa cct gta gca	2058
Ser Gln Leu Asn Ser Glu Ala Phe Leu Leu Glu Asn Lys Pro Val Ala	
599 604 609 614	
gaa aat aca gga att ctc aaa acc aat act ttg cta tca caa gaa tca	2106
Glu Asn Thr Gly Ile Leu Lys Thr Asn Thr Leu Leu Ser Gln Glu Ser	
615 620 625 630	
cta atg gct tct tca gta tca gct cca tgt aat gaa aag ctt att caa	2154
Leu Met Ala Ser Ser Val Ser Ala Pro Cys Asn Glu Lys Leu Ile Gln	
631 636 641 646	
gac caa ttt gtg gac ata agt ttt cca tcc caa gtt gta aat aca aac	2202
Asp Gln Phe Val Asp Ile Ser Phe Pro Ser Gln Val Val Asn Thr Asn	
647 652 657 662	
atg cag tca gta cag ctg aat aca gaa gat act gta aat act aaa tct	2250
Met Gln Ser Val Gln Leu Asn Thr Glu Asp Thr Val Asn Thr Lys Ser	
663 668 673 678	
gtg aat aat act gat gct act ggt ctt ata cag gga gtg aag tca gta	2298
Val Asn Asn Thr Asp Ala Thr Gly Leu Ile Gln Gly Val Lys Ser Val	
679 684 689 694	
gaa att gag aag gac gct cag tta aaa caa ttc ctt aca cca aaa act	2346
Glu Ile Glu Lys Asp Ala Gln Leu Lys Gln Phe Leu Thr Pro Lys Thr	
695 700 705 710	
gaa caa tta aaa cca gaa cgt gtc aca tct cag gta tct aat ttg aag	2394

Glu Gln Leu Lys Pro	Glu Arg Val Thr Ser	Gln Val Ser Asn Leu Lys	
711	716	721	726
aaa aaa gaa act aca	gca gat tct caa acc	aca aca tct aag tca tta	2442
Lys Lys Glu Thr Thr	Ala Asp Ser Gln Thr	Thr Thr Ser Lys Ser Leu	
727	732	737	742
cag aat cag tct ctg	aaa gaa aat cag aag	aag cca ttt gtg gga agt	2490
Gln Asn Gln Ser Leu	Lys Glu Asn Gln Lys	Lys Pro Phe Val Gly Ser	
743	748	753	758
tgg gtt aaa ggc tta	ata agc agg ggt gct	tct ttt atg cca ctc tgt	2538
Trp Val Lys Gly Leu	Ile Ser Arg Gly Ala	Ser Phe Met Pro Leu Cys	
759	764	769	774
gtt tca gct cat aat	aga aac act ata act	gat tta caa cct tca gtt	2586
Val Ser Ala His Asn	Arg Asn Thr Ile Thr	Asp Leu Gln Pro Ser Val	
775	780	785	790
aaa ggg gta aat aat	ttt ggt ggc ttt aaa	act aaa ggt ata aac cag	2634
Lys Gly Val Asn Asn	Phe Gly Gly Phe Lys	Thr Lys Gly Ile Asn Gln	
791	796	801	806
aag gcc agc cac gta	tcc aag aaa gct cgt	aag agt gca agt aag cct	2682
Lys Ala Ser His Val	Ser Lys Lys Ala Arg	Lys Ser Ala Ser Lys Pro	
807	812	817	822
cct ccc atc agt aag	cca cca gca ggc cct	cca tcg tct aat ggc aca	2730
Pro Pro Ile Ser Lys	Pro Pro Ala Gly Pro	Pro Ser Ser Asn Gly Thr	
823	828	833	838
gct gcc cac cca cat	gct cat gct gct tca	gaa gtt ttg gaa aag tct	2778
Ala Ala His Pro His	Ala His Ala Ala Ser	Glu Val Leu Glu Lys Ser	
839	844	849	854
gga agc acc tca tgt	gga gct caa ctc aac	cac agt tct tat ggg aat	2826
Gly Ser Thr Ser Cys	Gly Ala Gln Leu Asn	His Ser Ser Tyr Gly Asn	
855	860	865	870
ggt att tct tca gca	aac cat gaa gac ttg	gtg gaa ggt cag att cat	2874
Gly Ile Ser Ser Ala	Asn His Glu Asp Leu	Val Glu Gly Gln Ile His	
871	876	881	886
aaa ctt cgt cta aaa	ctt cgt aaa aag cta	aag gca gaa aag aag aaa	2922
Lys Leu Arg Leu Lys	Leu Arg Lys Lys Leu	Lys Ala Glu Lys Lys Lys	
887	892	897	902
tta gct gct ctt atg	tct tcc ccg caa agc	aga aca gtt cga agt gaa	2970
Leu Ala Ala Leu Met	Ser Ser Pro Gln Ser	Arg Thr Val Arg Ser Glu	
903	908	913	918
aat cta gaa cag gtg	ccc cag gat ggg tct	cca aat gat tgt gaa tca	3018
Asn Leu Glu Gln Val	Pro Gln Asp Gly Ser	Pro Asn Asp Cys Glu Ser	
919	924	929	934
ata gag gac ttg tta	aat gag cta cca tat	cca att gat att gcc aat	3066
Ile Glu Asp Leu Leu	Asn Glu Leu Pro Tyr	Pro Ile Asp Ile Ala Asn	

935	940	945	950	
gag tct gca tgc acc act gtt cct ggt gtt tcc ctg tac agt agt caa				3114
Glu Ser Ala Cys Thr Thr Val Pro Gly Val Ser Leu Tyr Ser Ser Gln				
951	956	961	966	
act cat gaa gaa att tta gcg gaa tta ttg tct cct aca cct gtt tca				3162
Thr His Glu Glu Ile Leu Ala Glu Leu Leu Ser Pro Thr Pro Val Ser				
967	972	977	982	
aca gag ctg tca gaa aat ggg gaa ggt gac ttt agg tat ttg gga atg				3210
Thr Glu Leu Ser Glu Asn Gly Glu Gly Asp Phe Arg Tyr Leu Gly Met				
983	988	993	998	
gga gat agt cat atc cca cca cca gta cca agt gaa ttc aat gat gtt				3258
Gly Asp Ser His Ile Pro Pro Pro Val Pro Ser Glu Phe Asn Asp Val				
999	1004	1009	1014	
tcc cag aac aca cat ctg aga cag gac cat aat tat tgt agc ccc acc				3306
Ser Gln Asn Thr His Leu Arg Gln Asp His Asn Tyr Cys Ser Pro Thr				
1015	1020	1025	1030	
aag aaa aat cca tgt gaa gtt cag cca gac tct ctg aca aat aat gcc				3354
Lys Lys Asn Pro Cys Glu Val Gln Pro Asp Ser Leu Thr Asn Asn Ala				
1031	1036	1041	1046	
tgc gtt aga aca tta aac ttg gag agt ccg atg aag act gat att ttc				3402
Cys Val Arg Thr Leu Asn Leu Glu Ser Pro Met Lys Thr Asp Ile Phe				
1047	1052	1057	1062	
gat gag ttt ttt tcc tcc tca gca tta aat gct tta gca aat gac aca				3450
Asp Glu Phe Phe Ser Ser Ser Ala Leu Asn Ala Leu Ala Asn Asp Thr				
1063	1068	1073	1078	
tta gac cta cct cat ttc gat gaa tat ctg ttt gag aat tat tga att				3498
Leu Asp Leu Pro His Phe Asp Glu Tyr Leu Phe Glu Asn Tyr *				
1079	1084	1089		
aatgcttggtt aacttttttcc atataatatt tattattattt agaagaactt acaatgtggtt				3558
caggtagtgt ttatacactg gacttgtgta attacttggtg taataaccat gaacaaaatg				3618
caagggtttaa ccttttggttc tgcccatgaa gcatgtaatc tttcttacac attaaaatca				3678
ctgaatgtgt taaaaaaaaa aaaaaa				3704

<210> 48
 <211> 1828
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (71)..(1792)


```

<400> 48
gggcggtggt gctttgtctc ctcagcactc tgctgtcact caaggaagta tcatcaagaa      60

caaggagggc  atg gat gct aag tca cta act gcc tgg tcc cgg aca ctg      109
             Met Asp Ala Lys Ser Leu Thr Ala Trp Ser Arg Thr Leu
               1             5             10

gtg acc ttc aag gat gta ttt gtg gac ttc acc agg gag gag tgg aag      157
Val Thr Phe Lys Asp Val Phe Val Asp Phe Thr Arg Glu Glu Trp Lys
  14             19             24             29

ctg ctg gac act gct cag cag atc gtg tac aga aat gtg atg ctg gag      205
Leu Leu Asp Thr Ala Gln Gln Ile Val Tyr Arg Asn Val Met Leu Glu
  30             35             40             45

aac tat aag aac ctg gtt tcc ttg ggt tat cag ctt act aag cca gat      253
Asn Tyr Lys Asn Leu Val Ser Leu Gly Tyr Gln Leu Thr Lys Pro Asp
  46             51             56             61

gtg atc ctc cgg ttg gag aag gga gaa gag ccc tgg ctg gtg gag aga      301
Val Ile Leu Arg Leu Glu Lys Gly Glu Glu Pro Trp Leu Val Glu Arg
  62             67             72             77

gaa att cac caa gag acc cat cct gat tca gag act gca ttt gaa atc      349
Glu Ile His Gln Glu Thr His Pro Asp Ser Glu Thr Ala Phe Glu Ile
  78             83             88             93

aaa tca tca gtt tcc agc agg agc att ttt aaa gat aag caa tcc tgt      397
Lys Ser Ser Val Ser Ser Arg Ser Ile Phe Lys Asp Lys Gln Ser Cys
  94             99             104            109

gac att aaa atg gaa gga atg gca agg aat gat ctc tgg tat ttg tca      445
Asp Ile Lys Met Glu Gly Met Ala Arg Asn Asp Leu Trp Tyr Leu Ser
 110             115            120            125

tta gaa gaa gtc tgg aaa tgt aga gac cag tta gac aag tat cag gaa      493
Leu Glu Glu Val Trp Lys Cys Arg Asp Gln Leu Asp Lys Tyr Gln Glu
 126             131            136            141

aac cca gag aga cat ttg agg caa gtg gca ttc acc caa aag aaa gta      541
Asn Pro Glu Arg His Leu Arg Gln Val Ala Phe Thr Gln Lys Lys Val
 142             147            152            157

ctt act cag gag aga gtc tct gaa agt ggt aaa tat ggg gga aac tgt      589
Leu Thr Gln Glu Arg Val Ser Glu Ser Gly Lys Tyr Gly Gly Asn Cys
 158             163            168            173

ctt ctt cct gct cag cta gta ctg aga gag tat ttc cat aaa cgt gac      637
Leu Leu Pro Ala Gln Leu Val Leu Arg Glu Tyr Phe His Lys Arg Asp
 174             179            184            189

tca cat act aaa agt tta aaa cat gat tta gtt ctt aat ggt cat cag      685
Ser His Thr Lys Ser Leu Lys His Asp Leu Val Leu Asn Gly His Gln
 190             195            200            205

gac agt tgt gca agt aac agt aat gaa tgt ggt caa act ttc tgt caa      733

```

Asp Ser Cys Ala Ser Asn Ser Asn Glu Cys Gly Gln Thr Phe Cys Gln	
206 211 216 221	
aac att cac ctt att cag ttt gca aga act cac aca ggt gat aaa tcc	781
Asn Ile His Leu Ile Gln Phe Ala Arg Thr His Thr Gly Asp Lys Ser	
222 227 232 237	
tac aaa tgc cct gat aat gac aac tct ctt act cat ggt tca tct ctt	829
Tyr Lys Cys Pro Asp Asn Asp Asn Ser Leu Thr His Gly Ser Ser Leu	
238 243 248 253	
ggt ata tca aag ggc ata cat aga gag aaa ccc tat gaa tgt aag gaa	877
Gly Ile Ser Lys Gly Ile His Arg Glu Lys Pro Tyr Glu Cys Lys Glu	
254 259 264 269	
tgt gga aaa ttc ttc agc tgg cgc tct aat ctt act agg cat cag ctt	925
Cys Gly Lys Phe Phe Ser Trp Arg Ser Asn Leu Thr Arg His Gln Leu	
270 275 280 285	
att cat act gga gaa aaa ccc tat gag tgt aaa gaa tgt gga aag tct	973
Ile His Thr Gly Glu Lys Pro Tyr Glu Cys Lys Glu Cys Gly Lys Ser	
286 291 296 301	
ttc agc cgg agt tct cac ctc att gga cat caa aag acc cat act ggt	1021
Phe Ser Arg Ser Ser His Leu Ile Gly His Gln Lys Thr His Thr Gly	
302 307 312 317	
gag gaa ccc tat gaa tgt aaa gaa tgt gga aaa tcc ttc agc tgg ttc	1069
Glu Glu Pro Tyr Glu Cys Lys Glu Cys Gly Lys Ser Phe Ser Trp Phe	
318 323 328 333	
tct cac ctt gtt act cat cag aga act cat aca gga gac aaa ctg tac	1117
Ser His Leu Val Thr His Gln Arg Thr His Thr Gly Asp Lys Leu Tyr	
334 339 344 349	
aca tgt aat cag tgt ggg aaa tct ttt gtt cat agc tct agg ctt att	1165
Thr Cys Asn Gln Cys Gly Lys Ser Phe Val His Ser Ser Arg Leu Ile	
350 355 360 365	
aga cac cag agg aca cat act gga gag aaa ccc tat gaa tgt cct gaa	1213
Arg His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Glu Cys Pro Glu	
366 371 376 381	
tgt ggg aaa tct ttc aga cag agc aca cat ctc att ctg cat cag aga	1261
Cys Gly Lys Ser Phe Arg Gln Ser Thr His Leu Ile Leu His Gln Arg	
382 387 392 397	
acc cat gtg aga gtg agg ccc tat gaa tgc aat gaa tgt gga aag tct	1309
Thr His Val Arg Val Arg Pro Tyr Glu Cys Asn Glu Cys Gly Lys Ser	
398 403 408 413	
tac agc cag aga tct cac ctt gtt gtg cat cat aga att cac act gga	1357
Tyr Ser Gln Arg Ser His Leu Val Val His His Arg Ile His Thr Gly	
414 419 424 429	
cta aaa cct ttt gag tgt aag gat tgt gga aaa tgt ttt agt cga agc	1405
Leu Lys Pro Phe Glu Cys Lys Asp Cys Gly Lys Cys Phe Ser Arg Ser	

430	435	440	445	
tct cac ctt tat tca cat caa aga acc cac act gga gag aaa cca tat				1453
Ser His Leu Tyr Ser His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr				
446	451	456	461	
gag tgt cat gat tgt gga aaa tct ttc agc cag agt tct gcc ctt att				1501
Glu Cys His Asp Cys Gly Lys Ser Phe Ser Gln Ser Ser Ala Leu Ile				
462	467	472	477	
gtg cat cag agg ata cac act gga gag aaa cca tat gaa tgc tgt cag				1549
Val His Gln Arg Ile His Thr Gly Glu Lys Pro Tyr Glu Cys Cys Gln				
478	483	488	493	
tgt ggg aaa gcc ttc atc cgg aag aat gac ctc att aag cac cag aga				1597
Cys Gly Lys Ala Phe Ile Arg Lys Asn Asp Leu Ile Lys His Gln Arg				
494	499	504	509	
att cat gtt gga gaa gag acc tat aaa tgt aat caa tgt ggc att atc				1645
Ile His Val Gly Glu Glu Thr Tyr Lys Cys Asn Gln Cys Gly Ile Ile				
510	515	520	525	
ttc agc cag aac tct cca ttt ata gtt cat caa ata gct cac act gga				1693
Phe Ser Gln Asn Ser Pro Phe Ile Val His Gln Ile Ala His Thr Gly				
526	531	536	541	
gag cag ttc tta aca tgc aat caa tgt ggg aca gcg ctt gtt aat acc				1741
Glu Gln Phe Leu Thr Cys Asn Gln Cys Gly Thr Ala Leu Val Asn Thr				
542	547	552	557	
tct aac ctt att gga tac cag aca aat cat att aga gaa aat gct tac				1789
Ser Asn Leu Ile Gly Tyr Gln Thr Asn His Ile Arg Glu Asn Ala Tyr				
558	563	568	573	
taa taaatatggg aatttttcac aaagaaaaaa aaaaaa				1828
*				
574				

<210> 49
 <211> 1426
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (71) .. (1390)

<400> 49	
gggcgggtggt gctttgtctc ctcagcactc tgctgtcact caaggaagta tcatcaagaa	60
caaggaggggc atg gat gct aag tca cta act gcc tgg tcc cgg aca ctg	109
Met Asp Ala Lys Ser Leu Thr Ala Trp Ser Arg Thr Leu	
1 5 10	

gtg acc ttc aag gat gta ttt gtg gac ttc acc agg gag gag tgg aag	157
Val Thr Phe Lys Asp Val Phe Val Asp Phe Thr Arg Glu Glu Trp Lys	
14 19 24 29	
ctg ctg gac act gct cag cag atc gtg tac aga aat gtg atg ctg gag	205
Leu Leu Asp Thr Ala Gln Gln Ile Val Tyr Arg Asn Val Met Leu Glu	
30 35 40 45	
aac tat aag aac ctg gtt tcc ttg ggt tat cag ctt act aag cca gat	253
Asn Tyr Lys Asn Leu Val Ser Leu Gly Tyr Gln Leu Thr Lys Pro Asp	
46 51 56 61	
gtg atc ctc cgg ttg gag aag gga gaa gag ccc tgg ctg gtg gag aga	301
Val Ile Leu Arg Leu Glu Lys Gly Glu Glu Pro Trp Leu Val Glu Arg	
62 67 72 77	
gaa att cac caa gag acc cat cct gat tca gag act gca ttt gaa atc	349
Glu Ile His Gln Glu Thr His Pro Asp Ser Glu Thr Ala Phe Glu Ile	
78 83 88 93	
aaa tca tca gtt tcc agc agg agc att ttt aaa gat aag caa tcc tgt	397
Lys Ser Ser Val Ser Ser Arg Ser Ile Phe Lys Asp Lys Gln Ser Cys	
94 99 104 109	
gac att aaa atg gaa gga atg gca agg aat gat ctc tgg tat ttg tca	445
Asp Ile Lys Met Glu Gly Met Ala Arg Asn Asp Leu Trp Tyr Leu Ser	
110 115 120 125	
tta gaa gaa gtc tgg aaa tgt aga gac cag tta gac aag tat cag gaa	493
Leu Glu Glu Val Trp Lys Cys Arg Asp Gln Leu Asp Lys Tyr Gln Glu	
126 131 136 141	
aac cca gag aga cat ttg agg cat cag ctt att cat act gga gaa aaa	541
Asn Pro Glu Arg His Leu Arg His Gln Leu Ile His Thr Gly Glu Lys	
142 147 152 157	
ccc tat gag tgt aaa gaa tgt gga aag tct ttc agc cgg agt tct cac	589
Pro Tyr Glu Cys Lys Glu Cys Gly Lys Ser Phe Ser Arg Ser Ser His	
158 163 168 173	
ctc att gga cat caa aag acc cat act ggt gag gaa ccc tat gaa tgt	637
Leu Ile Gly His Gln Lys Thr His Thr Gly Glu Glu Pro Tyr Glu Cys	
174 179 184 189	
aaa gaa tgt gga aaa tcc ttc agc tgg ttc tct cac ctt gtt act cat	685
Lys Glu Cys Gly Lys Ser Phe Ser Trp Phe Ser His Leu Val Thr His	
190 195 200 205	
cag aga act cat aca gga gac aaa ctg tac aca tgt aat cag tgt ggg	733
Gln Arg Thr His Thr Gly Asp Lys Leu Tyr Thr Cys Asn Gln Cys Gly	
206 211 216 221	
aaa tct ttt gtt cat agc tct agg ctt att aga cac cag agg aca cat	781
Lys Ser Phe Val His Ser Ser Arg Leu Ile Arg His Gln Arg Thr His	
222 227 232 237	

act gga gag aaa ccc tat gaa tgt cct gaa tgt ggg aaa tct ttc aga	829
Thr Gly Glu Lys Pro Tyr Glu Cys Pro Glu Cys Gly Lys Ser Phe Arg	
238 243 248 253	
cag agc aca cat ctc att ctg cat cag aga acc cat gtg aga gtg agg	877
Gln Ser Thr His Leu Ile Leu His Gln Arg Thr His Val Arg Val Arg	
254 259 264 269	
ccc tat gaa tgc aat gaa tgt gga aag tct tac agc cag aga tct cac	925
Pro Tyr Glu Cys Asn Glu Cys Gly Lys Ser Tyr Ser Gln Arg Ser His	
270 275 280 285	
ctt gtt gtg cat cat aga att cac act gga cta aaa cct ttt gag tgt	973
Leu Val Val His His Arg Ile His Thr Gly Leu Lys Pro Phe Glu Cys	
286 291 296 301	
aag gat tgt gga aaa tgt ttt agt cga agc tct cac ctt tat tca cat	1021
Lys Asp Cys Gly Lys Cys Phe Ser Arg Ser Ser His Leu Tyr Ser His	
302 307 312 317	
caa aga acc cac act gga gag aaa cca tat gag tgt cat gat tgt gga	1069
Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Glu Cys His Asp Cys Gly	
318 323 328 333	
aaa tct ttc agc cag agt tct gcc ctt att gtg cat cag agg ata cac	1117
Lys Ser Phe Ser Gln Ser Ser Ala Leu Ile Val His Gln Arg Ile His	
334 339 344 349	
act gga gag aaa cca tat gaa tgc tgt cag tgt ggg aaa gcc ttc atc	1165
Thr Gly Glu Lys Pro Tyr Glu Cys Cys Gln Cys Gly Lys Ala Phe Ile	
350 355 360 365	
cgg aag aat gac ctc att aag cac cag aga att cat gtt gga gaa gag	1213
Arg Lys Asn Asp Leu Ile Lys His Gln Arg Ile His Val Gly Glu Glu	
366 371 376 381	
acc tat aaa tgt aat caa tgt ggc att atc ttc agc cag aac tct cca	1261
Thr Tyr Lys Cys Asn Gln Cys Gly Ile Ile Phe Ser Gln Asn Ser Pro	
382 387 392 397	
ttt ata gtt cat caa ata gct cac act gga gag cag ttc tta aca tgc	1309
Phe Ile Val His Gln Ile Ala His Thr Gly Glu Gln Phe Leu Thr Cys	
398 403 408 413	
aat caa tgt ggg aca gcg ctt gtt aat acc tct aac ctt att gga tac	1357
Asn Gln Cys Gly Thr Ala Leu Val Asn Thr Ser Asn Leu Ile Gly Tyr	
414 419 424 429	
cag aca aat cat att aga gaa aat gct tac taa taaatatg ggaatttttc	1408
Gln Thr Asn His Ile Arg Glu Asn Ala Tyr *	
430 435 440	
acaaagaaaa aaaaaaaaa	1426

[illegible]

```
<220>
<221> misc_feature
<222> (1)...(2571)
<223> n = a,t,c or g
```

200

116	121	126	131	
ttg ttg aga cag aaa caa cta gaa gag aca aat ctt cag cta aga gaa				729
Leu Leu Arg Gln Lys Gln Leu Glu Glu Thr Asn Leu Gln Leu Arg Glu				
132	137	142	147	
aaa gct gga gat gtt cgt cga agc ctg cgt gac ttt gag ttg aca gaa				777
Lys Ala Gly Asp Val Arg Arg Ser Leu Arg Asp Phe Glu Leu Thr Glu				
148	153	158	163	
gag caa tat att aaa tta aaa gct ttt cct gaa gat cag ctt tct att				825
Glu Gln Tyr Ile Lys Leu Lys Ala Phe Pro Glu Asp Gln Leu Ser Ile				
164	169	174	179	
cct gaa tat gta tct gtt cgc ttc tat gag cta gtg aat cca tta aga				873
Pro Glu Tyr Val Ser Val Arg Phe Tyr Glu Leu Val Asn Pro Leu Arg				
180	185	190	195	
aag gaa atc tgt gaa cta caa gtg aaa aag aat atc cta gca gaa gaa				921
Lys Glu Ile Cys Glu Leu Gln Val Lys Lys Asn Ile Leu Ala Glu Glu				
196	201	206	211	
tta agt aca aac aaa aac caa ctg aag cag ctg aca gag aca tat gag				969
Leu Ser Thr Asn Lys Asn Gln Leu Lys Gln Leu Thr Glu Thr Tyr Glu				
212	217	222	227	
gaa gat cga aaa aac tac tct gaa gtt caa att aga tgt caa cgt ttg				1017
Glu Asp Arg Lys Asn Tyr Ser Glu Val Gln Ile Arg Cys Gln Arg Leu				
228	233	238	243	
gcc tta gaa tta gca gac aca aaa cag tta att cag caa ggt gac tac				1065
Ala Leu Glu Leu Ala Asp Thr Lys Gln Leu Ile Gln Gln Gly Asp Tyr				
244	249	254	259	
cgt caa gag aac tat gat aaa gtc aag agt gaa cgt gat gca ctt gaa				1113
Arg Gln Glu Asn Tyr Asp Lys Val Lys Ser Glu Arg Asp Ala Leu Glu				
260	265	270	275	
cag gaa gta att gag ctt agg aga aaa cat gaa ata ctt gaa gcc tct				1161
Gln Glu Val Ile Glu Leu Arg Arg Lys His Glu Ile Leu Glu Ala Ser				
276	281	286	291	
cac atg att caa aca aaa gaa cga agt gaa tta tca aaa gag gta gtc				1209
His Met Ile Gln Thr Lys Glu Arg Ser Glu Leu Ser Lys Glu Val Val				
292	297	302	307	
acc tta gag caa act gtt act tta ctg caa aag gat aaa gaa tat ctt				1257
Thr Leu Glu Gln Thr Val Thr Leu Leu Gln Lys Asp Lys Glu Tyr Leu				
308	313	318	323	
aat cgc caa aac atg gag ctt agt gtt cgc tgt gct cat gaa gag gat				1305
Asn Arg Gln Asn Met Glu Leu Ser Val Arg Cys Ala His Glu Glu Asp				
324	329	334	339	
cgc ctt gaa aga ctt caa gct caa ctg gaa gaa agc aaa aag gct aga				1353
Arg Leu Glu Arg Leu Gln Ala Gln Leu Glu Glu Ser Lys Lys Ala Arg				
340	345	350	355	


```

ttg gca aga aga gtg ctt caa tta gaa aaa caa aac tcg ctg att tta      2073
Leu Ala Arg Arg Val Leu Gln Leu Glu Lys Gln Asn Ser Leu Ile Leu
580                               585                               590                               595

aaa gat ctg gaa cat cga aag gac caa gta aca cag ctt tca cca gga      2121
Lys Asp Leu Glu His Arg Lys Asp Gln Val Thr Gln Leu Ser Pro Gly
596                               601                               606                               611

gct tga cagaggccaa ttcgctatta aaccagactc aacagcctta caggtatctc      2177
Ala *
612

attgaatcag tgcgtcagag agattctaag attgattcac tgacggaatc tattgcacaa      2237

cttgagaaaa ggatgtcagc aacttaaata aagaaaagtc agctttacta cagacggang      2297

gaatcaaaat ggcattagga tttaggacca acttctaaat catcgtgagg aattggcagc      2357

aatgaaacag attctcgtta agatgcatag taaacattct gagaacagct tacttctcac      2417

taaaacagaa ccaaaacatg tgacagaaaa tcagaaatca aagactttga atgtgcctaa      2477

agagcatgaa gacaatatat ttacacctaa accaacactc tttactaaaa aagaagcacc      2537

tgagtgggtct aagaaacaaa agatgaagac ctag                                2571

<210> 51
<211> 4515
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (93) .. (2354)

<400> 51
ggggaaagga catttgaggc tctcgggtccg gaattcccgg gtcgacccac gcgtccgatg      60

atgctgccga attcagagtt gttgctgatg cc  atg aaa gtc att ggc ttc aaa      113
                               Met Lys Val Ile Gly Phe Lys
                               1                               5

cct gag gag atc caa aca gtg tat aag att ttg gct gct att ctg cac      161
Pro Glu Glu Ile Gln Thr Val Tyr Lys Ile Leu Ala Ala Ile Leu His
8                               13                               18                               23

ttg gga aat tta aaa ttt gta gta gat ggt gac acg cct ctt att gag      209
Leu Gly Asn Leu Lys Phe Val Val Asp Gly Asp Thr Pro Leu Ile Glu
24                               29                               34                               39

aat ggc aaa gta gta tct atc ata gca gaa ttg ctc tct act aag aca      257
Asn Gly Lys Val Val Ser Ile Ile Ala Glu Leu Leu Ser Thr Lys Thr
40                               45                               50                               55

```

gat atg gtt gag aaa gcc ctt ctt tac cgg act ggg gcc aca ggc cgt Asp Met Val Glu Lys Ala Leu Leu Tyr Arg Thr Gly Ala Thr Gly Arg 56 61 66 71	305
gac atc att gac aag cag cac aca gaa caa gag gcc agc tac ggc aga Asp Ile Ile Asp Lys Gln His Thr Glu Gln Glu Ala Ser Tyr Gly Arg 72 77 82 87	353
gac gcc ttt gcc aag gca ata tat gag cgc ctt ttt tgt tgg atc gtt Asp Ala Phe Ala Lys Ala Ile Tyr Glu Arg Leu Phe Cys Trp Ile Val 88 93 98 103	401
act cgc atc aat gat att att gag gtc aag aac tat gac acc aca atc Thr Arg Ile Asn Asp Ile Ile Glu Val Lys Asn Tyr Asp Thr Thr Ile 104 109 114 119	449
cat ggg aaa aac act gtt att ggt gtc ttg gat atc tat ggc ttt gaa His Gly Lys Asn Thr Val Ile Gly Val Leu Asp Ile Tyr Gly Phe Glu 120 125 130 135	497
atc ttt gac aac aac agt ttt gaa caa ttc tgt atc aat tac tgc aat Ile Phe Asp Asn Asn Ser Phe Glu Gln Phe Cys Ile Asn Tyr Cys Asn 136 141 146 151	545
gag aaa ctg cag cag cta ttt att cag ctg gtt ctg aag caa gaa caa Glu Lys Leu Gln Gln Leu Phe Ile Gln Leu Val Leu Lys Gln Glu Gln 152 157 162 167	593
gag gaa tac cag cgg gaa ggg atc ccc tgg aaa cat att gac tac ttc Glu Glu Tyr Gln Arg Glu Gly Ile Pro Trp Lys His Ile Asp Tyr Phe 168 173 178 183	641
aac aat cag atc att gtt gac ctc gtg gag caa cag cac aaa ggg atc Asn Asn Gln Ile Ile Val Asp Leu Val Glu Gln Gln His Lys Gly Ile 184 189 194 199	689
att gca atc ctt gat gat gct tgc atg aat gtc ggc aaa gtc acc gat Ile Ala Ile Leu Asp Asp Ala Cys Met Asn Val Gly Lys Val Thr Asp 200 205 210 215	737
gaa atg ttt ctt gaa gca ctt aac agt aaa ttg ggc aaa cac gcc cat Glu Met Phe Leu Glu Ala Leu Asn Ser Lys Leu Gly Lys His Ala His 216 221 226 231	785
ttt tcc agc cga aag ctc tgt gcc tca gac aaa att ctg gag ttt gat Phe Ser Ser Arg Lys Leu Cys Ala Ser Asp Lys Ile Leu Glu Phe Asp 232 237 242 247	833
cga gat ttt cga att cga cat tat gca ggc gat gta gtc tat tct gtc Arg Asp Phe Arg Ile Arg His Tyr Ala Gly Asp Val Val Tyr Ser Val 248 253 258 263	881
att ggt ttt att gac aaa aat aaa gat act tta ttt caa gat ttc aag Ile Gly Phe Ile Asp Lys Asn Lys Asp Thr Leu Phe Gln Asp Phe Lys 264 269 274 279	929
cgc ctt atg tat aac agt tca aat cct gtg ctc aag aat atg tgg cct	977

Arg	Leu	Met	Tyr	Asn	Ser	Ser	Asn	Pro	Val	Leu	Lys	Asn	Met	Trp	Pro		
280					285					290					295		
gaa	ggc	aaa	ctg	agc	att	aca	gag	gtg	acc	aag	cga	cct	ctg	act	gct		1025
Glu	Gly	Lys	Leu	Ser	Ile	Thr	Glu	Val	Thr	Lys	Arg	Pro	Leu	Thr	Ala		
296					301					306					311		
gct	acc	ttg	ttt	aag	aat	tct	atg	att	gct	cta	gta	gac	aac	ctt	gca		1073
Ala	Thr	Leu	Phe	Lys	Asn	Ser	Met	Ile	Ala	Leu	Val	Asp	Asn	Leu	Ala		
312					317					322					327		
tca	aag	gaa	cca	tat	tac	gtt	cgt	tgc	atc	aaa	ccc	aat	gac	aag	aaa		1121
Ser	Lys	Glu	Pro	Tyr	Tyr	Val	Arg	Cys	Ile	Lys	Pro	Asn	Asp	Lys	Lys		
328					333					338					343		
tct	cca	cag	ata	ttt	gat	gat	gaa	cgc	tgc	cgg	cac	caa	gta	gaa	tat		1169
Ser	Pro	Gln	Ile	Phe	Asp	Asp	Glu	Arg	Cys	Arg	His	Gln	Val	Glu	Tyr		
344					349					354					359		
ctt	gga	cta	ctg	gaa	aat	gtg	aga	gtg	cgt	cgg	gca	gga	ttt	gcc	ttc		1217
Leu	Gly	Leu	Leu	Glu	Asn	Val	Arg	Val	Arg	Arg	Ala	Gly	Phe	Ala	Phe		
360					365					370					375		
cgc	cag	aca	tac	gag	aag	ttt	ctt	cac	agg	tat	aag	atg	atc	tct	gaa		1265
Arg	Gln	Thr	Tyr	Glu	Lys	Phe	Leu	His	Arg	Tyr	Lys	Met	Ile	Ser	Glu		
376					381					386					391		
ttc	acc	tgg	ccc	aac	cat	gac	ctt	cct	tca	gac	aaa	gag	gct	gtc	aag		1313
Phe	Thr	Trp	Pro	Asn	His	Asp	Leu	Pro	Ser	Asp	Lys	Glu	Ala	Val	Lys		
392					397					402					407		
aaa	cta	att	gaa	cgg	tgt	ggt	ttt	cag	gat	gat	gta	gct	tat	ggg	aag		1361
Lys	Leu	Ile	Glu	Arg	Cys	Gly	Phe	Gln	Asp	Asp	Val	Ala	Tyr	Gly	Lys		
408					413					418					423		
acc	aaa	att	ttc	att	cga	aca	ccc	cga	aca	ttg	ttt	acc	ttg	gaa	gaa		1409
Thr	Lys	Ile	Phe	Ile	Arg	Thr	Pro	Arg	Thr	Leu	Phe	Thr	Leu	Glu	Glu		
424					429					434					439		
ctc	cgt	gcc	cag	atg	ctc	ata	agg	att	gtc	ctc	ttt	cta	caa	aag	gtg		1457
Leu	Arg	Ala	Gln	Met	Leu	Ile	Arg	Ile	Val	Leu	Phe	Leu	Gln	Lys	Val		
440					445					450					455		
tgg	cgg	ggc	acc	ctg	gcc	cgc	atg	cgg	tac	aaa	aga	acc	aag	gca	gct		1505
Trp	Arg	Gly	Thr	Leu	Ala	Arg	Met	Arg	Tyr	Lys	Arg	Thr	Lys	Ala	Ala		
456					461					466					471		
ctg	aca	ata	atc	agg	tac	tac	cgg	cgc	tac	aaa	gtg	aag	tcg	tac	atc		1553
Leu	Thr	Ile	Ile	Arg	Tyr	Tyr	Arg	Arg	Tyr	Lys	Val	Lys	Ser	Tyr	Ile		
472					477					482					487		
cac	gag	gtg	gcc	aga	cgc	ttc	cat	ggc	gtc	aag	acc	atg	cga	gac	tac		1601
His	Glu	Val	Ala	Arg	Arg	Phe	His	Gly	Val	Lys	Thr	Met	Arg	Asp	Tyr		
488					493					498					503		
ggg	aag	cac	gtg	aag	tgg	cca	agc	cct	cct	aaa	gtt	ctt	cgc	cgt	ttt		1649
Gly	Lys	His	Val	Lys	Trp	Pro	Ser	Pro	Pro	Lys	Val	Leu	Arg	Arg	Phe		

504	509	514	519	
gag gag gcc ctg cag	acg att ttc aat aga	tgg aga gca tcc cag	ctc	1697
Glu Glu Ala Leu Gln	Thr Ile Phe Asn Arg	Trp Arg Ala Ser Gln	Leu	
520	525	530	535	
atc aag agc att ccg	gcc tca gac ctg ccc	cag gtc agg gca aag	gtt	1745
Ile Lys Ser Ile Pro	Ala Ser Asp Leu Pro	Gln Val Arg Ala Lys	Val	
536	541	546	551	
gca gcc gtg gaa atg	ttg aag ggt caa agg	gct gac ctc ggg ctc	cag	1793
Ala Ala Val Glu Met	Leu Lys Gly Gln Arg	Ala Asp Leu Gly Leu	Gln	
552	557	562	567	
agg gcc tgg gag ggc	aac tat ctt gct tca	aag cca gat aca cct	cag	1841
Arg Ala Trp Glu Gly	Asn Tyr Leu Ala Ser	Lys Pro Asp Thr Pro	Gln	
568	573	578	583	
acc tca ggc act ttt	gtc cct gtt gct aat	gaa ttg aaa cgg aag	gac	1889
Thr Ser Gly Thr Phe	Val Pro Val Ala Asn	Glu Leu Lys Arg Lys	Asp	
584	589	594	599	
aaa tac atg aat gtc	ctc ttt tcc tgt cac	gtc cgt aag gta aat	cga	1937
Lys Tyr Met Asn Val	Leu Phe Ser Cys His	Val Arg Lys Val Asn	Arg	
600	605	610	615	
ttt agt aag gtg gaa	gac aga gca att ttt	gtc act gac cgt cac	ctg	1985
Phe Ser Lys Val Glu	Asp Arg Ala Ile Phe	Val Thr Asp Arg His	Leu	
616	621	626	631	
tat aaa atg gat ccc	act aaa cag tac aag	gtg atg aag act atc	cct	2033
Tyr Lys Met Asp Pro	Thr Lys Gln Tyr Lys	Val Met Lys Thr Ile	Pro	
632	637	642	647	
cta tac aat ttg act	ggc ctg agt gtc tcc	aat gga aag gac caa	ctt	2081
Leu Tyr Asn Leu Thr	Gly Leu Ser Val Ser	Asn Gly Lys Asp Gln	Leu	
648	653	658	663	
gta gtg ttc cat acg	aaa gac aac aaa gac	ctc att gtc tgc ctc	ttc	2129
Val Val Phe His Thr	Lys Asp Asn Lys Asp	Leu Ile Val Cys Leu	Phe	
664	669	674	679	
agc aaa cag cca acc	cat gag agt cga att	gga gaa ctt gtt gga	gtg	2177
Ser Lys Gln Pro Thr	His Glu Ser Arg Ile	Gly Glu Leu Val Gly	Val	
680	685	690	695	
ctg gtg aat cat ttc	aag agt gag aag cgc	cac ctt caa gtg aac	gtc	2225
Leu Val Asn His Phe	Lys Ser Glu Lys Arg	His Leu Gln Val Asn	Val	
696	701	706	711	
acc aac cca gta cag	tgc agc ctg cac ggg	aag aag tgc acc gtc	tcc	2273
Thr Asn Pro Val Gln	Cys Ser Leu His Gly	Lys Lys Cys Thr Val	Ser	
712	717	722	727	
gtg gag acg cgg ctc	aac cag ccc cag ccc	gac ttc acc aag aat	cgc	2321
Val Glu Thr Arg Leu	Asn Gln Pro Gln Pro	Asp Phe Thr Lys Asn	Arg	
728	733	738	743	

tcg ggc ttc atc ctc agc gtg ccc ggg aac tga cgccccgc ggaggcctgg	2372
Ser Gly Phe Ile Leu Ser Val Pro Gly Asn *	
744 749 754	
cccggagccc ggccacactc cgagtcctgg gtcccagtc agctgctgcc tcccaacca	2432
tgcccgctag aaacctgctg cgagggcccc tcccagagga gccccgcccc tgtaagattt	2492
ccttcctggg tttctgcctt tggatcatc ttctctgtc cttactgtcc acggtccctg	2552
ttcaataagc caaagaccct ggtgccccgc ccagaccctt gggctgacgt ccagaccaat	2612
ctcaccaccag aggcaactgg atgggtgcctt tagttgggtgc ggatgccccg tggccaggtc	2672
aagtcagagc acctggacag gtgtcctccc tgctgctgac cctgcagagg gaaggggtgg	2732
ggatgcagga cccactctg cgaggagcccc atagccacct ctcttgcca aggtgagcca	2792
gccctgggga ccagctcag ggaggctctg ctcagagttc ggcggacca cccaacca	2852
actcccagcc gccagccaaa gccactgggt gagcagagtc acccacaggg ccagcccctc	2912
agccaggagc cagtggcagg aggcggaaca gcccatccag cagagtgagt ccaccccttc	2972
caggttctcc cctgggagac tccctttgcc accaaggccc ccaccagggc ctctgaccac	3032
cgctctggag aggacagtgt ggcattgtcc aaggatcatc ttacttaact cgcagcctgt	3092
ggctgtggtc ctcttataga tactttcacc gtttgccaggg ttgctaata gatacctgct	3152
gtcaccacac ttgggtcagg aaccctaata agaacgggga gctgccaggg tgagggcagc	3212
cctcagggtc ggccgcttcc cctctggacc acctcccgt gcgtttccta ctcagagaaa	3272
cagcaagggc ggggtcaaga cacgggatga cgggaagcag gaagcggggc agcagcacag	3332
cgtgggggtcc tggcactgca ggccaggcca ggatgcccac cccgccctct acacggcccc	3392
ttggggcctg cgcccgtaga actggtgcca gggagcactg ccagcttgcc agtttctgcc	3452
cagcaaaagc acgtatgctt caggggcctt ctgagaccac cttccccact gagccccagc	3512
tgctgagaag gccttgaggg aagtagaggc tgggagcaaa tgccccatgc ggtgagagga	3572
tgaggggagc ctacgcctca ggcatgtggt gagaggagga gggggaggga gccaacgcct	3632
caggtggagt gggcagaggt gcaagagagg gatgtactga agcttcttcc cgtcctgcca	3692
cagacacttc tctgccttc ccaccctgac ccggcagaac ccaccaagtg cctgtgtgca	3752
gcctcctgtg cctcaccag ggcctgacct cagagtggtc ccaacaacct ggtctcatgc	3812
ccactcccca tccctgcttc ccaaaaattg cactgtgtgc agtttgcaac aaagaatccc	3872
gctggcatcc tgtccttggg aaccctttct cattctccaa gcctggtcag ctgcctgcac	3932

```

aggcagaggt gccctcagcc cagattagca acactcatag ttttgccaat taccagtaga 3992
cactagtgga accatctaac tggaacttcc tctctccttc cacttatttc ctcaaacttg 4052
ttgctttaca ctagacacat gcaaattgtat gttttaaaca caccaaaaca gatcatgcc 4112
aatgagttgc ctgtcaaagg ctggaggggca ggaggagggc ctgggttttg gttctttcct 4172
cccagccttt ggatggtgcc ttggggccct tagccccagc gccagggcct cccagctgag 4232
gccacaggac aagcactttt ttatgatgta ctaaaagcca cagtatgtgg caactgcaaa 4292
aggatcagga atttagggta tgatctcggt cacgtgtccc gggcgctgag gggaaaggaa 4352
gcgggcatga ttgtagacaa tgaggggggt ctcttgatgt aatgaaatgc aattttatgg 4412
tttggtgcaa aaactcctat tttccagtaa attaacttta tttctaaagc atattttgat 4472
ttgccatcaa gagcaataaa gcattaaatc ttaaaaaaaaa aaa 4515

```

```

<210> 52
<211> 6827
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (85) .. (6585)

```

```

<400> 52
cgacacccgt cctgaatttc cgaggacgacg acttcgtcct gccgcaacgt ggcgcagtat 60

aacgccaaccc atcccgactt cccc      atg cag atc gag cag ctg gag cgc tac 111
                               Met Gln Ile Glu Gln Leu Glu Arg Tyr
                               1              5

att cag cga tat ctg gtt tat gcc ata ctc tgg tcc ctg tct gga gac 159
Ile Gln Arg Tyr Leu Val Tyr Ala Ile Leu Trp Ser Leu Ser Gly Asp
10              15              20              25

agc cgg cta aaa atg aga gca gag ctg ggt gaa tac atc aga aga atc 207
Ser Arg Leu Lys Met Arg Ala Glu Leu Gly Glu Tyr Ile Arg Arg Ile
26              31              36              41

acg acc gtg cct ctg ccc act gcg ccc aac ata ccc att atc gat tat 255
Thr Thr Val Pro Leu Pro Thr Ala Pro Asn Ile Pro Ile Ile Asp Tyr
42              47              52              57

gag gtg tcc atc agc gga gaa tgg tct ccg tgg cag gcc aag gtg cct 303
Glu Val Ser Ile Ser Gly Glu Trp Ser Pro Trp Gln Ala Lys Val Pro
58              63              68              73

cag att gaa gtg gag acg cac aag gtg gca gcc cct gat gtc gtc gtg 351
Gln Ile Glu Val Glu Thr His Lys Val Ala Ala Pro Asp Val Val Val

```

74						79						84						89	
cca	acg	ctg	gac	aca	gtc	cgc	cac	gaa	gcc	ctc	ttg	tac	act	tgg	ctg	399			
Pro	Thr	Leu	Asp	Thr	Val	Arg	His	Glu	Ala	Leu	Leu	Tyr	Thr	Trp	Leu				
90						95						100						105	
gcc	gaa	cac	aag	ccc	ctg	gtc	ttg	tgt	ggc	cct	cct	ggg	tct	ggc	aag	447			
Ala	Glu	His	Lys	Pro	Leu	Val	Leu	Cys	Gly	Pro	Pro	Gly	Ser	Gly	Lys				
106						111						116						121	
acc	atg	aca	ctc	ttc	agc	gcc	ctc	cgg	gcc	ttg	cct	gac	atg	gag	gtg	495			
Thr	Met	Thr	Leu	Phe	Ser	Ala	Leu	Arg	Ala	Leu	Pro	Asp	Met	Glu	Val				
122						127						132						137	
gtg	ggc	ctc	aac	ttc	tcc	agt	gct	act	act	cca	gag	ctg	ctt	ctg	aag	543			
Val	Gly	Leu	Asn	Phe	Ser	Ser	Ala	Thr	Thr	Pro	Glu	Leu	Leu	Leu	Lys				
138						143						148						153	
act	ttt	gat	cac	tac	tgc	gag	tac	agg	cgc	aca	cct	aat	ggg	gtg	gtt	591			
Thr	Phe	Asp	His	Tyr	Cys	Glu	Tyr	Arg	Arg	Thr	Pro	Asn	Gly	Val	Val				
154						159						164						169	
ttg	gct	cct	gtt	caa	ctt	gga	aag	tgg	ctg	gtg	ttg	ttc	tgt	gat	gaa	639			
Leu	Ala	Pro	Val	Gln	Leu	Gly	Lys	Trp	Leu	Val	Leu	Phe	Cys	Asp	Glu				
170						175						180						185	
atc	aac	ttg	cca	gat	atg	gat	aaa	tat	ggg	acc	cag	agg	gtc	ata	tcc	687			
Ile	Asn	Leu	Pro	Asp	Met	Asp	Lys	Tyr	Gly	Thr	Gln	Arg	Val	Ile	Ser				
186						191						196						201	
ttc	atc	aga	cag	atg	gtg	gag	cac	gga	ggc	ttt	tac	cgt	acc	tca	gat	735			
Phe	Ile	Arg	Gln	Met	Val	Glu	His	Gly	Gly	Phe	Tyr	Arg	Thr	Ser	Asp				
202						207						212						217	
caa	aca	tgg	gtg	aag	ctg	gag	aga	atc	cag	ttt	gtt	ggg	gct	tgt	aat	783			
Gln	Thr	Trp	Val	Lys	Leu	Glu	Arg	Ile	Gln	Phe	Val	Gly	Ala	Cys	Asn				
218						223						228						233	
ccc	ccc	aca	gac	cct	gga	aga	aag	ccc	ctc	tca	cac	agg	ttc	ctg	cgc	831			
Pro	Pro	Thr	Asp	Pro	Gly	Arg	Lys	Pro	Leu	Ser	His	Arg	Phe	Leu	Arg				
234						239						244						249	
cac	gtg	cct	gtc	gtg	tat	gtg	gat	tac	ccg	ggc	ccc	gcc	tcc	ctc	aca	879			
His	Val	Pro	Val	Val	Tyr	Val	Asp	Tyr	Pro	Gly	Pro	Ala	Ser	Leu	Thr				
250						255						260						265	
cag	atc	tac	ggc	acc	ttc	aac	cgc	gcc	atg	ctg	agg	ctc	att	cca	tcc	927			
Gln	Ile	Tyr	Gly	Thr	Phe	Asn	Arg	Ala	Met	Leu	Arg	Leu	Ile	Pro	Ser				
266						271						276						281	
ctg	cgg	acg	tat	gca	gag	ccg	ctc	act	gct	gcc	atg	gtg	gag	ttc	tac	975			
Leu	Arg	Thr	Tyr	Ala	Glu	Pro	Leu	Thr	Ala	Ala	Met	Val	Glu	Phe	Tyr				
282						287						292						297	
acc	atg	tct	cag	gag	aga	ttc	acc	cag	gat	aca	caa	cct	cac	tat	atc	1023			
Thr	Met	Ser	Gln	Glu	Arg	Phe	Thr	Gln	Asp	Thr	Gln	Pro	His	Tyr	Ile				
298						303						308						313	

tat tca ccc cgt gaa atg act agg tgg gtg aga ggc atc ttt gaa gcg	1071
Tyr Ser Pro Arg Glu Met Thr Arg Trp Val Arg Gly Ile Phe Glu Ala	
314 319 324 329	
ctg aga cct ctg gag acc ctg cct gtt gaa ggc ctc att cgg att tgg	1119
Leu Arg Pro Leu Glu Thr Leu Pro Val Glu Gly Leu Ile Arg Ile Trp	
330 335 340 345	
gca cat gaa gct ctg cgt ctc ttc caa gat aga ctc gta gag gat gag	1167
Ala His Glu Ala Leu Arg Leu Phe Gln Asp Arg Leu Val Glu Asp Glu	
346 351 356 361	
gag agg cgt tgg act gat gag aac atc gac acg gtt gct ctg aag cac	1215
Glu Arg Arg Trp Thr Asp Glu Asn Ile Asp Thr Val Ala Leu Lys His	
362 367 372 377	
ttc cct aac atc gac aga gag aag gca atg agc cga ccc atc ttg tac	1263
Phe Pro Asn Ile Asp Arg Glu Lys Ala Met Ser Arg Pro Ile Leu Tyr	
378 383 388 393	
agc aac tgg ctg tca aag gat tac atc cca gta gac caa gaa gag tta	1311
Ser Asn Trp Leu Ser Lys Asp Tyr Ile Pro Val Asp Gln Glu Glu Leu	
394 399 404 409	
aga gat tat gtc aaa gct agg ctg aag gtc ttt tat gaa gaa gaa ctt	1359
Arg Asp Tyr Val Lys Ala Arg Leu Lys Val Phe Tyr Glu Glu Glu Leu	
410 415 420 425	
gat gtt ccg ctg gtg ctg ttt aat gaa gtc cta gac cac gtg ctg agg	1407
Asp Val Pro Leu Val Leu Phe Asn Glu Val Leu Asp His Val Leu Arg	
426 431 436 441	
att gac aga ata ttc cgt caa cct caa ggc cac ttg ctt ctg att ggt	1455
Ile Asp Arg Ile Phe Arg Gln Pro Gln Gly His Leu Leu Leu Ile Gly	
442 447 452 457	
gtt agt gga gca gga aaa act acc ctg tct cgt ttc gtc gcc tgg atg	1503
Val Ser Gly Ala Gly Lys Thr Thr Leu Ser Arg Phe Val Ala Trp Met	
458 463 468 473	
aac ggt ttg agt gtg tac cag att aag gtc cat agg aag tac aca ggg	1551
Asn Gly Leu Ser Val Tyr Gln Ile Lys Val His Arg Lys Tyr Thr Gly	
474 479 484 489	
gaa gac ttt gat gaa gat cta cgg aca gtg ttg aga cgt tct ggc tgt	1599
Glu Asp Phe Asp Glu Asp Leu Arg Thr Val Leu Arg Arg Ser Gly Cys	
490 495 500 505	
aaa aat gaa aag ata gca ttt ata atg gat gaa tct aat gtg tta gat	1647
Lys Asn Glu Lys Ile Ala Phe Ile Met Asp Glu Ser Asn Val Leu Asp	
506 511 516 521	
tct gga ttc ctg gag cga atg aat acc ctt ctg gcc aat gga gag gtg	1695
Ser Gly Phe Leu Glu Arg Met Asn Thr Leu Leu Ala Asn Gly Glu Val	
522 527 532 537	

cct ggt ctc ttt gaa gga gac gag tat gcc acc ttg atg acg cag tgc	1743
Pro Gly Leu Phe Glu Gly Asp Glu Tyr Ala Thr Leu Met Thr Gln Cys	
538 543 548 553	
aaa gag ggg gca cag aag gaa ggc ctg atg ctg gac tcg cac gag gag	1791
Lys Glu Gly Ala Gln Lys Glu Gly Leu Met Leu Asp Ser His Glu Glu	
554 559 564 569	
ctc tac aag tgg ttc act agc cag gtt atc cgc aac ctc cac gtc gtg	1839
Leu Tyr Lys Trp Phe Thr Ser Gln Val Ile Arg Asn Leu His Val Val	
570 575 580 585	
ttc acc atg aac ccg tcc tcg gag gga ctc aag gac cgg gca gct aca	1887
Phe Thr Met Asn Pro Ser Ser Glu Gly Leu Lys Asp Arg Ala Ala Thr	
586 591 596 601	
tca cca gca ctt ttc aac agg tgt gtg ttg aat tgg ttt gga gac tgg	1935
Ser Pro Ala Leu Phe Asn Arg Cys Val Leu Asn Trp Phe Gly Asp Trp	
602 607 612 617	
tcc acc gaa gca ctg tat cag gtt ggc aaa gaa ttc aca agt aag atg	1983
Ser Thr Glu Ala Leu Tyr Gln Val Gly Lys Glu Phe Thr Ser Lys Met	
618 623 628 633	
gat ctg gag aag cca aat tac atc gtg cct gat tac atg cca gtt gtg	2031
Asp Leu Glu Lys Pro Asn Tyr Ile Val Pro Asp Tyr Met Pro Val Val	
634 639 644 649	
tat gat aag ctg ccg cag cca cca tcc cat cgg gaa gcc att gtg aac	2079
Tyr Asp Lys Leu Pro Gln Pro Pro Ser His Arg Glu Ala Ile Val Asn	
650 655 660 665	
agc tgt gtg ttt gtt cat cag act ctt cac cag gcg aat gct cgg cta	2127
Ser Cys Val Phe Val His Gln Thr Leu His Gln Ala Asn Ala Arg Leu	
666 671 676 681	
gca aag cga ggc ggc aga acg atg gcc atc acc cct cgc cac tac ctg	2175
Ala Lys Arg Gly Gly Arg Thr Met Ala Ile Thr Pro Arg His Tyr Leu	
682 687 692 697	
gac ttc atc aat cac tat gcc aac ctg ttc cac gag aag cgg agc gag	2223
Asp Phe Ile Asn His Tyr Ala Asn Leu Phe His Glu Lys Arg Ser Glu	
698 703 708 713	
ctg gag gag cag cag atg cac ttg aac gtg ggg ctc agg aag atc aaa	2271
Leu Glu Glu Gln Gln Met His Leu Asn Val Gly Leu Arg Lys Ile Lys	
714 719 724 729	
gag aca gtc gac cag gta gaa gaa ctg cgt cgt gac ttg agg ata aag	2319
Glu Thr Val Asp Gln Val Glu Glu Leu Arg Arg Asp Leu Arg Ile Lys	
730 735 740 745	
agc caa gag ctg gag gtg aag aat gca gca gcc aat gac aag ctg aaa	2367
Ser Gln Glu Leu Glu Val Lys Asn Ala Ala Ala Asn Asp Lys Leu Lys	
746 751 756 761	
aag atg gtg aaa gac cag cag gag gct gaa aag aag aag gtt atg agc	2415

Lys Met Val Lys Asp Gln Gln Glu Ala Glu	Lys Lys Lys Val Met Ser	
762	767	772 777
caa gaa atc cag gaa cag ctg cat aag cag	cag gag gta att gca gac	2463
Gln Glu Ile Gln Glu Gln Leu His Lys Gln	Gln Glu Val Ile Ala Asp	
778	783 788	793
aaa cag atg agt gtc aaa gaa gat ctt gat	aag gtg gaa cct gcc gtc	2511
Lys Gln Met Ser Val Lys Glu Asp Leu Asp	Lys Val Glu Pro Ala Val	
794	799	804 809
att gag gcc cag aat gct gtg aag tcg atc	aag aag cag cac ctg gtg	2559
Ile Glu Ala Gln Asn Ala Val Lys Ser Ile	Lys Lys Gln His Leu Val	
810	815	820 825
gag gtg agg tcc atg gcc aac cct cct gct	gct gtg aag ctg gcg ctg	2607
Glu Val Arg Ser Met Ala Asn Pro Pro Ala	Ala Val Lys Leu Ala Leu	
826	831	836 841
gag tcc atc tgc ctg ctg ctg ggg gaa agc	acc aca gac tgg aag cag	2655
Glu Ser Ile Cys Leu Leu Leu Gly Glu Ser	Thr Thr Asp Trp Lys Gln	
842	847	852 857
atc cgc tcc atc atc atg cgg gag aac ttc	atc ccc acc atc gtc aac	2703
Ile Arg Ser Ile Ile Met Arg Glu Asn Phe	Ile Pro Thr Ile Val Asn	
858	863	868 873
ttc tct gca gag gag atc agt gac gcc ata	agg gag aag atg aag aaa	2751
Phe Ser Ala Glu Glu Ile Ser Asp Ala Ile	Arg Glu Lys Met Lys Lys	
874	879	884 889
aat tac atg tcc aat cca agt tac aat tat	gaa att gtg aat cgg gct	2799
Asn Tyr Met Ser Asn Pro Ser Tyr Asn Tyr	Glu Ile Val Asn Arg Ala	
890	895	900 905
tcc ctg gct tgc ggc cct atg gtg aaa tgg	gca att gca cag ctt aac	2847
Ser Leu Ala Cys Gly Pro Met Val Lys Trp	Ala Ile Ala Gln Leu Asn	
906	911	916 921
tat gca gac atg tta aag aga gtg gag ccc	cta cgc aat gag ctg cag	2895
Tyr Ala Asp Met Leu Lys Arg Val Glu Pro	Leu Arg Asn Glu Leu Gln	
922	927	932 937
aag ctg gaa gat gac gcc aag gac aac cag	cag aag gcc aac gag gtg	2943
Lys Leu Glu Asp Asp Ala Lys Asp Asn Gln	Gln Lys Ala Asn Glu Val	
938	943	948 953
gag cag atg atc cga gac ctg gaa gcc agc	atc gcc cgc tac aag gag	2991
Glu Gln Met Ile Arg Asp Leu Glu Ala Ser	Ile Ala Arg Tyr Lys Glu	
954	959	964 969
gaa tac gcc gtc ctg atc tca gag gcc cag	gcc atc aag gca gac ctg	3039
Glu Tyr Ala Val Leu Ile Ser Glu Ala Gln	Ala Ile Lys Ala Asp Leu	
970	975	980 985
gca gct gtc gag gca aaa gta aac cgg agc	act gct ctt ctg aag agc	3087
Ala Ala Val Glu Ala Lys Val Asn Arg Ser	Thr Ala Leu Leu Lys Ser	

986	991	996	1001	
ttg tct gct gaa cgt gaa cga tgg gaa aaa aca agt gaa act ttc aaa				3135
Leu Ser Ala Glu Arg Glu Arg Trp Glu Lys Thr Ser Glu Thr Phe Lys				
1002	1007	1012	1017	
aac cag atg tcc acc att gct ggg gac tgt ctc ttg tca gct gcg ttc				3183
Asn Gln Met Ser Thr Ile Ala Gly Asp Cys Leu Leu Ser Ala Ala Phe				
1018	1023	1028	1033	
att gcc tac gcg ggt tac ttt gac cag cag atg cgt cag aac ttg ttc				3231
Ile Ala Tyr Ala Gly Tyr Phe Asp Gln Gln Met Arg Gln Asn Leu Phe				
1034	1039	1044	1049	
act acc tgg tcc cat cac cta cag caa gcc aac atc cag ttc cgt aca				3279
Thr Thr Trp Ser His His Leu Gln Gln Ala Asn Ile Gln Phe Arg Thr				
1050	1055	1060	1065	
gat att gcc agg acg gaa tac ctt tcc aat gct gat gag cgt ctt cgc				3327
Asp Ile Ala Arg Thr Glu Tyr Leu Ser Asn Ala Asp Glu Arg Leu Arg				
1066	1071	1076	1081	
tgg cag gcc agc tcc ttg cct gct gat gac ctt tgc aca gaa aat gcc				3375
Trp Gln Ala Ser Ser Leu Pro Ala Asp Asp Leu Cys Thr Glu Asn Ala				
1082	1087	1092	1097	
atc atg ctg aaa cga ttc aat agg tat ccg ctg atc att gac ccc tct				3423
Ile Met Leu Lys Arg Phe Asn Arg Tyr Pro Leu Ile Ile Asp Pro Ser				
1098	1103	1108	1113	
gga cag gcc aca gaa ttc att atg aat gaa tat aag gat cgt aag atc				3471
Gly Gln Ala Thr Glu Phe Ile Met Asn Glu Tyr Lys Asp Arg Lys Ile				
1114	1119	1124	1129	
aca cgg acc agc ttc ctg gat gac gcc ttc aga aag aac tta gag agt				3519
Thr Arg Thr Ser Phe Leu Asp Asp Ala Phe Arg Lys Asn Leu Glu Ser				
1130	1135	1140	1145	
gca ctg aga ttc ggt aac ccc ctt ctg gtc cag gat gtg gaa agc tac				3567
Ala Leu Arg Phe Gly Asn Pro Leu Leu Val Gln Asp Val Glu Ser Tyr				
1146	1151	1156	1161	
gat cca gtt ttg aac ccg gtg ctg aac cgt gaa gtg cgg cga aca ggg				3615
Asp Pro Val Leu Asn Pro Val Leu Asn Arg Glu Val Arg Arg Thr Gly				
1162	1167	1172	1177	
ggg aga gtg ctg atc act ctc ggg gac cag gac ata gac ctg tcg cca				3663
Gly Arg Val Leu Ile Thr Leu Gly Asp Gln Asp Ile Asp Leu Ser Pro				
1178	1183	1188	1193	
tcg ttt gtc atc ttc ctg tcc acc cgg gat cca act gtc gag ttc cca				3711
Ser Phe Val Ile Phe Leu Ser Thr Arg Asp Pro Thr Val Glu Phe Pro				
1194	1199	1204	1209	
cca gat ctc tgt tcc cgg gtt act ttt gta aac ttc aca gtt acc cgt				3759
Pro Asp Leu Cys Ser Arg Val Thr Phe Val Asn Phe Thr Val Thr Arg				
1210	1215	1220	1225	

agc	agt	tta	caa	agc	cag	tgt	cta	aat	gaa	gta	ctt	aaa	gca	gaa	aga	3807
Ser	Ser	Leu	Gln	Ser	Gln	Cys	Leu	Asn	Glu	Val	Leu	Lys	Ala	Glu	Arg	
1226					1231					1236					1241	
cct	gat	gtg	gac	gag	aaa	cga	tct	gat	ctt	ctt	aaa	ctt	caa	ggg	gaa	3855
Pro	Asp	Val	Asp	Glu	Lys	Arg	Ser	Asp	Leu	Leu	Lys	Leu	Gln	Gly	Glu	
1242					1247					1252					1257	
ttt	cag	ctc	cgt	ttg	cgt	cag	ctg	gaa	aaa	tct	cta	cta	caa	gct	ctg	3903
Phe	Gln	Leu	Arg	Leu	Arg	Gln	Leu	Glu	Lys	Ser	Leu	Leu	Gln	Ala	Leu	
1258					1263					1268					1273	
aac	gag	gtg	aaa	ggg	cgc	att	ttg	gat	gac	gac	acg	atc	ata	acc	act	3951
Asn	Glu	Val	Lys	Gly	Arg	Ile	Leu	Asp	Asp	Asp	Thr	Ile	Ile	Thr	Thr	
1274					1279					1284					1289	
ctg	gag	aac	ctg	aag	aga	gag	gct	gca	gag	gtc	acc	agg	aaa	gtt	gag	3999
Leu	Glu	Asn	Leu	Lys	Arg	Glu	Ala	Ala	Glu	Val	Thr	Arg	Lys	Val	Glu	
1290					1295					1300					1305	
gag	acg	gac	att	gtc	atg	cag	gag	gtg	gag	acc	gtg	tcc	cag	cag	tac	4047
Glu	Thr	Asp	Ile	Val	Met	Gln	Glu	Val	Glu	Thr	Val	Ser	Gln	Gln	Tyr	
1306					1311					1316					1321	
ctc	ccg	ctc	tcc	acc	gcc	tgc	agc	agc	atc	tac	ttc	acc	atg	gag	tcc	4095
Leu	Pro	Leu	Ser	Thr	Ala	Cys	Ser	Ser	Ile	Tyr	Phe	Thr	Met	Glu	Ser	
1322					1327					1332					1337	
ctc	aag	cag	ata	cac	ttc	ttg	tac	cag	tac	tcc	ctc	cag	ttt	ttc	ctg	4143
Leu	Lys	Gln	Ile	His	Phe	Leu	Tyr	Gln	Tyr	Ser	Leu	Gln	Phe	Phe	Leu	
1338					1343					1348					1353	
gac	att	tat	cac	aac	gtc	cta	tac	gag	aac	ccg	aac	ctg	aag	ggg	gtc	4191
Asp	Ile	Tyr	His	Asn	Val	Leu	Tyr	Glu	Asn	Pro	Asn	Leu	Lys	Gly	Val	
1354					1359					1364					1369	
acc	gac	cac	aca	cag	cgc	ctg	tcc	att	ata	aca	aag	gac	ctc	ttc	cag	4239
Thr	Asp	His	Thr	Gln	Arg	Leu	Ser	Ile	Ile	Thr	Lys	Asp	Leu	Phe	Gln	
1370					1375					1380					1385	
gtg	gcg	ttt	aac	cga	gtg	gct	cga	ggc	atg	ctg	cat	cag	gac	cac	att	4287
Val	Ala	Phe	Asn	Arg	Val	Ala	Arg	Gly	Met	Leu	His	Gln	Asp	His	Ile	
1386					1391					1396					1401	
acc	ttt	gcc	atg	ctg	ctg	gca	aga	atc	aaa	ctg	aag	ggc	acc	gtg	ggg	4335
Thr	Phe	Ala	Met	Leu	Leu	Ala	Arg	Ile	Lys	Leu	Lys	Gly	Thr	Val	Gly	
1402					1407					1412					1417	
gag	ccc	acc	tac	gat	gca	gaa	ttc	cag	cac	ttc	ttg	aga	gga	aat	gag	4383
Glu	Pro	Thr	Tyr	Asp	Ala	Glu	Phe	Gln	His	Phe	Leu	Arg	Gly	Asn	Glu	
1418					1423					142						

gag cag gcg gag gcg gtg gtg agg ctg agc tgc ctt ccc gcg ttt aag	4479
Glu Gln Ala Glu Ala Val Val Arg Leu Ser Cys Leu Pro Ala Phe Lys	
1450 1455 1460 1465	
gac ttg att gca aag gtt cag gca gac gag caa ttt ggc atc tgg ctg	4527
Asp Leu Ile Ala Lys Val Gln Ala Asp Glu Gln Phe Gly Ile Trp Leu	
1466 1471 1476 1481	
gac agc agc tcc ccg gag cag act gtg ccc tac ctc tgg agt gaa gaa	4575
Asp Ser Ser Ser Pro Glu Gln Thr Val Pro Tyr Leu Trp Ser Glu Glu	
1482 1487 1492 1497	
aca cct gca aca ccc att ggc cag gcc atc cac cgc ctg ctc ctg atc	4623
Thr Pro Ala Thr Pro Ile Gly Gln Ala Ile His Arg Leu Leu Leu Ile	
1498 1503 1508 1513	
cag gct ttc cgg ccc gat cgc ctg ttg gcc atg gcc cac atg ttt gtt	4671
Gln Ala Phe Arg Pro Asp Arg Leu Leu Ala Met Ala His Met Phe Val	
1514 1519 1524 1529	
tca aca aac ctt ggg gag tct ttc atg tcc atc atg gag cag ccg ctc	4719
Ser Thr Asn Leu Gly Glu Ser Phe Met Ser Ile Met Glu Gln Pro Leu	
1530 1535 1540 1545	
gac ctg acc cac att gtg ggc aca gag gtg aag ccc aac act cct gtc	4767
Asp Leu Thr His Ile Val Gly Thr Glu Val Lys Pro Asn Thr Pro Val	
1546 1551 1556 1561	
tta atg tgc tct gtg cct ggt tat gat gcc agt gga cat gtc gag gac	4815
Leu Met Cys Ser Val Pro Gly Tyr Asp Ala Ser Gly His Val Glu Asp	
1562 1567 1572 1577	
ctt gca gcc gag cag aac acg cag atc act tca att gca atc ggc tct	4863
Leu Ala Ala Glu Gln Asn Thr Gln Ile Thr Ser Ile Ala Ile Gly Ser	
1578 1583 1588 1593	
gca gaa ggc ttt aac caa gca gat aag gca ata aac acc gct gta aag	4911
Ala Glu Gly Phe Asn Gln Ala Asp Lys Ala Ile Asn Thr Ala Val Lys	
1594 1599 1604 1609	
tcg ggc agg tgg gtg atg ctg aag aat gtg cat ctg gcc cca ggg tgg	4959
Ser Gly Arg Trp Val Met Leu Lys Asn Val His Leu Ala Pro Gly Trp	
1610 1615 1620 1625	
ctg atg cag ctg gag aag aag ttg cat tcc ctg cag ccg cat gcc tgc	5007
Leu Met Gln Leu Glu Lys Lys Leu His Ser Leu Gln Pro His Ala Cys	
1626 1631 1636 1641	
ttc cga ctc ttc ctc acc atg gag atc aac ccc aag gtg cct gtg aat	5055
Phe Arg Leu Phe Leu Thr Met Glu Ile Asn Pro Lys Val Pro Val Asn	
1642 1647 1652 1657	
ctg ctc cgt gcg ggc cgc atc ttt gtg ttc gag cca ccg cca ggg gtg	5103
Leu Leu Arg Ala Gly Arg Ile Phe Val Phe Glu Pro Pro Pro Gly Val	
1658 1663 1668 1673	
aag gcc aac atg ctg agg acg ttc agc agc att ccc gtc tca cgg ata	5151

Lys Ala Asn Met Leu Arg Thr Phe Ser Ser Ile Pro Val Ser Arg Ile	
1674	1679 1684 1689
tgc aag tct ccc aac gag cgt gcc cgc ttg tac ttc ctg ctg gcc tgg	5199
Cys Lys Ser Pro Asn Glu Arg Ala Arg Leu Tyr Phe Leu Leu Ala Trp	
1690	1695 1700 1705
ttt cat gcg atc atc caa gaa cgc tta cga tac gca cca ctg ggg tgg	5247
Phe His Ala Ile Ile Gln Glu Arg Leu Arg Tyr Ala Pro Leu Gly Trp	
1706	1711 1716 1721
tca aag aag tat gaa ttt gga gag tct gac ctg cgg tca gct tgc gat	5295
Ser Lys Lys Tyr Glu Phe Gly Glu Ser Asp Leu Arg Ser Ala Cys Asp	
1722	1727 1732 1737
acg gtg gac acg tgg ctg gat gac acg gcc aag ggc agg cag aac atc	5343
Thr Val Asp Thr Trp Leu Asp Asp Thr Ala Lys Gly Arg Gln Asn Ile	
1738	1743 1748 1753
tca ccg gat aag atc ccg tgg tct gca cta aag acc tta atg gcc cag	5391
Ser Pro Asp Lys Ile Pro Trp Ser Ala Leu Lys Thr Leu Met Ala Gln	
1754	1759 1764 1769
tcc att tat ggc ggg cgc gtg gac aac gag ttt gac cag cgt ctg ctc	5439
Ser Ile Tyr Gly Gly Arg Val Asp Asn Glu Phe Asp Gln Arg Leu Leu	
1770	1775 1780 1785
aac acc ttc ctg gag cgc ctg ttc aca acc agg agt ttc gac agt gag	5487
Asn Thr Phe Leu Glu Arg Leu Phe Thr Thr Arg Ser Phe Asp Ser Glu	
1786	1791 1796 1801
ttt aag ctg gca tgc aag gtc gac gga cat aaa gac att caa atg cca	5535
Phe Lys Leu Ala Cys Lys Val Asp Gly His Lys Asp Ile Gln Met Pro	
1802	1807 1812 1817
gat ggc atc agg cga gag gag ttt gtg cag tgg gtg gag ttg ctc ccc	5583
Asp Gly Ile Arg Arg Glu Glu Phe Val Gln Trp Val Glu Leu Leu Pro	
1818	1823 1828 1833
gac acc cag acg ccc tcc tgg ctg ggc ctg ccc aac aac gcc gag aga	5631
Asp Thr Gln Thr Pro Ser Trp Leu Gly Leu Pro Asn Asn Ala Glu Arg	
1834	1839 1844 1849
gtc ctc ctt acc aca cag ggt gtg gac atg atc agt aaa atg ctg aag	5679
Val Leu Leu Thr Thr Gln Gly Val Asp Met Ile Ser Lys Met Leu Lys	
1850	1855 1860 1865
atg cag atg ttg gag gat gag gac gac ctg gcc tac gca gag act gag	5727
Met Gln Met Leu Glu Asp Glu Asp Asp Leu Ala Tyr Ala Glu Thr Glu	
1866	1871 1876 1881
aag aag acg agg aca gac tcc acg tcc gac ggg cgc cct gcc tgg atg	5775
Lys Lys Thr Arg Thr Asp Ser Thr Ser Asp Gly Arg Pro Ala Trp Met	
1882	1887 1892 1897
cgg aca ctg cac acc acc gcg tcc aac tgg ctg cac ctc atc ccc cag	5823
Arg Thr Leu His Thr Thr Ala Ser Asn Trp Leu His Leu Ile Pro Gln	

1898	1903	1908	1913	
acg ctg agc cac ctc aag cgc acc gtg gag aat atc aag gat cct ttg				5871
Thr Leu Ser His Leu Lys Arg Thr Val Glu Asn Ile Lys Asp Pro Leu				
1914	1919	1924	1929	
ttc agg ttc ttt gag aga gaa gtg aag atg ggc gca aag ctg ctt cag				5919
Phe Arg Phe Phe Glu Arg Glu Val Lys Met Gly Ala Lys Leu Leu Gln				
1930	1935	1940	1945	
gac gtt cgc cag gac ctt gca gat gtc gtc cag gtg tgc gaa gga aag				5967
Asp Val Arg Gln Asp Leu Ala Asp Val Val Gln Val Cys Glu Gly Lys				
1946	1951	1956	1961	
aag aag cag acc aac tac ttg cgc acg ctg atc aac gag cta gtg aaa				6015
Lys Lys Gln Thr Asn Tyr Leu Arg Thr Leu Ile Asn Glu Leu Val Lys				
1962	1967	1972	1977	
ggg atc ttg cct cgg agc tgg tcc cac tac acg gtg cct gcc ggc atg				6063
Gly Ile Leu Pro Arg Ser Trp Ser His Tyr Thr Val Pro Ala Gly Met				
1978	1983	1988	1993	
acc gtc atc cag tgg gtg tcc gac ttc agc gag agg atc aaa cag ctg				6111
Thr Val Ile Gln Trp Val Ser Asp Phe Ser Glu Arg Ile Lys Gln Leu				
1994	1999	2004	2009	
cag aac atc tca ctg gca gct gca tct ggt ggc gcc aag gag cta aag				6159
Gln Asn Ile Ser Leu Ala Ala Ala Ser Gly Gly Ala Lys Glu Leu Lys				
2010	2015	2020	2025	
aac atc cac gtg tgc ctg ggt ggc ctg ttc gtg cct gag gcg tac atc				6207
Asn Ile His Val Cys Leu Gly Gly Leu Phe Val Pro Glu Ala Tyr Ile				
2026	2031	2036	2041	
act gcc acc agg cag tat gtg gcc cag gcc aac agc tgg tcc ctg gag				6255
Thr Ala Thr Arg Gln Tyr Val Ala Gln Ala Asn Ser Trp Ser Leu Glu				
2042	2047	2052	2057	
gag ctc tgc ctg gaa gtc aac gtc acc acc tca cag ggc gcc acc ctt				6303
Glu Leu Cys Leu Glu Val Asn Val Thr Thr Ser Gln Gly Ala Thr Leu				
2058	2063	2068	2073	
gac gct tgc agc ttc gga gtc acg ggt ttg aaa ctt caa ggg gcc acg				6351
Asp Ala Cys Ser Phe Gly Val Thr Gly Leu Lys Leu Gln Gly Ala Thr				
2074	2079	2084	2089	
tgc aac aac aac aag ctg tca ctg tcc aat gcc atc tca acc gcc ctt				6399
Cys Asn Asn Asn Lys Leu Ser Leu Ser Asn Ala Ile Ser Thr Ala Leu				
2090	2095	2100	2105	
ccc ctg acg cag ctg cgc tgg gtc aag cag aca aac acc gag aag aag				6447
Pro Leu Thr Gln Leu Arg Trp Val Lys Gln Thr Asn Thr Glu Lys Lys				
2106	2111	2116	2121	
gcc agt gtg gta acc tta cct gtc tac ctg aac ttc acc cgt gca gac				6495
Ala Ser Val Val Thr Leu Pro Val Tyr Leu Asn Phe Thr Arg Ala Asp				
2122	2127	2132	2137	

```

ctc atc ttc acc gtg gac ttc gaa att gct aca aag gag gat cct cgc      6543
Leu Ile Phe Thr Val Asp Phe Glu Ile Ala Thr Lys Glu Asp Pro Arg
2138                2143                2148                2153

agc ttc tac gag cgg ggt gtc gca gtc ttg tgc aca gag taa acttttc      6592
Ser Phe Tyr Glu Arg Gly Val Ala Val Leu Cys Thr Glu  *
2154                2159                2164

tagctgcccc tttctgtaat agtgaaagtt ggtatttaac atttattcat ttttaaaata      6652

tttggaaggt ctgagcttgt gaaaagaaag tggttggtct gaggttggag gaagctgaat      6712

ggaatctgac ggttgggagt ggtggaaatt ggaaggatac caggaggtat ttgggaaggc      6772

caatggcgtg gctcctttga ggaaataaaa cactaagcat gaaaaaaaaa aaaaa      6827

```

```

<210> 53
<211> 3028
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (210)..(2531)

```

```

<400> 53
ccgtgccgga attcccgct cgacgatttc gtggctaagg cgccaggcac gggcaccacc      60
agggcgccca ggagccgccc gccgccggca tggaccagct gtactgccca ccgagcgct      120
gccagtcttt tggtagaac tagtcacaca gacctcaacc tgatgcgtgg agacaaggaa      180
atgcttttca gtgtgtccag aaagagaaa atg cag gtg tct tct gcg gag gtg      233
Met Gln Val Ser Ser Ala Glu Val
1                      5

cgc atc ggg ccc atg aga ctg acg cag gac cct att cag gtt ttg ctg      281
Arg Ile Gly Pro Met Arg Leu Thr Gln Asp Pro Ile Gln Val Leu Leu
9                      14                      19                      24

atc ttt gca aag gaa gat agt cag agc gat ggc ttc tgg tgg gcc tgc      329
Ile Phe Ala Lys Glu Asp Ser Gln Ser Asp Gly Phe Trp Trp Ala Cys
25                      30                      35                      40

gac aga gct ggt tat aga tgc aat att gct cgg act cca gag tca gcc      377
Asp Arg Ala Gly Tyr Arg Cys Asn Ile Ala Arg Thr Pro Glu Ser Ala
41                      46                      51                      56

ctt gaa tgc ttt ctt gat aag cat cat gaa att att gta att gat cat      425
Leu Glu Cys Phe Leu Asp Lys His His Glu Ile Ile Val Ile Asp His
57                      62                      67                      72

aga caa act cag aac ttc gat gca gaa gca gtg tgc agg tcg atc cgg      473

```


Arg	Gln	Thr	Gln	Asn	Phe	Asp	Ala	Glu	Ala	Val	Cys	Arg	Ser	Ile	Arg	
73					78					83					88	
gcc	aca	aat	ccc	tcc	gag	cac	acg	gtg	atc	ctc	gca	gtg	gtt	tcg	cga	521
Ala	Thr	Asn	Pro	Ser	Glu	His	Thr	Val	Ile	Leu	Ala	Val	Val	Ser	Arg	
89					94					99					104	
gta	tcg	gat	gac	cat	gaa	gag	gcg	tca	gtc	ctt	cct	ctt	ctc	cac	gca	569
Val	Ser	Asp	Asp	His	Glu	Glu	Ala	Ser	Val	Leu	Pro	Leu	Leu	His	Ala	
105					110					115					120	
ggc	ttc	aac	agg	aga	ttt	atg	gag	aat	agc	agc	ata	att	gct	tgc	tat	617
Gly	Phe	Asn	Arg	Arg	Phe	Met	Glu	Asn	Ser	Ser	Ile	Ile	Ala	Cys	Tyr	
121					126					131					136	
aat	gaa	ctg	att	caa	ata	gaa	cat	ggg	gaa	gtt	cgc	tcc	cag	ttc	aaa	665
Asn	Glu	Leu	Ile	Gln	Ile	Glu	His	Gly	Glu	Val	Arg	Ser	Gln	Phe	Lys	
137					142					147					152	
tta	cgg	gcc	tgt	aat	tca	gtg	ttt	aca	gca	tta	gat	cac	tgt	cat	gaa	713
Leu	Arg	Ala	Cys	Asn	Ser	Val	Phe	Thr	Ala	Leu	Asp	His	Cys	His	Glu	
153					158					163					168	
gcc	ata	gaa	ata	aca	agc	gat	gac	cac	gtg	att	cag	tat	gtc	aac	cca	761
Ala	Ile	Glu	Ile	Thr	Ser	Asp	Asp	His	Val	Ile	Gln	Tyr	Val	Asn	Pro	
169					174					179					184	
gcc	ttc	gaa	agg	atg	atg	ggc	tac	cac	aaa	ggg	gag	ctc	ctg	gga	aaa	809
Ala	Phe	Glu	Arg	Met	Met	Gly	Tyr	His	Lys	Gly	Glu	Leu	Leu	Gly	Lys	
185					190					195					200	
gaa	ctc	gct	gat	ctg	ccc	aaa	agc	gat	aag	aac	cgg	gca	gac	ctt	ctc	857
Glu	Leu	Ala	Asp	Leu	Pro	Lys	Ser	Asp	Lys	Asn	Arg	Ala	Asp	Leu	Leu	
201					206					211					216	
gac	acc	atc	aat	aca	tgc	atc	aag	aag	gga	aag	gag	tgg	cag	ggg	gtt	905
Asp	Thr	Ile	Asn	Thr	Cys	Ile	Lys	Lys	Gly	Lys	Glu	Trp	Gln	Gly	Val	
217					222					227					232	
tac	tat	gcc	aga	cgg	aaa	tcc	ggg	gac	agc	atc	caa	cag	cac	gtg	aag	953
Tyr	Tyr	Ala	Arg	Arg	Lys	Ser	Gly	Asp	Ser	Ile	Gln	Gln	His	Val	Lys	
233					238					243					248	
atc	acc	cca	gtg	att	ggc	caa	gga	ggg	aaa	att	agg	cat	ttt	gtc	tcg	1001
Ile	Thr	Pro	Val	Ile	Gly	Gln	Gly	Gly	Lys	Ile	Arg	His	Phe	Val	Ser	
249					254					259					264	
ctc	aag	aaa	ctg	tgt	tgt	acc	act	gac	aat	aat	aag	cag	att	cac	aag	1049
Leu	Lys	Lys	Leu	Cys	Cys	Thr	Thr	Asp	Asn	Asn	Lys	Gln	Ile	His	Lys	
265					270					275					280	
att	cat	cgt	gat	tca	gga	gac	aat	tct	cag	aca	gag	cct	cat	tca	ttc	1097
Ile	His	Arg	Asp	Ser	Gly	Asp	Asn	Ser	Gln	Thr	Glu	Pro	His	Ser	Phe	
281					286					291					296	
aga	tat	aag	aac	agg	agg	aaa	gag	tcc	att	gac	gtg	aaa	tcg	ata	tca	1145
Arg	Tyr	Lys	Asn	Arg	Arg	Lys	Glu	Ser	Ile	Asp	Val	Lys	Ser	Ile	Ser	

297	302	307	312	
tct cga ggc agt gat	gca cca agc ctg cag	aat cgt cgc tat ccg tcc	1193	
Ser Arg Gly Ser Asp	Ala Pro Ser Leu Gln	Asn Arg Arg Tyr Pro Ser		
313	318	323	328	
atg gcg agg atc cac	tcc atg acc atc gag	gct ccc atc aca aag gtt	1241	
Met Ala Arg Ile His	Ser Met Thr Ile Glu	Ala Pro Ile Thr Lys Val		
329	334	339	344	
ata aat ata atc aat	gca gcc caa gaa aac	agc cca gtc aca gta gcg	1289	
Ile Asn Ile Ile Asn	Ala Ala Gln Glu Asn	Ser Pro Val Thr Val Ala		
345	350	355	360	
gaa gcc ttg gac aga	gtt cta gag att tta	cgg acc aca gaa ctg tac	1337	
Glu Ala Leu Asp Arg	Val Leu Glu Ile Leu	Arg Thr Thr Glu Leu Tyr		
361	366	371	376	
tcc cct cag ctg ggt	acc aaa gat gaa gat	ccc cac acc agt gat ctt	1385	
Ser Pro Gln Leu Gly	Thr Lys Asp Glu Asp	Pro His Thr Ser Asp Leu		
377	382	387	392	
gtt gga ggc ctg atg	act gac ggc ttg aga	aga ctg tca gga aac gag	1433	
Val Gly Gly Leu Met	Thr Asp Gly Leu Arg	Arg Leu Ser Gly Asn Glu		
393	398	403	408	
tat gtg ttt act aag	aat gtg cac cag agt	cac agt cac ctt gca atg	1481	
Tyr Val Phe Thr Lys	Asn Val His Gln Ser	His Ser His Leu Ala Met		
409	414	419	424	
cca ata acc atc aat	gat gtt ccc cct tgt	atc tct caa tta ctt gat	1529	
Pro Ile Thr Ile Asn	Asp Val Pro Pro Cys	Ile Ser Gln Leu Leu Asp		
425	430	435	440	
aat gag gag agt tgg	gac ttc aac atc ttt	gaa ttg gaa gcc att acg	1577	
Asn Glu Glu Ser Trp	Asp Phe Asn Ile Phe	Glu Leu Glu Ala Ile Thr		
441	446	451	456	
cat aaa agg cca ttg	gtt tat ctg ggc tta	aag gtc ttc tct cgg ttt	1625	
His Lys Arg Pro Leu	Val Tyr Leu Gly Leu	Lys Val Phe Ser Arg Phe		
457	462	467	472	
gga gta tgt gag ttt	tta aac tgt tct gaa	acc act ctt cgg gcc tgg	1673	
Gly Val Cys Glu Phe	Leu Asn Cys Ser Glu	Thr Thr Leu Arg Ala Trp		
473	478	483	488	
ttc caa gtg atc gaa	gcc aac tac cac tct	tcc aat gcc tac cac aac	1721	
Phe Gln Val Ile Glu	Ala Asn Tyr His Ser	Ser Asn Ala Tyr His Asn		
489	494	499	504	
tcc acc cat gct gcc	gac gtc ctg cac gcc	acc gct ttc ttt ctt gga	1769	
Ser Thr His Ala Ala	Asp Val Leu His Ala	Thr Ala Phe Phe Leu Gly		
505	510	515	520	
aag gaa aga gta aag	gga agc ctc gat cag	ttg gat gag gtg gca gcc	1817	
Lys Glu Arg Val Lys	Gly Ser Leu Asp Gln	Leu Asp Glu Val Ala Ala		
521	526	531	536	

ctc att gct gcc aca gtc cat gac gtg gat cac ccg gga agg acc aac Leu Ile Ala Ala Thr Val His Asp Val Asp His Pro Gly Arg Thr Asn 537 542 547 552	1865
tct ttc ctc tgc aat gca ggc agt gag ctt gct gtg ctc tac aat gac Ser Phe Leu Cys Asn Ala Gly Ser Glu Leu Ala Val Leu Tyr Asn Asp 553 558 563 568	1913
act gct gtt ctg gag agt cac cac acc gcc ctg gcc ttc cag ctc acg Thr Ala Val Leu Glu Ser His His Thr Ala Leu Ala Phe Gln Leu Thr 569 574 579 584	1961
gtc aag gac acc aaa tgc aac att ttc aag aat att gac agg aac cat Val Lys Asp Thr Lys Cys Asn Ile Phe Lys Asn Ile Asp Arg Asn His 585 590 595 600	2009
tat cga acg ctg cgc cag gct att att gac atg gtt ttg gca aca gag Tyr Arg Thr Leu Arg Gln Ala Ile Ile Asp Met Val Leu Ala Thr Glu 601 606 611 616	2057
atg aca aaa cac ttt gaa cat gtg aat aag ttt gtg aac agc atc aac Met Thr Lys His Phe Glu His Val Asn Lys Phe Val Asn Ser Ile Asn 617 622 627 632	2105
aag cca atg gca gct gag att gaa ggc agc gac tgt gaa tgc aac cct Lys Pro Met Ala Ala Glu Ile Glu Gly Ser Asp Cys Glu Cys Asn Pro 633 638 643 648	2153
gct ggg aag aac ttc cct gaa aac caa atc ctg atc aaa cgc atg atg Ala Gly Lys Asn Phe Pro Glu Asn Gln Ile Leu Ile Lys Arg Met Met 649 654 659 664	2201
att aag tgt gct gac gtg gcc aac cca tgc cgc ccc ttg gac ctg tgc Ile Lys Cys Ala Asp Val Ala Asn Pro Cys Arg Pro Leu Asp Leu Cys 665 670 675 680	2249
att gaa tgg gct ggg agg atc tct gag gag tat ttt gca cag act gat Ile Glu Trp Ala Gly Arg Ile Ser Glu Glu Tyr Phe Ala Gln Thr Asp 681 686 691 696	2297
gaa gag aag aga cag gga cta cct gtg gtg atg cca gtg ttt gac cgg Glu Glu Lys Arg Gln Gly Leu Pro Val Val Met Pro Val Phe Asp Arg 697 702 707 712	2345
aat acc tgt agc atc ccc aag tct cag atc tct ttc att gac tac ttc Asn Thr Cys Ser Ile Pro Lys Ser Gln Ile Ser Phe Ile Asp Tyr Phe 713 718 723 728	2393
ata aca gac atg ttt gat gct tgg gat gcc ttt gca cat ctg cca gcc Ile Thr Asp Met Phe Asp Ala Trp Asp Ala Phe Ala His Leu Pro Ala 729 734 739 744	2441
ctg atg caa cat ttg gct gac aac tac aaa cac tgg aag aca cta gat Leu Met Gln His Leu Ala Asp Asn Tyr Lys His Trp Lys Thr Leu Asp 745 750 755 760	2489

```

gac cta aag tgc aaa agt ttg agg ctt cca tct gac agc taa agccaag 2538
Asp Leu Lys Cys Lys Ser Leu Arg Leu Pro Ser Asp Ser *
761 766 771

ccacagaggg ggcctcttga ccgacaaaagg acactgtgaa tcacagtagc gtaaacaaga 2598

ggccttcctt tctaatagaca atgacaggta ttggtgaagg agctaattgtt taatatttga 2658

ccttgaatca ttcaagtccc caaatttcat tcttagaaaag ttatgttcca tgaagaaaaa 2718

tatatgttct tttgaatact taatgacaga acaaatactt ggcaaactcc tttgctctgc 2778

tgtcatcctg tgtacccttg tcaatccatg gagctgggtc actgtaacta gcaggccaca 2838

ggaagcaaag ccttgggtgcc tgtgagctca tctcccagga tgggtgactaa gtagcttagc 2898

tagtgatcag ctcatccttt accataaaaag tcatcattgc tgttttagctt gactgttttc 2958

ctcaagaaca tcgatctgaa ggattcataa ggagcttattc tgaacagatt tatctaagaa 3018

aaaaaaaaa 3028

```

```

<210> 54
<211> 1259
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (385)..(1203)

```

```

<220>
<221> misc_feature
<222> (1)...(1259)
<223> n = a,t,c or g

```

```

<400> 54
atttggccct cgagcagnag attcggaaacg atggagaaaa gaaaaagaga gagagaaaaa 60

aaagtccatt tggcatgttt cagaccaagt gaccagtcac caatcaattt ttcttcattg 120

tgtttggata ttttgaagtc acatagacac caactaatat ctgtcaccca ctgtgtcatc 180

ggatggatcg ggtgacactc caaatcagtc gtgcaggtag ttctgagtgt gcagccatta 240

gccaatgttg agtcacctca tgttgacagc gttggctgac tggctgcctt tccccctgcc 300

agggagaagc gcattggcat tgacctggtg cagcacacag tggagcatga gctgataaag 360

gaggctgaga tcatccaggg catt atg gct ctg ctg acc cgt acc ttg gag 411
Met Ala Leu Leu Thr Arg Thr Leu Glu
1 5

gag gct tcc gag cag att cgg atg aac cgc tct gcc aag tac aat ctt 459

```

Glu 10	Ala	Ser	Glu	Gln	Ile 15	Arg	Met	Asn	Arg	Ser 20	Ala	Lys	Tyr	Asn	Leu 25	
gag Glu 26	aag Lys	gat Asp	ttg Leu	aag Lys	gac Asp 31	aag Lys	ttt Phe	gtg Val	gcc Ala	ctg Leu 36	acc Thr	ata Ile	gat Asp	gat Asp	atc Ile 41	507
tgc Cys 42	ttc Phe	tcg Ser	ctc Leu	aac Asn	aac Asn 47	aac Asn	tca Ser	cca Pro	aac Asn	atc Ile 52	aga Arg	tat Tyr	tct Ser	gag Glu	aac Asn 57	555
gcc Ala 58	gtg Val	agg Arg	att Ile	gag Glu	cca Pro 63	aac Asn	tcc Ser	gtg Val	agt Ser	ctg Leu 68	gaa Glu	gac Asp	tgg Trp	ttg Leu	gac Asp 73	603
ttc Phe 74	tcc Ser	agc Ser	acc Thr	aat Asn	gtg Val 79	gag Glu	aag Lys	gct Ala	gac Asp	aag Lys 84	cag Gln	cgg Arg	aac Asn	aac Asn	tcc Ser 89	651
ctg Leu 90	atg Met	ctg Leu	aaa Lys	gcc Ala	ctg Leu 95	gtg Val	gat Asp	cga Arg	atc Ile	ctg Leu 100	tcc Ser	atg Met	aca Thr	gcc Ala	aat Asn 105	699
gat Asp 106	ctg Leu	cgc Arg	aag Lys	cag Gln	tgt Cys 111	gat Asp	gtg Val	gtg Val	cac His	acg Thr 116	gca Ala	ttc Phe	aag Lys	aat Asn	ggg Gly 121	747
ctg Leu 122	aag Lys	gat Asp	aca Thr	aag Lys	gat Asp 127	gcc Ala	agg Arg	gac Asp	aag Lys	ctg Leu 132	gct Ala	gat Asp	cat His	ctg Leu	gcc Ala 137	795
aag Lys 138	gtc Val	atg Met	gaa Glu	gag Glu	att Ile 143	gct Ala	tcc Ser	cag Gln	gag Glu	aaa Lys 148	aat Asn	att Ile	aca Thr	gct Ala	ctt Leu 153	843
gaa Glu 154	aag Lys	gcc Ala	atc Ile	ctt Leu	gac Asp 159	caa Gln	gaa Glu	ggg Gly	cca Pro	gcc Ala 164	aag Lys	gtg Val	gct Ala	cat His	acg Thr 169	891
cgc Arg 170	ttg Leu	gag Glu	acc Thr	agg Arg	aca Thr 175	cac His	cgg Arg	ccg Pro	aac Asn	gtg Val 180	gag Glu	ctg Leu	tgt Cys	cgt Arg	gat Asp 185	939
gtc Val 186	gca Ala	caa Gln	tat Tyr	agg Arg	cta Leu 191	atg Met	aag Lys	gag Glu	gtt Val	caa Gln 196	gag Glu	atc Ile	acc Thr	cac His	aat Asn 201	987
gtc Val 202	gca Ala	aga Arg	ttg Leu	aag Lys	gaa Glu 207	act Thr	tta Leu	gcc Ala	caa Gln	gct Ala 212	cag Gln	gca Ala	gag Glu	ctg Leu	aaa Lys 217	1035
ggg Gly 218	ctg Leu	cat His	cgc Arg	aga Arg	cag Gln 223	ctt Leu	gcc Ala	ctg Leu	cag Gln	gag Glu 228	gag Glu	atc Ile	cag Gln	gtc Val	aaa Lys 233	1083
gag Glu	aac Asn	acc Thr	att Ile	tat Tyr	atc Ile	gac Asp	gaa Glu	gtg Val	ctg Leu	tgt Cys	atg Met	cag Gln	atg Met	agg Arg	aaa Lys	1131

234	239	244	249	
tcc atc cca ctt cgg gat ggg gaa gac cat ggg gtc tgg gct ggg ggc				1179
Ser Ile Pro Leu Arg Asp Gly Glu Asp His Gly Val Trp Ala Gly Gly				
250	255	260	265	
ctc cgc cct gat gct gtc tgc taa tagtaggggt agttccaatt ctcattaaac				1233
Leu Arg Pro Asp Ala Val Cys *				
266	271			
cacattgtaa acagtaaaaa aaaaaa				1259

<210> 55
 <211> 1387
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (518)..(1054)

<400> 55	
ggcgcgctga tgagccccgc ttatatacga ctactatag ggaccacttt gtacaagaaa	60
gctgggtacg cgtaagcttg ggccccctcga gggatactct agagcggccg cccgggagtc	120
cgagcgccag ctgcgcctcc gcctctgctt cctcaacgag atcttgggca ccgagagggga	180
ctacgtgggc accttgcgct tcttgagtc ggcattcctg catcgcatcc ggcagaacgt	240
ggcgcactca gtggagaagg gcctcacgga ggagaatgtc aaggctcctgt tctcgaacat	300
cgaagacatc ctggaagttc ataaggattt cttggccgcc ttggagtatt gtttacaccc	360
ggagccgcag tctcagcatg aacttgggaa tgttttctta aaattcaagg acaagttctg	420
cgtgtacgag gagtattgca gcaaccatga gaaagccctg aggctgctgg tggagctgaa	480
caagatccct accgtgcgcg ccttcctttt gagctgc atg ctt ctg gga ggc cgg	535
Met Leu Leu Gly Gly Arg	
1	
aag acc acg gac atc cct ttg gaa ggc tac ctg ttg tct ccg atc cag	583
Lys Thr Thr Asp Ile Pro Leu Glu Gly Tyr Leu Leu Ser Pro Ile Gln	
7 12 17 22	
agg atc tgc aag tac ccg ctc ctc ctt aag gag ctg gcc aag agg act	631
Arg Ile Cys Lys Tyr Pro Leu Leu Leu Lys Glu Leu Ala Lys Arg Thr	
23 28 33 38	
ccc ggc aag cac cca gac cac ccc gcg gtc cag agt gcc ctg cag gcc	679
Pro Gly Lys His Pro Asp His Pro Ala Val Gln Ser Ala Leu Gln Ala	
39 44 49 54	

atg aag acc gtt tgc tcc aac atc aat gag acc aag cgg cag atg gag	727
Met Lys Thr Val Cys Ser Asn Ile Asn Glu Thr Lys Arg Gln Met Glu	
55 60 65 70	
aag ctg gaa gcc ctg gag cag ctg cag tcc cac atc gaa ggc tgg gag	775
Lys Leu Glu Ala Leu Glu Gln Leu Gln Ser His Ile Glu Gly Trp Glu	
71 76 81 86	
ggt tcc aac ctc aca gac atc tgc act cag ctc ctc ctg caa ggg act	823
Gly Ser Asn Leu Thr Asp Ile Cys Thr Gln Leu Leu Leu Gln Gly Thr	
87 92 97 102	
ttg tta aag atc tct gcg ggc aac atc cag gaa agg gcc ttc ttc ctc	871
Leu Leu Lys Ile Ser Ala Gly Asn Ile Gln Glu Arg Ala Phe Phe Leu	
103 108 113 118	
ttc gac aac ctt ctc gtc tac tgc aag cgg aaa tcc agg gtc acc ggg	919
Phe Asp Asn Leu Leu Val Tyr Cys Lys Arg Lys Ser Arg Val Thr Gly	
119 124 129 134	
agc aag aag tcc acc aag agg acc aaa tcc atc aac ggc tcc ctc tac	967
Ser Lys Lys Ser Thr Lys Arg Thr Lys Ser Ile Asn Gly Ser Leu Tyr	
135 140 145 150	
atc ttc agg ggt cga atc aac act gaa gtc atg gag gtg gag aat gtg	1015
Ile Phe Arg Gly Arg Ile Asn Thr Glu Val Met Glu Val Glu Asn Val	
151 156 161 166	
gaa gat ggg aca ggt agc ccc tcc ccc agc ctt gcc tga gccctgcctg	1064
Glu Asp Gly Thr Gly Ser Pro Ser Pro Ser Leu Ala *	
167 172 177	
agccctgcct gtcctctggc actctctctg tttcatttaa atatattttt ttcttttctc	1124
atgagatgta atctacctac agaaaagtgc ccagagcata gatgcatgaa gcgaacatct	1184
gggtggttag cattcaagtt aagaaataaa acactgcacc ccaaatacctt cctccttgca	1244
atgccttctt ccccttagaa gtaaccactg tctgaatttt gtgatgatca ttttcttgct	1304
ttttaagac atttttacct cctaagcatt tatgactaaa cattttaatt aaaatttcta	1364
tttttgagcc ttaaaaaaaaa aaa	1387

<210> 56
 <211> 4862
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (182) .. (2809)

 <400> 56

aagctggttac	gcttcgaggt	accggtccgg	aattcccggg	tcgacgattt	cgttgaaggg		60									
cctgtagccg	gggggttcct	ggccggatcc	cggtctaccc	ttagcccaga	ctcgttccgg		120									
accccagccc	ggcccgaac	actctgggcg	agacggcggt	ggcaactctc	cccttgccgc		180									
c	atg	cac	gac	gct	ttc	gag	cca	gtg	ccg	atc	cta	gaa	aag	ctg	cct	226
	Met	His	Asp	Ala	Phe	Glu	Pro	Val	Pro	Ile	Leu	Glu	Lys	Leu	Pro	
	1				5					10						
ctg	caa	atc	gac	tgt	ctg	gct	gcc	tgg	gag	gaa	tgg	ctt	ctt	gtg	gga	274
Leu	Gln	Ile	Asp	Cys	Leu	Ala	Ala	Trp	Glu	Glu	Trp	Leu	Leu	Val	Gly	
16					21					26					31	
acc	aaa	caa	gga	cat	ctt	ctt	ctc	tat	agg	att	cgg	aag	gac	gtt	ggc	322
Thr	Lys	Gln	Gly	His	Leu	Leu	Leu	Tyr	Arg	Ile	Arg	Lys	Asp	Val	Gly	
32					37					42					47	
tgc	aac	aga	ttt	gaa	gtg	aca	cta	gag	aaa	tcc	aat	aag	aac	ttc	tcc	370
Cys	Asn	Arg	Phe	Glu	Val	Thr	Leu	Glu	Lys	Ser	Asn	Lys	Asn	Phe	Ser	
48					53					58					63	
aaa	aag	att	cag	cag	atc	cat	gtg	gtt	tcc	cag	ttt	aag	att	ctg	gtc	418
Lys	Lys	Ile	Gln	Gln	Ile	His	Val	Val	Ser	Gln	Phe	Lys	Ile	Leu	Val	
64					69					74					79	
agc	ttg	tta	gaa	aat	aac	att	tat	gtc	cat	gac	cta	ttg	aca	ttt	caa	466
Ser	Leu	Leu	Glu	Asn	Asn	Ile	Tyr	Val	His	Asp	Leu	Leu	Thr	Phe	Gln	
80					85					90					95	
caa	atc	act	acg	gtt	tca	aag	gca	aag	gga	gca	tca	ctg	ttt	act	tgt	514
Gln	Ile	Thr	Thr	Val	Ser	Lys	Ala	Lys	Gly	Ala	Ser	Leu	Phe	Thr	Cys	
96					101					106					111	
gac	ctc	cag	cac	aca	gag	acc	ggc	gag	gag	gtg	tta	cgg	atg	tgt	gtg	562
Asp	Leu	Gln	His	Thr	Glu	Thr	Gly	Glu	Glu	Val	Leu	Arg	Met	Cys	Val	
112					117					122					127	
gca	gta	aaa	aag	agg	ctg	cag	ctc	tat	ttc	tgg	aag	gac	aga	gaa	ttt	610
Ala	Val	Lys	Lys	Arg	Leu	Gln	Leu	Tyr	Phe	Trp	Lys	Asp	Arg	Glu	Phe	
128					133					138					143	
cat	gaa	ttg	cag	ggg	gac	ttt	agt	gtg	cca	gat	gtg	ccc	aag	tcc	atg	658
His	Glu	Leu	Gln	Gly	Asp	Phe	Ser	Val	Pro	Asp	Val	Pro	Lys	Ser	Met	
144					149					154					159	
gcg	tgg	tgt	gaa	aat	tct	atc	tgt	gtg	ggc	ttc	aag	aga	gac	tac	tac	706
Ala	Trp	Cys	Glu	Asn	Ser	Ile	Cys	Val	Gly	Phe	Lys	Arg	Asp	Tyr	Tyr	
160					165					170					175	
cta	ata	agg	gtg	gat	gga	aag	ggg	tcc	atc	aaa	gag	ctc	ttt	cca	aca	754
Leu	Ile	Arg	Val	Asp	Gly	Lys	Gly	Ser	Ile	Lys	Glu	Leu	Phe	Pro	Thr	
176					181					186					191	
gga	aaa	cag	ctg	gag	ccc	tta	gtt	gca	cct	ctg	gca	gat	gga	aaa	gtg	802
Gly	Lys	Gln	Leu	Glu	Pro	Le										

gct gtg ggc cag gat gat ctc acc gtg gta ctc aat gag gaa ggg atc	850
Ala Val Gly Gln Asp Asp Leu Thr Val Val Leu Asn Glu Glu Gly Ile	
208 213 218 223	
tgc aca cag aaa tgt gcc ctg aac tgg acg gac ata cca gtg gcc atg	898
Cys Thr Gln Lys Cys Ala Leu Asn Trp Thr Asp Ile Pro Val Ala Met	
224 229 234 239	
gag cac cag cct ccc tac atc att gca gtg ttg cct cga tat gtt gag	946
Glu His Gln Pro Pro Tyr Ile Ile Ala Val Leu Pro Arg Tyr Val Glu	
240 245 250 255	
atc cga aca ttt gaa ccg agg ctt ctg gtc caa agc att gaa ttg caa	994
Ile Arg Thr Phe Glu Pro Arg Leu Leu Val Gln Ser Ile Glu Leu Gln	
256 261 266 271	
agg ccc cgt ttc att acc tca gga gga tca aac att atc tat gtg gcc	1042
Arg Pro Arg Phe Ile Thr Ser Gly Gly Ser Asn Ile Ile Tyr Val Ala	
272 277 282 287	
agc aat cat ttt gtt tgg aga ctc atc cct gtc ccc atg gca acc caa	1090
Ser Asn His Phe Val Trp Arg Leu Ile Pro Val Pro Met Ala Thr Gln	
288 293 298 303	
atc caa caa ctt ctc cag gac aag cag ttt gaa ttg gct ctg cag ctc	1138
Ile Gln Gln Leu Leu Gln Asp Lys Gln Phe Glu Leu Ala Leu Gln Leu	
304 309 314 319	
gca gaa atg aaa gat gat tct gac agt gaa aag cag caa caa att cat	1186
Ala Glu Met Lys Asp Asp Ser Asp Ser Glu Lys Gln Gln Gln Ile His	
320 325 330 335	
cac atc aag aac ttg tat gcc ttc aac ctc ttc tgc cag aag cgt ttt	1234
His Ile Lys Asn Leu Tyr Ala Phe Asn Leu Phe Cys Gln Lys Arg Phe	
336 341 346 351	
gat gag tcc atg cag gtc ttt gct aaa ctt ggc aca gat ccc acc cat	1282
Asp Glu Ser Met Gln Val Phe Ala Lys Leu Gly Thr Asp Pro Thr His	
352 357 362 367	
gtg atg ggc ctg tac cct gac ctg ctg ccc aca gac tac aga aag cag	1330
Val Met Gly Leu Tyr Pro Asp Leu Leu Pro Thr Asp Tyr Arg Lys Gln	
368 373 378 383	
ttg cag tat ccc aac cca ttg cct gtg ctc tcc ggg gct gaa ttg gag	1378
Leu Gln Tyr Pro Asn Pro Leu Pro Val Leu Ser Gly Ala Glu Leu Glu	
384 389 394 399	
aag gct cac tta gct ctg att gac tac ctg aca cag aaa cga agt caa	1426
Lys Ala His Leu Ala Leu Ile Asp Tyr Leu Thr Gln Lys Arg Ser Gln	
400 405 410 415	
ttg gta aag aag ctg aat gac tct gat cac cag tca agc acc tca ccg	1474
Leu Val Lys Lys Leu Asn Asp Ser Asp His Gln Ser Ser Thr Ser Pro	
416 421 426 431	

ctc atg gaa ggc act ccc acc atc aaa tcc aag aag aag ctg cta caa	1522
Leu Met Glu Gly Thr Pro Thr Ile Lys Ser Lys Lys Lys Leu Leu Gln	
432 437 442 447	
atc atc gac acc acc ctg ctc aag tgc tat ctc cat aca aat gtg gcc	1570
Ile Ile Asp Thr Thr Leu Leu Lys Cys Tyr Leu His Thr Asn Val Ala	
448 453 458 463	
ctg gtg gcc ccc ttg cta cgc ctg gag aac aat cac tgc cac atc gag	1618
Leu Val Ala Pro Leu Leu Arg Leu Glu Asn Asn His Cys His Ile Glu	
464 469 474 479	
gag agc gag cac gtg ctg aag aag gct cac aag tac agt gag ctt atc	1666
Glu Ser Glu His Val Leu Lys Lys Ala His Lys Tyr Ser Glu Leu Ile	
480 485 490 495	
atc ctg tat gag aag aag ggg ctc cac gag aaa gct ctg cag gtg ctc	1714
Ile Leu Tyr Glu Lys Lys Gly Leu His Glu Lys Ala Leu Gln Val Leu	
496 501 506 511	
gtg gac cag tcc aag aaa gcc aac tcc cct ctg aaa ggc cac gag agg	1762
Val Asp Gln Ser Lys Lys Ala Asn Ser Pro Leu Lys Gly His Glu Arg	
512 517 522 527	
aca gtg cag tat ctg cag cat ctg ggc aca gaa aac ctg cat ttg att	1810
Thr Val Gln Tyr Leu Gln His Leu Gly Thr Glu Asn Leu His Leu Ile	
528 533 538 543	
ttc tcc tac tca gtg tgg gtg ctg aga gac ttc cca gaa gat ggc ctg	1858
Phe Ser Tyr Ser Val Trp Val Leu Arg Asp Phe Pro Glu Asp Gly Leu	
544 549 554 559	
aag ata ttt act gaa gat ctc ccg gaa gtg gag tct ctg cca cgt gat	1906
Lys Ile Phe Thr Glu Asp Leu Pro Glu Val Glu Ser Leu Pro Arg Asp	
560 565 570 575	
cga gtc ctc ggc ttc tta ata gag aat ttt aag ggt ctg gct att cct	1954
Arg Val Leu Gly Phe Leu Ile Glu Asn Phe Lys Gly Leu Ala Ile Pro	
576 581 586 591	
tat ctg gaa cac atc atc cat gtt tgg gag gag aca ggc tct cgg ttc	2002
Tyr Leu Glu His Ile Ile His Val Trp Glu Glu Thr Gly Ser Arg Phe	
592 597 602 607	
cac aac tgc ctg atc cag cta tac tgt gag aag gtg caa ggt ctg atg	2050
His Asn Cys Leu Ile Gln Leu Tyr Cys Glu Lys Val Gln Gly Leu Met	
608 613 618 623	
aag gag tat ctc ctg tcc ttc cct gca ggc aaa acc cca gtc cca gct	2098
Lys Glu Tyr Leu Leu Ser Phe Pro Ala Gly Lys Thr Pro Val Pro Ala	
624 629 634 639	
gga gag gaa gag ggt gag ctg gga gaa tac cgg caa aag ctc ctc atg	2146
Gly Glu Glu Glu Gly Glu Leu Gly Glu Tyr Arg Gln Lys Leu Leu Met	
640 645 650 655	
ttc ttg gag att tcc agc tac tat gat cca ggc cgg ctc atc tgt gat	2194

Phe	Leu	Glu	Ile	Ser	Ser	Tyr	Tyr	Asp	Pro	Gly	Arg	Leu	Ile	Cys	Asp		
656					661					666					671		
ttt	ccc	ttt	gat	ggc	ctc	tta	gaa	gaa	cga	gct	ctc	ctg	ttg	ggg	cgc	2242	
Phe	Pro	Phe	Asp	Gly	Leu	Leu	Glu	Glu	Arg	Ala	Leu	Leu	Leu	Gly	Arg		
672					677					682					687		
atg	ggg	aaa	cat	gaa	caa	gct	ctt	ttc	att	tat	gtc	cac	atc	ttg	aag	2290	
Met	Gly	Lys	His	Glu	Gln	Ala	Leu	Phe	Ile	Tyr	Val	His	Ile	Leu	Lys		
688					693					698					703		
gat	aca	agg	atg	gct	gag	gag	tac	tgc	cac	aaa	cac	tat	gac	cga	aac	2338	
Asp	Thr	Arg	Met	Ala	Glu	Glu	Tyr	Cys	His	Lys	His	Tyr	Asp	Arg	Asn		
704					709					714					719		
aaa	gat	ggc	aac	aaa	gat	gtg	tat	ctg	tcc	ctg	ctt	cgg	atg	tac	ctg	2386	
Lys	Asp	Gly	Asn	Lys	Asp	Val	Tyr	Leu	Ser	Leu	Leu	Arg	Met	Tyr	Leu		
720					725					730					735		
tcg	ccc	ccc	agc	att	cac	tgc	ctg	ggg	cca	atc	aag	ctg	gaa	cta	ctg	2434	
Ser	Pro	Pro	Ser	Ile	His	Cys	Leu	Gly	Pro	Ile	Lys	Leu	Glu	Leu	Leu		
736					741					746					751		
gag	cca	aaa	gcc	aac	ctc	cag	gcc	gct	ctg	cag	gtc	ctc	gag	cta	cac	2482	
Glu	Pro	Lys	Ala	Asn	Leu	Gln	Ala	Ala	Leu	Gln	Val	Leu	Glu	Leu	His		
752					757					762					767		
cac	agc	aaa	ctg	gac	acc	acc	aag	gcc	ctc	aac	ctt	ctg	cca	gca	aac	2530	
His	Ser	Lys	Leu	Asp	Thr	Thr	Lys	Ala	Leu	Asn	Leu	Leu	Pro	Ala	Asn		
768					773					778					783		
act	cag	atc	aat	gac	ata	cgc	atc	ttc	ctg	gaa	aag	gtc	ttg	gaa	gaa	2578	
Thr	Gln	Ile	Asn	Asp	Ile	Arg	Ile	Phe	Leu	Glu	Lys	Val	Leu	Glu	Glu		
784					789					794					799		
aat	gca	caa	aag	aaa	cgg	ttc	aat	caa	gtg	ctc	aag	aac	ctt	ctc	cat	2626	
Asn	Ala	Gln	Lys	Lys	Arg	Phe	Asn	Gln	Val	Leu	Lys	Asn	Leu	Leu	His		
800					805					810					815		
gca	gaa	ttc	ctg	agg	gtc	cag	gaa	gag	cgg	att	tta	cac	cag	cag	gtg	2674	
Ala	Glu	Phe	Leu	Arg	Val	Gln	Glu	Glu	Arg	Ile	Leu	His	Gln	Gln	Val		
816					821					826					831		
aag	tgc	atc	atc	aca	gag	gag	aag	gtg	tgc	atg	gtg	tgt	aag	aag	aag	2722	
Lys	Cys	Ile	Ile	Thr	Glu	Glu	Lys	Val	Cys	Met	Val	Cys	Lys	Lys	Lys		
832					837					842					847		
att	ggg	aac	agt	gca	ttt	gca	aga	tac	ccc	aat	gga	gtg	gtc	gtc	cat	2770	
Ile	Gly	Asn	Ser	Ala	Phe	Ala	Arg	Tyr	Pro	Asn	Gly	Val	Val	Val	His		
848					853					858					863		
tac	ttc	tgt	tcc	aaa	gag	gta	aac	cca	gct	gac	act	tga	gcccagcatc			2819	
Tyr	Phe	Cys	Ser	Lys	Glu	Val	Asn	Pro	Ala	Asp	Thr	*					
864					869					874							
ctg	ggg	gat	ccc	agc	ggat	gga	cag	ctt	ggct	ctccc	agaga	ggt	gaagg	gag	cacct	ggcct	2879

taggaatcct	ggctgccacc	accacaaggc	tccccatttg	gacattactg	gctatcttgt	2939
gccctggaac	aactctgaat	taattagact	catgggtctgg	cattgccagc	tttttaatgg	2999
gaaaagagat	tagttatacc	ttataaccatt	atgtttgtggg	caattccaga	gaattcagta	3059
cctgcttggg	caggaggatg	tgcaccatct	tgcctttgca	caccagtcac	ctgaacaagg	3119
aaacttgca	caagtgtttg	taaccatggg	gttggttcac	aagggctttt	ctattaagta	3179
catgacttca	caaggaccgc	tcagcatggc	tcaactggaga	gttccatgag	agaacagcac	3239
tcaagcttct	ggccgcatgg	acccgatggc	tgcattctg	tgtagtgttt	tacgtctcca	3299
tggtaaactgt	gccctgcacc	cctcggtagc	cgccctgtta	gttttcagtc	tccttttctt	3359
tctcaccatt	tatcacttcc	ctcactgccc	taccagget	ttctctccca	cttccctgac	3419
tctgggaata	actaatattt	aagcaaggta	agatgagaag	caaggggtct	cagttctagg	3479
aatacagtgc	tagttgattg	tcaggatatgt	tgtaaataga	ccctctttgg	ccatacactc	3539
catgcctaga	tgctcggag	agcatcattc	tctgcctagg	caaggccctg	catcccttgc	3599
ctcaggccgg	gctgagtgtg	actgcagctc	ctgaggatgg	gcctgccctg	tctggggtat	3659
gcgtgatccc	tagatacatg	ttcccacaga	ggtgcctgct	ccgtcttcgc	tcaccagaca	3719
ctcaggcagg	ctggcttagt	ctttgtgcgt	ggcgattttg	tgctctgggc	cctttctctt	3779
tttccagcca	gtttccattc	acttgccctt	cagcctgccc	tggccgtcac	tcccagctt	3839
tgttcagcaa	tgggtgtggt	ggagagtgtg	gctgggatag	cgcaggaagg	tgggtcccgg	3899
caacacgcag	gggatgagtg	gacctggaac	tgacaatggc	gtgctgccaa	gtgttcctga	3959
gaggtgttta	ggcacagcag	aggggacgcg	gggggcaaga	acagcaggac	gctgggttaa	4019
aaataactca	ccgccaacc	tgtggagcag	tgtggggcat	cctgccagag	gtgcacaggc	4079
tggagtttca	ggcactgcag	gctgatgaca	cacagggaga	gtggccctgc	ctcctgtcct	4139
ccccgggggt	tttgcagact	cgaagtctca	ctgcaccagt	gtctttgatg	gtggtgaggg	4199
tgggtgatgg	tgcccagcac	caacagtttt	agtggcctgt	ccttgacctg	ccgtggctct	4259
ttgtaaacta	tggctccatg	ctgtgtgaca	gatcaacgtg	ctgatggtaa	gtagactagg	4319
cttccccagg	catgccgtcc	gtgggggcct	gaagagacag	tgagtgccat	tggccccatt	4379
cgcagatgtg	ggagactctg	ctcaggcctg	tgaggctggg	cagcccttca	ccagagttcg	4439
gaggagcagt	gtgtggcgcc	acgtcccgc	tggccatacc	cacacagaag	cagtgtgtcc	4499
cggggcctca	tctgggccag	cttggactct	gcttcctcca	ggagcagcag	ggaagctctg	4559
ggccacctcc	ctggatagca	ggaacttgac	ctgccatgtg	tgccctgcct	tcctggccag	4619

ctgtgcttgt tatcttccat tctcacaac tgtctttgaa gcaatagaat aaagaatgtg 4679
 tgttttcttt cctggtatac atacatgata ccatgctccc aagctccatt cttccttccc 4739
 tcaactctct gccctccaca gagctatgga gaaggctgga gatgaaagct ttgtagtgag 4799
 gactgataaa gatctcatca ctgctcctta taataaacct aataaagcaa gaaaaaaaaa 4859
 aaa 4862

<210> 57
 <211> 1899
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (69)..(1064)

<400> 57
 ccactttgta caagaaagct gggtacgcgt aagcttgggc ccctcgaggg atactctaga 60
 gcggccgc atg agc cgc gcg cgt ggg gcg ctg tgc cgg gcc tgc ctc gcg 110
 Met Ser Arg Ala Arg Gly Ala Leu Cys Arg Ala Cys Leu Ala
 1 5 10
 ctg gcc gcg gcc ctg gcc gcg ctg ctg tta ctg ccg ctg ccg ctg ccc 158
 Leu Ala Ala Ala Leu Ala Ala Leu Leu Leu Leu Pro Leu Pro Leu Pro
 15 20 25 30
 cgc gcg ccc gcc ccg gcc cgg acc ccc gcc ccg gcc ccg cgc gcg ccc 206
 Arg Ala Pro Ala Pro Ala Arg Thr Pro Ala Pro Ala Pro Arg Ala Pro
 31 36 41 46
 ccg tcc cgg ccc gct gcc ccc agc ctg cgg cct gac gac gtc ttc atc 254
 Pro Ser Arg Pro Ala Ala Pro Ser Leu Arg Pro Asp Asp Val Phe Ile
 47 52 57 62
 gcc gtc aag acc acc cgg aag aac cac ggg ccg cgc ctg cgg ctg ctg 302
 Ala Val Lys Thr Thr Arg Lys Asn His Gly Pro Arg Leu Arg Leu Leu
 63 68 73 78
 ctg cgc acc tgg atc tcc cgg gcc cgc cag cag acg ttt atc ttc acc 350
 Leu Arg Thr Trp Ile Ser Arg Ala Arg Gln Gln Thr Phe Ile Phe Thr
 79 84 89 94
 gac ggg gac gac cct gag ctc gag ctc cag ggc ggc gac cgt gtc atc 398
 Asp Gly Asp Asp Pro Glu Leu Glu Leu Gln Gly Gly Asp Arg Val Ile
 95 100 105 110
 aac acc aac tgc tgc gcg gtg cgc act cgt cag gcc ctc tgc tgc aag 446
 Asn Thr Asn Cys Ser Ala Val Arg Thr Arg Gln Ala Leu Cys Cys Lys
 111 116 121 126

1	5	10	
tgg ctt tgg gct ttt cgt acc cac agt caa gtc agt tca cgt cgc ctc			637
Trp Leu Trp Ala Phe Arg Thr His Ser Gln Val Ser Ser Arg Arg Leu			
16	21	26	31
ccg cac aca cgc gtt cat aaa acg aaa ctg gag ttt cac gaa gca att			685
Pro His Thr Arg Val His Lys Thr Lys Leu Glu Phe His Glu Ala Ile			
32	37	42	47
ctt agg ctt agc gtc cag gaa cgc tgt aga cgg tct att cta ttc tac			733
Leu Arg Leu Ser Val Gln Glu Arg Cys Arg Arg Ser Ile Leu Phe Tyr			
48	53	58	63
ccc tat tct act cgg ttc gat tct gtt cct aag aaa atg ccg atc tcg			781
Pro Tyr Ser Thr Arg Phe Asp Ser Val Pro Lys Lys Met Pro Ile Ser			
64	69	74	79
acc cac ttg tac ttc cac gag cgg agc tgc agc cag cag ctc tgc agg			829
Thr His Leu Tyr Phe His Glu Arg Ser Cys Ser Gln Gln Leu Cys Arg			
80	85	90	95
acc ccg cac tgc ccg cca ccg tcc cct ctg gca gtg cct tcc tcc tcc			877
Thr Pro His Cys Pro Pro Pro Ser Pro Leu Ala Val Pro Ser Ser Ser			
96	101	106	111
cgc ttt ccc caa ctg ctc cac tcg agg aaa ccg gag gac agg ttc agc			925
Arg Phe Pro Gln Leu Leu His Ser Arg Lys Pro Glu Asp Arg Phe Ser			
112	117	122	127
tca ctg aaa ggg gtc cca aca gag gtg aag atc caa gaa atg acg aag			973
Ser Leu Lys Gly Val Pro Thr Glu Val Lys Ile Gln Glu Met Thr Lys			
128	133	138	143
ctg ggc cac gag ctg atg ctg tgt gcg cca gat gac cag gag ctc ctc			1021
Leu Gly His Glu Leu Met Leu Cys Ala Pro Asp Asp Gln Glu Leu Leu			
144	149	154	159
aag ggc tgt gcc tgc gcc cag aag cag cta cac ttc atg gac cag ttg			1069
Lys Gly Cys Ala Cys Ala Gln Lys Gln Leu His Phe Met Asp Gln Leu			
160	165	170	175
ctc gat acc atc cgg agc ctg acc att ggg tgc tcc agt tgc tcg agc			1117
Leu Asp Thr Ile Arg Ser Leu Thr Ile Gly Cys Ser Ser Cys Ser Ser			
176	181	186	191
ctg atg gag cac ttc gag gac acc agg gag aag aac gag gcc ttg ctg			1165
Leu Met Glu His Phe Glu Asp Thr Arg Glu Lys Asn Glu Ala Leu Leu			
192	197	202	207
ggg gag ctc ttc tct agc ccc cac ctg cag atg ctc ctg aat cca gag			1213
Gly Glu Leu Phe Ser Ser Pro His Leu Gln Met Leu Leu Asn Pro Glu			
208	213	218	223
tgc gac ccg tgg ccc ctg gac atg cag ccc ctc ctc aac aag cag agt			1261
Cys Asp Pro Trp Pro Leu Asp Met Gln Pro Leu Leu Asn Lys Gln Ser			
224	229	234	239

gat gac tgg cag tgg gcc agt gcc tct gcc aag tcc gag gag gag gag	1309
Asp Asp Trp Gln Trp Ala Ser Ala Ser Ala Lys Ser Glu Glu Glu Glu	
240 245 250 255	
aag ctg gcg gag ctt gcc agg cag ctg cag gag agt gct gcc aag ttg	1357
Lys Leu Ala Glu Leu Ala Arg Gln Leu Gln Glu Ser Ala Ala Lys Leu	
256 261 266 271	
cac gcg ctt aga acg gag tac ttt gca cag cat gag caa ggg gct gct	1405
His Ala Leu Arg Thr Glu Tyr Phe Ala Gln His Glu Gln Gly Ala Ala	
272 277 282 287	
gcg ggc gca gcc gac atc agc acc cta gac cag aag ctg cgt ctg gtc	1453
Ala Gly Ala Ala Asp Ile Ser Thr Leu Asp Gln Lys Leu Arg Leu Val	
288 293 298 303	
act tcc gac ttc cac cag cta atc ttg gct ttt ctc caa gtc tac gac	1501
Thr Ser Asp Phe His Gln Leu Ile Leu Ala Phe Leu Gln Val Tyr Asp	
304 309 314 319	
gac gag ctg ggc gag tgc tgc cag cgc cca ggc cct gac ctc cac ccg	1549
Asp Glu Leu Gly Glu Cys Cys Gln Arg Pro Gly Pro Asp Leu His Pro	
320 325 330 335	
tgc ggc ccc atc atc cag gcc acg cac cag aat ctg act tcc tac agc	1597
Cys Gly Pro Ile Ile Gln Ala Thr His Gln Asn Leu Thr Ser Tyr Ser	
336 341 346 351	
caa ctg ctg caa gtg gtc atg gca gtt gct gac acc tct gcg aag gcc	1645
Gln Leu Leu Gln Val Val Met Ala Val Ala Asp Thr Ser Ala Lys Ala	
352 357 362 367	
gtg gag acc gtg aag aag cag caa ggc gag cag atc tgc tgg ggt ggc	1693
Val Glu Thr Val Lys Lys Gln Gln Gly Glu Gln Ile Cys Trp Gly Gly	
368 373 378 383	
agc agc tcc gtc atg agt cta gct acc aag atg aat gaa cta atg gag	1741
Ser Ser Ser Val Met Ser Leu Ala Thr Lys Met Asn Glu Leu Met Glu	
384 389 394 399	
aaa tag aaagtcttca gtgatggcct acgccaaagc acaggatggg gcgggcagga	1797
Lys *	
400	
agccctctcc caagatcgag ttggccgagg atggatgatt gtggcagcag aagccgttgc	1857
agccccacgt tgtgctctag gcagggacct ttggccctt tggggaggga gagacagacg	1917
ggcggtttga cttggacaca aagaaagcct tggtttctaa gcaaaaaaaaa aaaa	1971

<210> 59
 <211> 1188
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (158)..(907)

<400> 59

```
agaaatttgt tttttaagt caggaagcat ctaaatatgg tgtcctccgg aaaaaagtat      60
tccaggaaat ctgggaagcc gtctgtggaa gatcagttta cgagagccta tgactttgag      120
actgaagata agaaagatct gagtggatca gaggaag atg tta ttg aag gtg cag      175
                               Met Leu Leu Lys Val Gln
                               1
tac atc tca tgt tgg gca gtg atg tcc ttc agt tca ttt gtt ttg aac      223
Tyr Ile Ser Cys Trp Ala Val Met Ser Phe Ser Ser Phe Val Leu Asn
   7                               12                               17                               22
cca ttg aga cta tcg tac aac tta gtt tgt aaa gca ttt tca ggt atg      271
Pro Leu Arg Leu Ser Tyr Asn Leu Val Cys Lys Ala Phe Ser Gly Met
  23                               28                               33                               38
gtc ttc cct ccc ccg gta ttt gtg gtt aca gaa cct gct gac acg gat      319
Val Phe Pro Pro Pro Val Phe Val Val Thr Glu Pro Ala Asp Thr Asp
  39                               44                               49                               54
ggc cag ctg tac ttg tgt ttc tca ttt gat cct tat att gca gta tcg      367
Gly Gln Leu Tyr Leu Cys Phe Ser Phe Asp Pro Tyr Ile Ala Val Ser
  55                               60                               65                               70
gag tta cag aag ctt att cgg caa ctc ttg ctt ttg cag tta ttt cca      415
Glu Leu Gln Lys Leu Ile Arg Gln Leu Leu Leu Leu Gln Leu Phe Pro
  71                               76                               81                               86
aaa tat ctg ata tat att gac att aac aag gct ctt ctt gcc aag aga      463
Lys Tyr Leu Ile Tyr Ile Asp Ile Asn Lys Ala Leu Leu Ala Lys Arg
  87                               92                               97                               102
aag aga cta gaa atg tat acc aag gct tct ctc aaa act agt aac cag      511
Lys Arg Leu Glu Met Tyr Thr Lys Ala Ser Leu Lys Thr Ser Asn Gln
 103                               108                               113                               118
aaa att gaa cat gtt tgg aaa aca caa caa gat caa agg cag aag ctt      559
Lys Ile Glu His Val Trp Lys Thr Gln Gln Asp Gln Arg Gln Lys Leu
 119                               124                               129                               134
aac caa gaa tat tct cag cag ttt ctg act ttg ttt cag cag tgg gat      607
Asn Gln Glu Tyr Ser Gln Gln Phe Leu Thr Leu Phe Gln Gln Trp Asp
 135                               140                               145                               150
tta gat atg cag aaa gct gag gaa caa gaa gaa aaa ata ctt aat atg      655
Leu Asp Met Gln Lys Ala Glu Glu Gln Glu Glu Lys Ile Leu Asn Met
 151                               156                               161                               166
ttt cga cag caa caa aag att ctt caa caa tct aga att gtt cag agc      703
Phe Arg Gln Gln Gln Lys Ile Leu Gln Gln Ser Arg Ile Val Gln Ser
```


6	11	16	21	
cca tac ttc atc ctg cag cgg agg aag ggc cac gcc ggc gat gga ggc				390
Pro Tyr Phe Ile Leu Gln Arg Arg Lys Gly His Ala Gly Asp Gly Gly				
22	27	32	37	
ggc ggc ggc gga ctg gcg ggc ctg ctg gtg ggt acc ctt gat gtt gtg				438
Gly Gly Gly Gly Leu Ala Gly Leu Leu Val Gly Thr Leu Asp Val Val				
38	43	48	53	
ttg gac tcc agc gcc cgg gtc gct cct tac cga atc ttg tac cag act				486
Leu Asp Ser Ser Ala Arg Val Ala Pro Tyr Arg Ile Leu Tyr Gln Thr				
54	59	64	69	
cca gac tcc ctg ggt cta ctg gac cat cgc ctg tgg gtg gtt cca gga				534
Pro Asp Ser Leu Gly Leu Leu Asp His Arg Leu Trp Val Val Pro Gly				
70	75	80	85	
aag aaa tca ctg aac act ggg aat ggc ttg agc aaa atc tct tgc aga				582
Lys Lys Ser Leu Asn Thr Gly Asn Gly Leu Ser Lys Ile Ser Cys Arg				
86	91	96	101	
cac ttt cca tct ttg aaa atg aga atg ata tca cca cat ttg tga gag				630
His Phe Pro Ser Leu Lys Met Arg Met Ile Ser Pro His Leu *				
102	107	112		
gaaaaataca gggcatcatt gcagaataca acaaaatcaa tgatgtaaag gaagatgatg				690
acacggagaa gtttaaagaa gccattgtga aatttcatag gctgtttggg atgccagagg				750
aagagaaact cgtcaactat tactcttgca gctattggaa ggggag				796
<210> 61				
<211> 2624				
<212> DNA				
<213> Homo sapiens				
<220>				
<221> CDS				
<222> (271)..(2202)				
<400> 61				
tatttataat atgtggagga gagagagctc accatgctca ggtaaaggga tgaagcctct				60
ggtatgtcag aaccatgctg tcttccatga gacttccttt gtgaagagca tccattttaa				120
agacttttat gaatacatgg tttcaatcaa gtccccagag aacacatttg tcttctgagc				180
tgctggcagt tttgagaatc tgatgacctc cgaggggacc ctgcactcag ccatcaaagt				240
gttcttgccc ctctggacac tcataattca		atg gta gat gca ggt gga gtt		291
		Met Val Asp Ala Gly Gly Val		
	1	5		

gag aac atc acc cag ctt ccc cag gag ctt cct cag atg atg gct gca	339
Glu Asn Ile Thr Gln Leu Pro Gln Glu Leu Pro Gln Met Met Ala Ala	
8 13 18 23	
gca gcc gat ggt ttg ggg agt ata gcg ata gac acg acc cag ctc aac	387
Ala Ala Asp Gly Leu Gly Ser Ile Ala Ile Asp Thr Thr Gln Leu Asn	
24 29 34 39	
atg tcc gtg aca gat ccc aca gcc tgg gct aca gcc atg aat aac ctg	435
Met Ser Val Thr Asp Pro Thr Ala Trp Ala Thr Ala Met Asn Asn Leu	
40 45 50 55	
ggc atg gtt ccc gta ggg ttg cct gga cag cag ctc gtg tct gac tca	483
Gly Met Val Pro Val Gly Leu Pro Gly Gln Gln Leu Val Ser Asp Ser	
56 61 66 71	
atc tgt gtc cca ggc ttt gat cca agc ctc aac atg atg act gga atc	531
Ile Cys Val Pro Gly Phe Asp Pro Ser Leu Asn Met Met Thr Gly Ile	
72 77 82 87	
acc ccc att aac cca atg ata cca ggc ctt gga ctg gta cct ccc cca	579
Thr Pro Ile Asn Pro Met Ile Pro Gly Leu Gly Leu Val Pro Pro Pro	
88 93 98 103	
cca cca aca gaa gtg gct gtt gtc aaa gaa ata atc cac tgc aaa agc	627
Pro Pro Thr Glu Val Ala Val Val Lys Glu Ile Ile His Cys Lys Ser	
104 109 114 119	
tgt act ctt ttt cct caa aat cca aat ctt cca cct cct tcc aca aga	675
Cys Thr Leu Phe Pro Gln Asn Pro Asn Leu Pro Pro Pro Ser Thr Arg	
120 125 130 135	
gaa cga cct cct ggg tgt aag acc gtg ttt gtc gga gga tta cca gaa	723
Glu Arg Pro Pro Gly Cys Lys Thr Val Phe Val Gly Gly Leu Pro Glu	
136 141 146 151	
aat gct act gag gaa att att caa gaa gtc ttt gaa cag tgc ggt gat	771
Asn Ala Thr Glu Glu Ile Ile Gln Glu Val Phe Glu Gln Cys Gly Asp	
152 157 162 167	
att aca gca att cgg aaa agc aag aag aat ttt tgt cac att cgc ttt	819
Ile Thr Ala Ile Arg Lys Ser Lys Lys Asn Phe Cys His Ile Arg Phe	
168 173 178 183	
gca gag gaa ttc atg gtt gat aaa gcc att tac ctt tct ggt tat agg	867
Ala Glu Glu Phe Met Val Asp Lys Ala Ile Tyr Leu Ser Gly Tyr Arg	
184 189 194 199	
atg cga tta ggg tct agc acc gac aaa aag gat tca ggc cgc ctt cat	915
Met Arg Leu Gly Ser Ser Thr Asp Lys Lys Asp Ser Gly Arg Leu His	
200 205 210 215	
gtg gac ttt gcc cag gcc agg gat gac ttc tat gag tgg gaa tgc aag	963
Val Asp Phe Ala Gln Ala Arg Asp Asp Phe Tyr Glu Trp Glu Cys Lys	
216 221 226 231	
cag agg atg cgt gcc cgg gag gag cgg cac cgg cgc aag ctg gag gag	1011

Gln Arg Met Arg Ala Arg Glu Glu Arg His Arg Arg Lys Leu Glu Glu	
232 237 242 247	
gac cgg ctc agg ccc cca tcc ccg cct gcc ata atg cac tac tcg gag	1059
Asp Arg Leu Arg Pro Pro Ser Pro Pro Ala Ile Met His Tyr Ser Glu	
248 253 258 263	
cac gaa gcc gct ctg ctg gct gaa aag ctg aaa gat gat agc aag ttt	1107
His Glu Ala Ala Leu Leu Ala Glu Lys Leu Lys Asp Asp Ser Lys Phe	
264 269 274 279	
tca gag gct atc aca gtg ctg ctt tcc tgg att gaa cga ggg gaa gtg	1155
Ser Glu Ala Ile Thr Val Leu Leu Ser Trp Ile Glu Arg Gly Glu Val	
280 285 290 295	
aat cgg cgc tct gca aac cag ttc tat tcc atg gtg cag tcg gcc aac	1203
Asn Arg Arg Ser Ala Asn Gln Phe Tyr Ser Met Val Gln Ser Ala Asn	
296 301 306 311	
agc cac gtc cgc cgg cta atg aat gaa aaa gcc acc cat gag caa gag	1251
Ser His Val Arg Arg Leu Met Asn Glu Lys Ala Thr His Glu Gln Glu	
312 317 322 327	
atg gag gaa gcc aag gag aat ttt aaa aat gcc tta act ggg att ctc	1299
Met Glu Glu Ala Lys Glu Asn Phe Lys Asn Ala Leu Thr Gly Ile Leu	
328 333 338 343	
act caa ttt gag cag att gtg gcc gtt ttc aac gct tct acc aga caa	1347
Thr Gln Phe Glu Gln Ile Val Ala Val Phe Asn Ala Ser Thr Arg Gln	
344 349 354 359	
aaa gct tgg gac cat ttc tcg aaa gcc cag cgc aag aac ata gac att	1395
Lys Ala Trp Asp His Phe Ser Lys Ala Gln Arg Lys Asn Ile Asp Ile	
360 365 370 375	
tgg cga aag cat tct gag gag ctc cgg aat gct caa agt gag cag ctc	1443
Trp Arg Lys His Ser Glu Glu Leu Arg Asn Ala Gln Ser Glu Gln Leu	
376 381 386 391	
atg ggc atc cgc cgc gaa gaa gaa atg gaa atg tct gat gat gag aac	1491
Met Gly Ile Arg Arg Glu Glu Glu Met Glu Met Ser Asp Asp Glu Asn	
392 397 402 407	
tgt gac agc cct aca aag aaa atg aga gtc gat gaa tca gcc ctg gct	1539
Cys Asp Ser Pro Thr Lys Lys Met Arg Val Asp Glu Ser Ala Leu Ala	
408 413 418 423	
gcc cag gcc tac gct ctg aaa gag gag aat gac agt ctc cgc tgg cag	1587
Ala Gln Ala Tyr Ala Leu Lys Glu Glu Asn Asp Ser Leu Arg Trp Gln	
424 429 434 439	
ctg gat gcc tac agg aat gag gtg gag ctg ctg aaa caa gaa aaa gaa	1635
Leu Asp Ala Tyr Arg Asn Glu Val Glu Leu Leu Lys Gln Glu Lys Glu	
440 445 450 455	
cag ctt ttc cga aca gaa gaa aac ctc acc aag gac cag caa ctg cag	1683
Gln Leu Phe Arg Thr Glu Glu Asn Leu Thr Lys Asp Gln Gln Leu Gln	

456											461											466											471																																										
ttt	ctg	cag	caa	acc	atg	caa	ggc	atg	cag	cag	caa	ttg	cta	acc	atc	1731																																																											
Phe	Leu	Gln	Gln	Thr	Met	Gln	Gly	Met	Gln	Gln	Gln	Leu	Leu	Thr	Ile																																																												
472											477											482											487																																										
cag	gag	gag	tta	aac	aac	aaa	aag	tca	gaa	ttg	gaa	caa	gca	aag	gaa	1779																																																											
Gln	Glu	Glu	Leu	Asn	Asn	Lys	Lys	Ser	Glu	Leu	Glu	Gln	Ala	Lys	Glu																																																												
488											493											498											503																																										
gag	cag	tcc	cat	aca	caa	gcg	tta	cta	aaa	gtc	ctg	cag	gaa	caa	tta	1827																																																											
Glu	Gln	Ser	His	Thr	Gln	Ala	Leu	Leu	Lys	Val	Leu	Gln	Glu	Gln	Leu																																																												
504											509											514											519																																										
aaa	ggc	acc	aag	gaa	ttg	gtc	gag	acc	aat	ggc	cac	agc	cat	gag	gat	1875																																																											
Lys	Gly	Thr	Lys	Glu	Leu	Val	Glu	Thr	Asn	Gly	His	Ser	His	Glu	Asp																																																												
520											525											530											535																																										
tca	aat	gaa	atc	aat	gtg	ttg	aca	gtt	gca	tta	gtc	aac	caa	gac	cga	1923																																																											
Ser	Asn	Glu	Ile	Asn	Val	Leu	Thr	Val	Ala	Leu	Val	Asn	Gln	Asp	Arg																																																												
536											541											546											551																																										
gag	aac	aat	att	gag	aaa	aga	agc	caa	ggc	tta	aaa	tca	gag	aaa	gaa	1971																																																											
Glu	Asn	Asn	Ile	Glu	Lys	Arg	Ser	Gln	Gly	Leu	Lys	Ser	Glu	Lys	Glu																																																												
552											557											562											567																																										
gct	ctg	cta	ata	ggc	atc	ata	tca	acg	ttt	ctt	cac	gtc	cat	cct	ttt	2019																																																											
Ala	Leu	Leu	Ile	Gly	Ile	Ile	Ser	Thr	Phe	Leu	His	Val	His	Pro	Phe																																																												
568											573											578											583																																										
gga	gcc	aac	ata	gaa	tat	ctt	tgg	tca	tac	atg	cag	cag	ctg	gac	tcc	2067																																																											
Gly	Ala	Asn	Ile	Glu	Tyr	Leu	Trp	Ser	Tyr	Met	Gln	Gln	Leu	Asp	Ser																																																												
584											589											594											599																																										
aag	ata	tct	gca	aat	gaa	ata	gaa	atg	ctt	ttg	atg	agg	ctg	cca	cgc	2115																																																											
Lys	Ile	Ser	Ala	Asn	Glu	Ile	Glu	Met	Leu	Leu	Met	Arg	Leu	Pro	Arg																																																												
600											605											610											615																																										
atg	ttc	aaa	cag	gaa	ttc	acg	ggc	gtg	gga	gcc	acg	ctg	gaa	aaa	aga	2163																																																											
Met	Phe	Lys	Gln	Glu	Phe	Thr	Gly	Val	Gly	Ala	Thr	Leu	Glu	Lys	Arg																																																												
616											621											626											631																																										
tgg	aag	ttg	tgt	gcc	ttt	gaa	gga	att	aaa	acc	acc	taa	ctgcgaagag	2212																																																													
Trp	Lys	Leu	Cys	Ala	Phe	Glu	Gly	Ile	Lys	Thr	Thr	*																																																															
632											637											642																																																					
caaagcatct																ctggaaatga										aaccatgtga										acctggccag										ggcgggtgcga										cggggaagca										2272									
ggaggtgtgg																ggttgggtccc										gcacgcaacc										tttgtggagc										catcgaagcc										tgccttttagt										2332									
tatatctgtg																gcgttctctt										gtaagtggaa										atgtaattgt										gtaccagttt										cttaaaataa										2392									
acaaagcttc																atactgtgac										agatctgttt										cctatgaaaa										ccaaacaatg										attccacagt										2452									
cataatgatg																gcaaaatctt										aaaatgtgct										acatttgaga										atagctcacc										aagcaaaata										2512									
tttaaaqtta																atgatgggtgt										agcaatgatt										gttgctaggc										tacagagttg										tatatgtaat										2572									

gtatagctga aatcattaaa tgacattttc ctgaaagtct ttctgtttta gt

2624

<210> 62
<211> 2565
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(2565)

<400> 62

atg cca ggc ggg ggt cct cag ggc gcc cca gcc gcc gcc ggc ggc ggc 48
Met Pro Gly Gly Gly Pro Gln Gly Ala Pro Ala Ala Ala Gly Gly Gly
1 5 10

ggc gtg agc cac cgc gca ggc agc cgg gat tgc tta cca cct gca gcg 96
Gly Val Ser His Arg Ala Gly Ser Arg Asp Cys Leu Pro Pro Ala Ala
17 22 27 32

tgc ttt cgg agg cgg cgg ctg gca cgg agg ccg ggc tac atg aga agc 144
Cys Phe Arg Arg Arg Arg Leu Ala Arg Arg Pro Gly Tyr Met Arg Ser
33 38 43 48

tcg aca ggg cct ggg atc ggg ttc ctt tcc cca gca gtg ggc aca ctg 192
Ser Thr Gly Pro Gly Ile Gly Phe Leu Ser Pro Ala Val Gly Thr Leu
49 54 59 64

ttc cgg ttc cca gga ggg gtg tct ggc gag gag tcc cac cac tcg gag 240
Phe Arg Phe Pro Gly Gly Val Ser Gly Glu Glu Ser His His Ser Glu
65 70 75 80

tcc agg gcc aga cag tgt ggc ctt gac tcg aga ggc ctc ttg gtc cgg 288
Ser Arg Ala Arg Gln Cys Gly Leu Asp Ser Arg Gly Leu Leu Val Arg
81 86 91 96

agc cct gtt tcc aag agt gca gca gcc cct act gtg acc tct gtg aga 336
Ser Pro Val Ser Lys Ser Ala Ala Ala Pro Thr Val Thr Ser Val Arg
97 102 107 112

gga acc tcg gcg cac ttt ggg att cag ctc aga ggt ggc acc aga ttg 384
Gly Thr Ser Ala His Phe Gly Ile Gln Leu Arg Gly Gly Thr Arg Leu
113 118 123 128

cct gac agg ctt agc tgg ccg tgt ggc cct ggg agt gct ggg tgg cag 432
Pro Asp Arg Leu Ser Trp Pro Cys Gly Pro Gly Ser Ala Gly Trp Gln
129 134 139 144

caa gag ttt gca gcc atg gat agt tct gag acc ctg gac gcc agc tgg 480
Gln Glu Phe Ala Ala Met Asp Ser Ser Glu Thr Leu Asp Ala Ser Trp
145 150 155 160

gag gca gcc tgc agc gat gga gca agg cgt gtc cgg gca gca ggc tct 528

Glu Ala Ala Cys Ser Asp Gly Ala Arg Arg Val Arg Ala Ala Gly Ser	
161 166 171 176	
ctg cca tca gca gag ttg agt agc aac agc tgc agc cct ggc tgt ggc	576
Leu Pro Ser Ala Glu Leu Ser Ser Asn Ser Cys Ser Pro Gly Cys Gly	
177 182 187 192	
cct gag gtc ccc cca acc cct cct ggc tct cac agt gcc ttt acc tca	624
Pro Glu Val Pro Pro Thr Pro Pro Gly Ser His Ser Ala Phe Thr Ser	
193 198 203 208	
agc ttt agc ttt att cgg ctc tcg ctt ggc tct gcc ggg gaa cgt gga	672
Ser Phe Ser Phe Ile Arg Leu Ser Leu Gly Ser Ala Gly Glu Arg Gly	
209 214 219 224	
gaa gca gaa ggc tgc cca cca tcc aga gag gct gag tcc cat tgc cag	720
Glu Ala Glu Gly Cys Pro Pro Ser Arg Glu Ala Glu Ser His Cys Gln	
225 230 235 240	
agc ccc cag gag atg gga gcc aaa gct gcc agc ttg gac ggg cct cac	768
Ser Pro Gln Glu Met Gly Ala Lys Ala Ala Ser Leu Asp Gly Pro His	
241 246 251 256	
gag gac ccg cga tgt ctc tct cag ccc ttc agt ctc ttg gct aca cgg	816
Glu Asp Pro Arg Cys Leu Ser Gln Pro Phe Ser Leu Leu Ala Thr Arg	
257 262 267 272	
gtc tct gca gac ttg gcc cag gcc gca agg aac agc tcc agg cca gag	864
Val Ser Ala Asp Leu Ala Gln Ala Ala Arg Asn Ser Ser Arg Pro Glu	
273 278 283 288	
cgt gac atg cat tct tta cca gac atg gac cct ggc tcc tcc agt tct	912
Arg Asp Met His Ser Leu Pro Asp Met Asp Pro Gly Ser Ser Ser Ser	
289 294 299 304	
ctg gat ccc tca ctg gct ggc tgt ggt ggt gat ggg agc agc ggc tca	960
Leu Asp Pro Ser Leu Ala Gly Cys Gly Gly Asp Gly Ser Ser Gly Ser	
305 310 315 320	
ggg gat gcc cac tct tgg gac acc ctg ctc agg aaa tgg gag cca gtg	1008
Gly Asp Ala His Ser Trp Asp Thr Leu Leu Arg Lys Trp Glu Pro Val	
321 326 331 336	
ctg cgg gac tgc ctg ctg aga aac cgg agg cag atg gag gta ata tcc	1056
Leu Arg Asp Cys Leu Leu Arg Asn Arg Arg Gln Met Glu Val Ile Ser	
337 342 347 352	
tta aga tta aaa ctt cag aaa ctt cag gaa gat gca gtt gag aat gat	1104
Leu Arg Leu Lys Leu Gln Lys Leu Gln Glu Asp Ala Val Glu Asn Asp	
353 358 363 368	
gat tat gat aaa gct gag acg tta caa caa aga tta gaa gac ctg gaa	1152
Asp Tyr Asp Lys Ala Glu Thr Leu Gln Gln Arg Leu Glu Asp Leu Glu	
369 374 379 384	
caa gag aaa atc agc ctg cac ttt caa ctt cct tca agg cag cca gct	1200
Gln Glu Lys Ile Ser Leu His Phe Gln Leu Pro Ser Arg Gln Pro Ala	

385		390		395		400	
ctt agc agt ttc ctg ggt cac ctg gca gca caa gtc cag gct gcc ttg	1248						
Leu Ser Ser Phe Leu Gly His Leu Ala Ala Gln Val Gln Ala Ala Leu							
401		406		411		416	
cgc cgt ggg gcc act cag cag gcc agc gga gat gac acc cac acc cca	1296						
Arg Arg Gly Ala Thr Gln Gln Ala Ser Gly Asp Asp Thr His Thr Pro							
417		422		427		432	
ctg aga atg gag ccg agg ctg ttg gaa ccc act gct cag gac agc ttg	1344						
Leu Arg Met Glu Pro Arg Leu Leu Glu Pro Thr Ala Gln Asp Ser Leu							
433		438		443		448	
cac gtg tcc atc acg aga cga gac tgg ctt ctt cag gaa aag cag cag	1392						
His Val Ser Ile Thr Arg Arg Asp Trp Leu Leu Gln Glu Lys Gln Gln							
449		454		459		464	
cta cag aaa gaa atc gaa gct ctc caa gca agg atg ttt gtg ctg gaa	1440						
Leu Gln Lys Glu Ile Glu Ala Leu Gln Ala Arg Met Phe Val Leu Glu							
465		470		475		480	
gcc aaa gat caa cag ctg aga agg gaa ata gag gag caa gag cag caa	1488						
Ala Lys Asp Gln Gln Leu Arg Arg Glu Ile Glu Glu Gln Glu Gln Gln							
481		486		491		496	
ctc cag tgg cag ggc tgc gac ctg acc cca ctg gtg ggc cag ctg tcc	1536						
Leu Gln Trp Gln Gly Cys Asp Leu Thr Pro Leu Val Gly Gln Leu Ser							
497		502		507		512	
ctg ggt cag ctg cag gag gtc agc aag gcc ttg cag gac acc ctg gcc	1584						
Leu Gly Gln Leu Gln Glu Val Ser Lys Ala Leu Gln Asp Thr Leu Ala							
513		518		523		528	
tca gcc ggt cag att ccc ttc cat gca gag cca ccg gaa acc ata agg	1632						
Ser Ala Gly Gln Ile Pro Phe His Ala Glu Pro Pro Glu Thr Ile Arg							
529		534		539		544	
agc ctc cag gaa aga ata aaa tcc ctc aac ttg tca ctt aaa gaa atc	1680						
Ser Leu Gln Glu Arg Ile Lys Ser Leu Asn Leu Ser Leu Lys Glu Ile							
545		550		555		560	
act act aag gtg tgt atg agt gag aaa ttc tgc agc acc ctg agg aag	1728						
Thr Thr Lys Val Cys Met Ser Glu Lys Phe Cys Ser Thr Leu Arg Lys							
561		566		571		576	
aaa gtt aac gat att gaa acc caa cta cca gcc ttg ctt gaa gcc aaa	1776						
Lys Val Asn Asp Ile Glu Thr Gln Leu Pro Ala Leu Leu Glu Ala Lys							
577		582		587		592	
atg cat gcc ata tca gga aac cat ttc tgg acg gct aaa gac ctc acc	1824						
Met His Ala Ile Ser Gly Asn His Phe Trp Thr Ala Lys Asp Leu Thr							
593		598		603		608	
gag gag att aga tca tta aca tca gag aga gaa ggg ctg gag gga ctc	1872						
Glu Glu Ile Arg Ser Leu Thr Ser Glu Arg Glu Gly Leu Glu Gly Leu							
609		614		619		624	

ctc agc aag ctg ttg gtg ttg agt tcc agg aat gtc aaa aag ctg gga Leu Ser Lys Leu Leu Val Leu Ser Ser Arg Asn Val Lys Lys Leu Gly 625 630 635 640	1920
agt gtt aaa gaa gat tac aac aga ctg aga aga gaa gtg gag cac cag Ser Val Lys Glu Asp Tyr Asn Arg Leu Arg Arg Glu Val Glu His Gln 641 646 651 656	1968
gag act gcc tat gaa aca agt gtg aag gaa aat act atg aag tac atg Glu Thr Ala Tyr Glu Thr Ser Val Lys Glu Asn Thr Met Lys Tyr Met 657 662 667 672	2016
gaa aca ctt aag aat aaa ctg tgc agc tgc aag tgt cca ctg ctt ggg Glu Thr Leu Lys Asn Lys Leu Cys Ser Cys Lys Cys Pro Leu Leu Gly 673 678 683 688	2064
aaa gtg tgg gaa gct gac ttg gaa gct tgt cga ttg ctt atc cag tgc Lys Val Trp Glu Ala Asp Leu Glu Ala Cys Arg Leu Leu Ile Gln Cys 689 694 699 704	2112
cta cag ctc cag gaa gcc agg gga agc ctg tct gta gaa gat gag agg Leu Gln Leu Gln Glu Ala Arg Gly Ser Leu Ser Val Glu Asp Glu Arg 705 710 715 720	2160
cag atg gat gac tta gag gga gct gct cct cct att ccc ccc agg ctc Gln Met Asp Asp Leu Glu Gly Ala Ala Pro Pro Ile Pro Pro Arg Leu 721 726 731 736	2208
cac tcc gag gat aaa agg aag acc cct ttg aag gta ttg gaa gaa tgg His Ser Glu Asp Lys Arg Lys Thr Pro Leu Lys Val Leu Glu Glu Trp 737 742 747 752	2256
aag act cac ctc atc ccc tct ctg cac tgt gct gga ggt gaa cag aaa Lys Thr His Leu Ile Pro Ser Leu His Cys Ala Gly Gly Glu Gln Lys 753 758 763 768	2304
gag gaa tct tac atc ctt tct gca gaa ctt gga gaa aag tgt gaa gac Glu Glu Ser Tyr Ile Leu Ser Ala Glu Leu Gly Glu Lys Cys Glu Asp 769 774 779 784	2352
ata ggc aag aag cta ttg tac ttg gaa gat caa ctt cac aca gca atc Ile Gly Lys Lys Leu Leu Tyr Leu Glu Asp Gln Leu His Thr Ala Ile 785 790 795 800	2400
cac agt cat gat gaa gat ctc att cag tct ctc agg agg gag ctc cag His Ser His Asp Glu Asp Leu Ile Gln Ser Leu Arg Arg Glu Leu Gln 801 806 811 816	2448
atg gtg aag gaa act ctg cag gcc atg atc ctg cag ctc cag cca gca Met Val Lys Glu Thr Leu Gln Ala Met Ile Leu Gln Leu Gln Pro Ala 817 822 827 832	2496
aag gag gcg gga gaa aga gaa gct gca gct tcc tgc atg aca gct ggt Lys Glu Ala Gly Glu Arg Glu Ala Ala Ala Ser Cys Met Thr Ala Gly 833 838 843 848	2544

gtc cac gaa gca caa gcc tga
 Val His Glu Ala Gln Ala *
 849 854

2565

<210> 63
 <211> 1126
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (46) .. (999)

<400> 63
 taagcttgcg gccgccggcg ggccggggccc gcgcacagcg cccgc atg tac aac 54
 Met Tyr Asn
 1

atg atg gag acg gag ctg aag ccg ccg ggc ccg cag caa act tcg ggg 102
 Met Met Glu Thr Glu Leu Lys Pro Pro Gly Pro Gln Gln Thr Ser Gly
 4 9 14 19

ggc ggc ggc ggc aac tcc acc gcg gcg gcg gcc ggc ggc aac cag aaa 150
 Gly Gly Gly Gly Asn Ser Thr Ala Ala Ala Gly Gly Asn Gln Lys
 20 25 30 35

aac agc ccg gac cgc gtc aag ccg ccc atg aat gcc ttc atg gtg tgg 198
 Asn Ser Pro Asp Arg Val Lys Arg Pro Met Asn Ala Phe Met Val Trp
 36 41 46 51

tcc cgc ggg cag ccg cgc aag atg gcc cag gag aac ccc aag atg cac 246
 Ser Arg Gly Gln Arg Arg Lys Met Ala Gln Glu Asn Pro Lys Met His
 52 57 62 67

aac tcg gag atc agc aag cgc ctg ggc gcc gag tgg aaa ctt ttg tcg 294
 Asn Ser Glu Ile Ser Lys Arg Leu Gly Ala Glu Trp Lys Leu Leu Ser
 68 73 78 83

gag acg gag aag ccg ccg ttc atc gac gag gct aag ccg ctg cga gcg 342
 Glu Thr Glu Lys Arg Pro Phe Ile Asp Glu Ala Lys Arg Leu Arg Ala
 84 89 94 99

ctg cac atg aag gag cac ccg gat tat aaa tac ccg ccc ccg ccg aaa 390
 Leu His Met Lys Glu His Pro Asp Tyr Lys Tyr Arg Pro Arg Arg Lys
 100 105 110 115

acc aag acg ctc atg aag aag gat aag tac acg ctg ccc ggc ggc ctg 438
 Thr Lys Thr Leu Met Lys Lys Asp Lys Tyr Thr Leu Pro Gly Gly Leu
 116 121 126 131

ctg gcc ccc ggc ggc aat agc atg gcg agc ggg gtc ggc gtg ggc gcc 486
 Leu Ala Pro Gly Gly Asn Ser Met Ala Ser Gly Val Gly Val Gly Ala
 132 137 142 147

004060" 9E64E9E0

ggc Gly 148	ctg Leu	ggc Gly	gcg Ala	ggc Gly	gtg Val 153	aac Asn	cag Gln	cgc Arg	atg Met	gac Asp 158	agt Ser	tac Tyr	gcg Ala	cac His	atg Met 163	534	
aac Asn 164	ggc Gly	tgg Trp	agc Ser	aac Asn	ggc Gly 169	agc Ser	tac Tyr	agc Ser	atg Met	atg Met 174	cag Gln	gac Asp	cag Gln	ctg Leu	ggc Gly 179	582	
tac Tyr 180	ccg Pro	cag Gln	cac His	ccg Pro	ggc Gly 185	ctc Leu	aat Asn	gcg Ala	cac His	ggc Gly 190	gca Ala	gcg Ala	cag Gln	atg Met	cag Gln 195	630	
ccc Pro 196	atg Met	cac His	cgc Arg	tac Tyr	gac Asp 201	gtg Val	agc Ser	gcc Ala	ctg Leu	cag Gln 206	tac Tyr	aac Asn	tcc Ser	atg Met	acc Thr 211	678	
agc Ser 212	tcg Ser	cag Gln	acc Thr	tac Tyr	atg Met 217	aac Asn	ggc Gly	tcg Ser	ccc Pro	acc Thr 222	tac Tyr	agc Ser	atg Met	tcc Ser	tac Tyr 227	726	
tcg Ser 228	cag Gln	cag Gln	ggc Gly	acc Thr	cct Pro 233	ggc Gly	atg Met	gct Ala	ctt Leu	ggc Gly 238	tcc Ser	atg Met	ggc Gly	tcg Ser	gtg Val 243	774	
gtc Val 244	aag Lys	tcc Ser	gag Glu	gcc Ala	agc Ser 249	tcc Ser	agc Ser	ccc Pro	cct Pro	gtg Val 254	gtt Val	acc Thr	tct Ser	tcc Ser	tcc Ser 259	822	
cac His 260	tcc Ser	agg Arg	gcg Ala	ccc Pro	tgc Cys 265	cag Gln	gcc Ala	ggg Gly	gac Asp	ctc Leu 270	cgg Arg	gac Asp	atg Met	atc Ile	agc Ser 275	870	
atg Met 276	tat Tyr	ctc Leu	ccc Pro	ggc Gly	gcc Ala 281	gag Glu	gtg Val	ccg Pro	gaa Glu	ccc Pro 286	gcc Ala	gcc Ala	ccc Pro	agc Ser	aga Arg 291	918	
ctt Leu 292	cac His	atg Met	tcc Ser	cag Gln	cac His 297	tac Tyr	cag Gln	agc Ser	ggc Gly	ccg Pro 302	gtg Val	ccc Pro	ggc Gly	acg Thr	gcc Ala 307	966	
att Ile 308	aac Asn	ggc Gly	aca Thr	ctg Leu	ccc Pro 313	ctc Leu	tca Ser	cac His	atg Met	tga * 318	gggccgga	cagcgaactg				1017	
gaggggggag			aaatttttcaa			agaaaaacga			gggaaatggg			aggggtgcaa			aagaggagag		1077
taagaaacag			catggagaaa			acccggtacg			ctcaaaaaga			aaaaaaaaa					1126

```
<210> 64
<211> 3276
<212> DNA
<213> Homo sapiens
```

<220>
 <221> CDS
 <222> (1)..(2760)

<400> 64

atg gtg cag cgc atg tgg gcc gag gcg gcc ggg cct gct ggc ggc gcc	48
Met Val Gln Arg Met Trp Ala Glu Ala Ala Gly Pro Ala Gly Gly Ala	
1 5 10	
gag ccg ctg ttt ccg ggc tcc cgg cgg agc cgc agc gtg tgg gac gcc	96
Glu Pro Leu Phe Pro Gly Ser Arg Arg Ser Arg Ser Val Trp Asp Ala	
17 22 27 32	
gtg cgc ctg gag gtg ggc gtc ccc gac agc tgc ccg gtg gtg ctg cac	144
Val Arg Leu Glu Val Gly Val Pro Asp Ser Cys Pro Val Val Leu His	
33 38 43 48	
agc ttc acg cag cta gac ccc gac ctg ccg cgc ccg gag agc tcc acg	192
Ser Phe Thr Gln Leu Asp Pro Asp Leu Pro Arg Pro Glu Ser Ser Thr	
49 54 59 64	
cag gag atc ggt gag gag ctg atc aac gga gtc atc tac tcc atc tcc	240
Gln Glu Ile Gly Glu Glu Leu Ile Asn Gly Val Ile Tyr Ser Ile Ser	
65 70 75 80	
ctg cgc aag gtg cag ctg cac cac gga ggc aac aag ggg cag cgc tgg	288
Leu Arg Lys Val Gln Leu His His Gly Gly Asn Lys Gly Gln Arg Trp	
81 86 91 96	
ctc ggg tat gag aat gag tgc gcc ctg aac ctt tat gag act tgc aag	336
Leu Gly Tyr Glu Asn Glu Ser Ala Leu Asn Leu Tyr Glu Thr Cys Lys	
97 102 107 112	
gtg cgg acc gtg aag gct ggc acg ctg gag aag ctg gtg gag cac ctg	384
Val Arg Thr Val Lys Ala Gly Thr Leu Glu Lys Leu Val Glu His Leu	
113 118 123 128	
gtg cca gcc ttc cag ggc agc gac ctc tcc tac gtc acc atc ttc ctg	432
Val Pro Ala Phe Gln Gly Ser Asp Leu Ser Tyr Val Thr Ile Phe Leu	
129 134 139 144	
tgt acc tat aga gcc ttc acc acc acc caa cag gtc ctg gac ctg ctg	480
Cys Thr Tyr Arg Ala Phe Thr Thr Thr Gln Gln Val Leu Asp Leu Leu	
145 150 155 160	
ttc aaa agg tac ggt aga tgt gac gcc ctc acg gcc tcc tct aga tac	528
Phe Lys Arg Tyr Gly Arg Cys Asp Ala Leu Thr Ala Ser Ser Arg Tyr	
161 166 171 176	
ggc tgc atc ctc ccc tat tcc gac gag gat ggt gga ccc cag gac caa	576
Gly Cys Ile Leu Pro Tyr Ser Asp Glu Asp Gly Gly Pro Gln Asp Gln	
177 182 187 192	
ctt aaa aat gcc atc tcc tcc atc ctg ggc acc tgg ctg gac cag tac	624
Leu Lys Asn Ala Ile Ser Ser Ile Leu Gly Thr Trp Leu Asp Gln Tyr	
193 198 203 208	

tcg gag gat ttc tgt caa cct ccg gac ttt ccc tgc ctc aag cag ctg Ser Glu Asp Phe Cys Gln Pro Pro Asp Phe Pro Cys Leu Lys Gln Leu 209 214 219 224	672
gtg gcc tac gtg cag ctc aac atg cca ggc tca gac ctg gag cgc cgt Val Ala Tyr Val Gln Leu Asn Met Pro Gly Ser Asp Leu Glu Arg Arg 225 230 235 240	720
gcc cac ctt ctc ctg gcc cag ctg gag cac tcg gaa ccc att gag gca Ala His Leu Leu Leu Ala Gln Leu Glu His Ser Glu Pro Ile Glu Ala 241 246 251 256	768
gag cct gag ggt gag gag gac tgg gct ctg tca cca gtg cca gct cta Glu Pro Glu Gly Glu Glu Asp Trp Ala Leu Ser Pro Val Pro Ala Leu 257 262 267 272	816
aaa cca act cca gag ctc gag cta gct cta aca cca gct cga gca ccc Lys Pro Thr Pro Glu Leu Glu Leu Ala Leu Thr Pro Ala Arg Ala Pro 273 278 283 288	864
agc cca gtg ccg gct cca gcc ccg gag cca gag cca gct cca aca cca Ser Pro Val Pro Ala Pro Ala Pro Glu Pro Glu Pro Ala Pro Thr Pro 289 294 299 304	912
gct cca ggt tca gag cta gaa gta gct cca gca cca gct ccg gag ctc Ala Pro Gly Ser Glu Leu Glu Val Ala Pro Ala Pro Ala Pro Glu Leu 305 310 315 320	960
cag cag gct cca gag cca gct gtg gga cta gaa tcg gct cca gcg cca Gln Gln Ala Pro Glu Pro Ala Val Gly Leu Glu Ser Ala Pro Ala Pro 321 326 331 336	1008
gct ctg gaa cta gag cca gct cca gaa cag gat cca gct ccc tca caa Ala Leu Glu Leu Glu Pro Ala Pro Glu Gln Asp Pro Ala Pro Ser Gln 337 342 347 352	1056
act cta gag ctg gag cca gct cca gca cca gtt cca tca tta cag cct Thr Leu Glu Leu Glu Pro Ala Pro Ala Pro Val Pro Ser Leu Gln Pro 353 358 363 368	1104
tcc tgg cct tca cct gtg gtt gca gag aac ggg ctg agt gag gag aag Ser Trp Pro Ser Pro Val Val Ala Glu Asn Gly Leu Ser Glu Glu Lys 369 374 379 384	1152
cct cac ctc ttg gtg ttc cct cca gat ctg gtg gca gag cag ttt aca Pro His Leu Leu Val Phe Pro Pro Asp Leu Val Ala Glu Gln Phe Thr 385 390 395 400	1200
ctg atg gat gcg gaa ctg ttc aag aag gtg gtg ccc tac cac tgc ctg Leu Met Asp Ala Glu Leu Phe Lys Lys Val Val Pro Tyr His Cys Leu 401 406 411 416	1248
ggc tcc atc tgg tcc cag cgg gac aag aag ggc aag gag cac ctg gcg Gly Ser Ile Trp Ser Gln Arg Asp Lys Lys Gly Lys Glu His Leu Ala 417 422 427 432	1296
ccc acc atc cgc gcc act gtc acc cag ttc aac agt gtg gcc aac tgt	1344

Pro Thr Ile Arg Ala Thr Val Thr Gln Phe Asn Ser Val Ala Asn Cys	
433 438 443 448	
gtc atc acc acc tgc ctc ggg aac cga agc acg aaa gcc cca gac agg	1392
Val Ile Thr Thr Cys Leu Gly Asn Arg Ser Thr Lys Ala Pro Asp Arg	
449 454 459 464	
gcc agg gtg gtg gag cac tgg atc gag gtg gcc agg gag tgc cgg atc	1440
Ala Arg Val Val Glu His Trp Ile Glu Val Ala Arg Glu Cys Arg Ile	
465 470 475 480	
ctc aag aac ttc tcg tca ctg tat gcc atc ctc tcg gcc ctg cag agc	1488
Leu Lys Asn Phe Ser Ser Leu Tyr Ala Ile Leu Ser Ala Leu Gln Ser	
481 486 491 496	
aac tcc atc cac cgt ctg aag aag acg tgg gaa gac gtt tcc agg gac	1536
Asn Ser Ile His Arg Leu Lys Lys Thr Trp Glu Asp Val Ser Arg Asp	
497 502 507 512	
agt ttc cgg atc ttt cag aag ctg tca gag atc ttc tca gat gag aac	1584
Ser Phe Arg Ile Phe Gln Lys Leu Ser Glu Ile Phe Ser Asp Glu Asn	
513 518 523 528	
aac tac tca ttg agc cgg gag ctg ctc atc aag gag ggc acc tcc aag	1632
Asn Tyr Ser Leu Ser Arg Glu Leu Leu Ile Lys Glu Gly Thr Ser Lys	
529 534 539 544	
ttt gcc acc ctg gag atg aac ccc aag aga gcc cag aaa cgg ccg aag	1680
Phe Ala Thr Leu Glu Met Asn Pro Lys Arg Ala Gln Lys Arg Pro Lys	
545 550 555 560	
gag acg ggc atc atc cag ggc acc gtt ccc tac ctg ggc acg ttc ctc	1728
Glu Thr Gly Ile Ile Gln Gly Thr Val Pro Tyr Leu Gly Thr Phe Leu	
561 566 571 576	
acc gac ctg gtg atg ctg gac act gcc atg aag gac tat ctg tat ggc	1776
Thr Asp Leu Val Met Leu Asp Thr Ala Met Lys Asp Tyr Leu Tyr Gly	
577 582 587 592	
aga ctc atc aac ttt gag aag agg agg aag gag ttc gag gtg atc gcc	1824
Arg Leu Ile Asn Phe Glu Lys Arg Arg Lys Glu Phe Glu Val Ile Ala	
593 598 603 608	
cag atc aag ctg ctg cag tcg gcc tgc aac aac tac agc atc gcg cca	1872
Gln Ile Lys Leu Leu Gln Ser Ala Cys Asn Asn Tyr Ser Ile Ala Pro	
609 614 619 624	
gat gag caa ttt ggg gcc tgg ttc cgg gcc gtg gag cgg ctc agc gag	1920
Asp Glu Gln Phe Gly Ala Trp Phe Arg Ala Val Glu Arg Leu Ser Glu	
625 630 635 640	
act gag agc tac aac ctg tcg tgc gag ctg gag ccc cca tcc gag tca	1968
Thr Glu Ser Tyr Asn Leu Ser Cys Glu Leu Glu Pro Pro Ser Glu Ser	
641 646 651 656	
gcc agc aac acc ctc agg acc aag aag aac aca gcc att gtc aag cgc	2016
Ala Ser Asn Thr Leu Arg Thr Lys Lys Asn Thr Ala Ile Val Lys Arg	

657	662	667	672	
tgg agc gac cgc cag gcc ccc agc act gag ctc agt acc agt ggc agc				2064
Trp Ser Asp Arg Gln Ala Pro Ser Thr Glu Leu Ser Thr Ser Gly Ser				
673	678	683	688	
tcc cac tcc aag tcc tgt gac cag ctc agg tgt ggc ccc tac ctc agc				2112
Ser His Ser Lys Ser Cys Asp Gln Leu Arg Cys Gly Pro Tyr Leu Ser				
689	694	699	704	
agc ggg gac atc gct gac gcg ctc agc gtg cac tcg gcc ggc tcc tct				2160
Ser Gly Asp Ile Ala Asp Ala Leu Ser Val His Ser Ala Gly Ser Ser				
705	710	715	720	
agc tcc gac gtg gag gag atc aac atc agc ttc gtc ccg gag tct cct				2208
Ser Ser Asp Val Glu Glu Ile Asn Ile Ser Phe Val Pro Glu Ser Pro				
721	726	731	736	
gat ggc cag gaa aag aag ttc tgg gaa tca gcc tca cag tca tcc ccg				2256
Asp Gly Gln Glu Lys Lys Phe Trp Glu Ser Ala Ser Gln Ser Ser Pro				
737	742	747	752	
gag acc tcc ggc atc agc tca gcc tcc agc agc acc tcg tcc tcc tca				2304
Glu Thr Ser Gly Ile Ser Ser Ala Ser Ser Ser Thr Ser Ser Ser Ser				
753	758	763	768	
gcc tcc acc acg ccc gtg gct gcc aca cgc acc cac aag cgc tct gtc				2352
Ala Ser Thr Thr Pro Val Ala Ala Thr Arg Thr His Lys Arg Ser Val				
769	774	779	784	
tca ggg ctc tgc aac tcc agc tcc gcg ctg ccg ctc tac aac cag cag				2400
Ser Gly Leu Cys Asn Ser Ser Ser Ala Leu Pro Leu Tyr Asn Gln Gln				
785	790	795	800	
gtg ggc gac tgc tgt atc atc cgc gtc agc ctg gac gtg gac aat ggc				2448
Val Gly Asp Cys Cys Ile Ile Arg Val Ser Leu Asp Val Asp Asn Gly				
801	806	811	816	
aac atg tac aag agc atc ctg gtg acc agc caa gat aag gct ccg gct				2496
Asn Met Tyr Lys Ser Ile Leu Val Thr Ser Gln Asp Lys Ala Pro Ala				
817	822	827	832	
gta atc cgc aag gcc atg gac aaa cac aac ctg gag gag gag gag ccg				2544
Val Ile Arg Lys Ala Met Asp Lys His Asn Leu Glu Glu Glu Glu Pro				
833	838	843	848	
gag gac tat gag ctg ctg cag att ctc tca gat gac cgg aag ctg aag				2592
Glu Asp Tyr Glu Leu Leu Gln Ile Leu Ser Asp Asp Arg Lys Leu Lys				
849	854	859	864	
atc cct gaa aac gcc aac gtc ttc tat gcc atg aac tct acc gcc aac				2640
Ile Pro Glu Asn Ala Asn Val Phe Tyr Ala Met Asn Ser Thr Ala Asn				
865	870	875	880	
tat gac ttt gtc ctc aag aag cgg acc ttc acc aag gga gtg aag gtc				2688
Tyr Asp Phe Val Leu Lys Lys Arg Thr Phe Thr Lys Gly Val Lys Val				
881	886	891	896	

aag cac gga gcc agc tcc acc ctc cct cgc atg aag cag aaa gga ctc 2736
 Lys His Gly Ala Ser Ser Thr Leu Pro Arg Met Lys Gln Lys Gly Leu
 897 902 907 912

aag att gcc aag ggc atc ttc tga gggcatcctc ccagggtctg gctggctggt 2790
 Lys Ile Ala Lys Gly Ile Phe *
 913 918

agccaagcac ttatggacca gagtggccca ggccagctgg gcgccttcct cccacctgcc 2850

agcccagggt accccagact ccagtttcat cctgaacctc tcccgtgct gggattgacg 2910

cctgccattg gtcaggctga cctggcctcc cgtggaccac tcgctgcctt aggtgccttc 2970

tgctctctgg aaccagagga cttagctgact tttgccaagg agcagtgcc aacgggcatgg 3030

catggtgccc tgctgcccc cgggcaccac ctctgtacac ttccctgaca ccttcccagg 3090

tgtgggtcac tgccacctgt gcccatgggc accccagagc accactgtg accactgcag 3150

ttctctcatg cccacaggca ctggcctgtg accttgcag ggggtccggc cctcccacc 3210

actctagcct ttctcaggct gcaccaaaga ttccatcatc agggccaact gagagtgagg 3270

gagtct 3276

<210> 65
 <211> 4863
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (185)..(4096)

<400> 65
 ggagatagcg cctgtcagtc ggtgggtcgg tcctcgcgcc ggccctcccc ctccccggtc 60

tccgggggag gcgcggtgga gtccgcccc ggggttctcc gatgggggag aagcggcgac 120

ggcggcagtg gagtaaccga gccggagcgt gagcggcccc ggtgccccgt tccccacgga 180

ggcc atg ggc gac cca gcc ccc gcc cgc agc ctg gac gac atc gac ctg 229
 Met Gly Asp Pro Ala Pro Ala Arg Ser Leu Asp Asp Ile Asp Leu
 1 5 10

tcc gcc ctg cgg gac cct gct ggg atc ttt gag ctt gtg gag gtg gtc 277
 Ser Ala Leu Arg Asp Pro Ala Gly Ile Phe Glu Leu Val Glu Val Val
 16 21 26 31

ggc aat gga acc tac gga cag gtg tac aag ggt cgg cat gtc aag acg 325
 Gly Asn Gly Thr Tyr Gly Gln Val Tyr Lys Gly Arg His Val Lys Thr
 32 37 42 47

gag Gly 48	cag Gln	ctg Leu	gct Ala	gcc Ala	atc Ile 53	aag Lys	gtc Val	atg Met	gat Asp	gtc Val 58	acg Thr	gag Glu	gac Asp	gag Glu	gag Glu 63	373
gaa Glu 64	gag Glu	atc Ile	aaa Lys	cag Gln	gag Glu 69	atc Ile	aac Asn	atg Met	ctg Leu	aaa Lys 74	aag Lys	tac Tyr	tct Ser	cac His	cac His 79	421
cgc Arg 80	aac Asn	atc Ile	gcc Ala	acc Thr	tac Tyr 85	tac Tyr	gga Gly	gcc Ala	ttc Phe	atc Ile 90	aag Lys	aag Lys	agc Ser	ccc Pro	ccg Pro 95	469
gga Gly 96	aac Asn	gat Asp	gac Asp	cag Gln	ctc Leu 101	tgg Trp	ctg Leu	gtg Val	atg Met	gag Glu 106	ttc Phe	tgt Cys	ggg Gly	gct Ala	ggt Gly 111	517
tca Ser 112	gtg Val	act Thr	gac Asp	ctg Leu	gta Val 117	aag Lys	aac Asn	aca Thr	aaa Lys	ggc Gly 122	aac Asn	gcc Ala	ctg Leu	aag Lys	gag Glu 127	565
gac Asp 128	tgt Cys	atc Ile	gcc Ala	tat Tyr	atc Ile 133	tgc Cys	agg Arg	gag Glu	atc Ile	ctc Leu 138	agg Arg	ggg Gly	ctg Leu	gcc Ala	cat His 143	613
ctc Leu 144	cat His	gcc Ala	cac His	aag Lys	gtg Val 149	atc Ile	cat His	cga Arg	gac Asp	atc Ile 154	aag Lys	ggg Gly	cag Gln	aat Asn	gtg Val 159	661
ctg Leu 160	ctg Leu	aca Thr	gag Glu	aat Asn	gct Ala 165	gag Glu	gtc Val	aag Lys	cta Leu	gtg Val 170	gat Asp	ttt Phe	ggg Gly	gtg Val	agt Ser 175	709
gct Ala 176	cag Gln	ctg Leu	gac Asp	cgc Arg	acc Thr 181	gtg Val	ggc Gly	aga Arg	cgg Arg	aac Asn 186	act Thr	ttc Phe	att Ile	ggg Gly	act Thr 191	757
ccc Pro 192	tac Tyr	tgg Trp	atg Met	gct Ala	cca Pro 197	gag Glu	gtc Val	atc Ile	gcc Ala	tgt Cys 202	gat Asp	gag Glu	aac Asn	cct Pro	gat Asp 207	805
gcc Ala 208	acc Thr	tat Tyr	gat Asp	tac Tyr	agg Arg 213	agt Ser	gat Asp	att Ile	tgg Trp	tct Ser 218	cta Leu	gga Gly	atc Ile	aca Thr	gcc Ala 223	853
atc Ile 224	gag Glu	atg Met	gca Ala	gag Glu	gga Gly 229	gcc Ala	ccc Pro	cct Pro	ctg Leu	tgt Cys 234	gac Asp	atg Met	cac His	ccc Pro	atg Met 239	901
cga Arg 240	gcc Ala	ctc Leu	ttc Phe	ctc Leu	att Ile 245	cct Pro	cgg Arg	aac Asn	cct Pro	ccg Pro 250	ccc Pro	agg Arg	ctc Leu	aag Lys	tcc Ser 255	949
aag Lys 256	aag Lys	tgg Trp	tct Ser	aag Lys	aag Lys 261	ttc Phe	att Ile	gac Asp	ttc Phe	att Ile 266	gac Asp	aca Thr	tgt Cys	ctc Leu	atc Ile 271	997

Leu	Leu	Pro	Gly	Asp	Arg	Lys	Pro	Leu	Tyr	His	Tyr	Gly	Arg	Gly	Met	
496					501					506					511	
aat	ccc	gct	gac	aaa	cca	gcc	tgg	gcc	cga	gag	gta	gaa	gag	aga	aca	1765
Asn	Pro	Ala	Asp	Lys	Pro	Ala	Trp	Ala	Arg	Glu	Val	Glu	Glu	Arg	Thr	
512					517					522					527	
agg	atg	aac	aag	cag	cag	aac	tct	ccc	ttg	gcc	aag	agc	aag	cca	ggc	1813
Arg	Met	Asn	Lys	Gln	Gln	Asn	Ser	Pro	Leu	Ala	Lys	Ser	Lys	Pro	Gly	
528					533					538					543	
agc	acg	ggg	cct	gag	ccc	ccc	atc	ccc	cag	gcc	tcc	cca	ggg	ccc	cca	1861
Ser	Thr	Gly	Pro	Glu	Pro	Pro	Ile	Pro	Gln	Ala	Ser	Pro	Gly	Pro	Pro	
544					549					554					559	
gga	ccc	ctt	tcc	cag	act	cct	cct	atg	cag	agg	ccg	gtg	gag	ccc	cag	1909
Gly	Pro	Leu	Ser	Gln	Thr	Pro	Pro	Met	Gln	Arg	Pro	Val	Glu	Pro	Gln	
560					565					570					575	
gag	gga	ccg	cac	aag	agc	ctg	gtg	gca	cac	cgg	gtc	cca	ctg	aag	cca	1957
Glu	Gly	Pro	His	Lys	Ser	Leu	Val	Ala	His	Arg	Val	Pro	Leu	Lys	Pro	
576					581					586					591	
tat	gca	gca	cct	gta	ccc	cga	tcc	cag	tcc	ctg	cag	gac	cag	ccc	acc	2005
Tyr	Ala	Ala	Pro	Val	Pro	Arg	Ser	Gln	Ser	Leu	Gln	Asp	Gln	Pro	Thr	
592					597					602					607	
cga	aac	ctg	gct	gcc	ttc	cca	gcc	tcc	cat	gac	ccc	gac	cct	gcc	atc	2053
Arg	Asn	Leu	Ala	Ala	Phe	Pro	Ala	Ser	His	Asp	Pro	Asp	Pro	Ala	Ile	
608					613					618					623	
ccc	gca	ccc	act	gcc	acg	ccc	agt	gcc	cga	gga	gct	gtc	atc	cgc	cag	2101
Pro	Ala	Pro	Thr	Ala	Thr	Pro	Ser	Ala	Arg	Gly	Ala	Val	Ile	Arg	Gln	
624					629					634					639	
aat	tca	gac	ccc	acc	tct	gaa	gga	cct	ggc	ccc	agc	ccg	aat	ccc	cca	2149
Asn	Ser	Asp	Pro	Thr	Ser	Glu	Gly	Pro	Gly	Pro	Ser	Pro	Asn	Pro	Pro	
640					645					650					655	
gcc	tgg	gtc	cgc	cca	gat	aac	gag	gcc	cca	ccc	aag	gtg	cct	cag	agg	2197
Ala	Trp	Val	Arg	Pro	Asp	Asn	Glu	Ala	Pro	Pro	Lys	Val	Pro	Gln	Arg	
656					661					666					671	
acc	tca	tct	atc	gcc	act	gcc	ctt	aac	acc	agt	ggg	gcc	gga	ggg	tcc	2245
Thr	Ser	Ser	Ile	Ala	Thr	Ala	Leu	Asn	Thr	Ser	Gly	Ala	Gly	Gly	Ser	
672					677					682					687	
cgg	cca	gcc	cag	gca	gtc	cgt	gcc	agt	aac	ccc	gac	ctc	agg	agg	agc	2293
Arg	Pro	Ala	Gln	Ala	Val	Arg	Ala	Ser	Asn	Pro	Asp	Leu	Arg	Arg	Ser	
688					693					698					703	
gac	cct	ggc	tgg	gaa	cgc	tcg	gac	agc	gtc	ctt	cca	gcc	tct	cac	ggg	2341
Asp	Pro	Gly	Trp	Glu	Arg	Ser	Asp	Ser	Val	Leu	Pro	Ala	Ser	His	Gly	
704					709					714					719	
cac	ctc	ccc	cag	gct	ggc	tca	ctg	gag	cgg	aac	cgc	gtg	gga	gtc	tcc	2389
His	Leu	Pro	Gln	Ala	Gly	Ser	Leu	Glu	Arg	Asn	Arg	Val	Gly	Val	Ser	

720	725	730	735	
tcc aaa ccg gac agc	tcc cct gtg ctc	tcc cct ggg aat aaa gcc aag		2437
Ser Lys Pro Asp Ser	Ser Pro Val Leu Ser	Pro Gly Asn Lys Ala Lys		
736	741	746	751	
ccc gac gac cac cgc	tca cgg cca ggc cgg	ccc gca agc tat aag cga		2485
Pro Asp Asp His Arg	Ser Arg Pro Gly Arg	Pro Ala Ser Tyr Lys Arg		
752	757	762	767	
gca att ggt gag gac	ttt gtg ttg ctg aaa	gag cgg act ctg gac gag		2533
Ala Ile Gly Glu Asp	Phe Val Leu Leu Lys	Glu Arg Thr Leu Asp Glu		
768	773	778	783	
gcc cct cgg cct ccc	aag aag gcc atg gac	tac tcg tcg tcc agc gag		2581
Ala Pro Arg Pro Pro	Lys Lys Ala Met Asp	Tyr Ser Ser Ser Ser Glu		
784	789	794	799	
gag gtg gaa agc agt	gag gac gac gag gag	gaa ggc gaa ggc ggg cca		2629
Glu Val Glu Ser Ser	Glu Asp Asp Glu Glu	Glu Gly Glu Gly Gly Pro		
800	805	810	815	
gca gag ggg agc aga	gat acc cct ggg ggc	cgc agc gat ggg gat aca		2677
Ala Glu Gly Ser Arg	Asp Thr Pro Gly Gly	Arg Ser Asp Gly Asp Thr		
816	821	826	831	
gac agc gtc agc acc	atg gtg gtc cac gac	gtc gag gag atc acc ggg		2725
Asp Ser Val Ser Thr	Met Val Val His Asp	Val Glu Glu Ile Thr Gly		
832	837	842	847	
acc cag ccc cca tac	ggg ggc ggc acc atg	gtg gtc cag cgc acc cct		2773
Thr Gln Pro Pro Tyr	Gly Gly Gly Thr Met	Val Val Gln Arg Thr Pro		
848	853	858	863	
gaa gag gag cgg aac	ctg ctg cat gct gac	agc aat ggg tac aca aac		2821
Glu Glu Glu Arg Asn	Leu Leu His Ala Asp	Ser Asn Gly Tyr Thr Asn		
864	869	874	879	
ctg cct gac gtg gtc	cag ccc agc cac tca	ccc acc gag aac agc aaa		2869
Leu Pro Asp Val Val	Gln Pro Ser His Ser	Pro Thr Glu Asn Ser Lys		
880	885	890	895	
ggc caa agc cca ccc	tcg aag gat ggg agt	ggt gac tac cag tct cgt		2917
Gly Gln Ser Pro Pro	Ser Lys Asp Gly Ser	Gly Asp Tyr Gln Ser Arg		
896	901	906	911	
ggg ctg gta aag gcc	cct ggc aag agc tcg	ttc acg atg ttt gtg gat		2965
Gly Leu Val Lys Ala	Pro Gly Lys Ser Ser	Phe Thr Met Phe Val Asp		
912	917	922	927	
cta ggg atc tac cag	cct gga ggc agt ggg	gac agc atc ccc atc aca		3013
Leu Gly Ile Tyr Gln	Pro Gly Gly Ser Gly	Asp Ser Ile Pro Ile Thr		
928	933	938	943	
gcc cta gtg ggt gga	gag ggc act cgg ctc	gac cag ctg cag tac gac		3061
Ala Leu Val Gly Gly	Glu Gly Thr Arg Leu	Asp Gln Leu Gln Tyr Asp		
944	949	954	959	

gtg agg aag ggt tct gtg gtc aac gtg aat ccc acc aac acc cgg gcc	3109
Val Arg Lys Gly Ser Val Val Asn Val Asn Pro Thr Asn Thr Arg Ala	
960 965 970 975	
cac agt gag acc cct gag atc cgg aag tac aag aag cga ttc aac tcc	3157
His Ser Glu Thr Pro Glu Ile Arg Lys Tyr Lys Lys Arg Phe Asn Ser	
976 981 986 991	
gag atc ctc tgt gca gcc ctt tgg ggg gtc aac ctg ctg gtg ggc acg	3205
Glu Ile Leu Cys Ala Ala Leu Trp Gly Val Asn Leu Leu Val Gly Thr	
992 997 1002 1007	
gag aac ggg ctg atg ttg ctg gac cga agt ggg cag ggc aag gtg tat	3253
Glu Asn Gly Leu Met Leu Leu Asp Arg Ser Gly Gln Gly Lys Val Tyr	
1008 1013 1018 1023	
gga ctc att ggg cgg cga cgc ttc cag cag atg gat gtg ctg gag ggg	3301
Gly Leu Ile Gly Arg Arg Arg Phe Gln Gln Met Asp Val Leu Glu Gly	
1024 1029 1034 1039	
ctc aac ctg ctc atc acc atc tca ggg aaa agg aac aaa ctg cgg gtg	3349
Leu Asn Leu Leu Ile Thr Ile Ser Gly Lys Arg Asn Lys Leu Arg Val	
1040 1045 1050 1055	
tat tac ctg tcc tgg ctc cgg aac aag att ctg cac aat gac cca gaa	3397
Tyr Tyr Leu Ser Trp Leu Arg Asn Lys Ile Leu His Asn Asp Pro Glu	
1056 1061 1066 1071	
gtg gag aag aag cag ggc tgg acc acc gtg ggg gac atg gag ggc tgc	3445
Val Glu Lys Lys Gln Gly Trp Thr Thr Val Gly Asp Met Glu Gly Cys	
1072 1077 1082 1087	
ggg cac tac cgt gtt gtg aaa tac gag cgg att aag ttc ctg gtc atc	3493
Gly His Tyr Arg Val Val Lys Tyr Glu Arg Ile Lys Phe Leu Val Ile	
1088 1093 1098 1103	
gcc ctc aag agc tcc gtg gag gtg tat gcc tgg gcc ccc aaa ccc tac	3541
Ala Leu Lys Ser Ser Val Glu Val Tyr Ala Trp Ala Pro Lys Pro Tyr	
1104 1109 1114 1119	
cac aaa ttc atg gcc ttc aag tcc ttt gcc gac ctc ccc cac cgc cct	3589
His Lys Phe Met Ala Phe Lys Ser Phe Ala Asp Leu Pro His Arg Pro	
1120 1125 1130 1135	
ctg ctg gtc gac ctg aca gta gag gag ggg cag cgg ctc aag gtc atc	3637
Leu Leu Val Asp Leu Thr Val Glu Glu Gly Gln Arg Leu Lys Val Ile	
1136 1141 1146 1151	
tat ggc tcc agt gct ggc ttc cat gct gtg gat gtc gac tcg ggg aac	3685
Tyr Gly Ser Ser Ala Gly Phe His Ala Val Asp Val Asp Ser Gly Asn	
1152 1157 1162 1167	
agc tat gac atc tac atc cct gtg cac atc cag agc cag atc acg ccc	3733
Ser Tyr Asp Ile Tyr Ile Pro Val His Ile Gln Ser Gln Ile Thr Pro	
1168 1173 1178 1183	

cat gcc atc atc ttc ctc ccc aac acc gac ggc atg gag atg ctg ctg	3781
His Ala Ile Ile Phe Leu Pro Asn Thr Asp Gly Met Glu Met Leu Leu	
1184 1189 1194 1199	
tgc tac gag gac gag ggt gtc tac gtc aac acg tac ggg cgc atc att	3829
Cys Tyr Glu Asp Glu Gly Val Tyr Val Asn Thr Tyr Gly Arg Ile Ile	
1200 1205 1210 1215	
aag gat gtg gtg ctg cag tgg ggg gag atg cct act tct gtg gcc tac	3877
Lys Asp Val Val Leu Gln Trp Gly Glu Met Pro Thr Ser Val Ala Tyr	
1216 1221 1226 1231	
atc tgc tcc aac cag ata atg ggc tgg ggt gag aaa gcc att gag atc	3925
Ile Cys Ser Asn Gln Ile Met Gly Trp Gly Glu Lys Ala Ile Glu Ile	
1232 1237 1242 1247	
cgc tct gtg gag acg ggc cac ctc gac ggg gtc ttc atg cac aaa cga	3973
Arg Ser Val Glu Thr Gly His Leu Asp Gly Val Phe Met His Lys Arg	
1248 1253 1258 1263	
gct cag agg ctc aag ttc ctg tgt gag cgg aat gac aag gtg ttt ttt	4021
Ala Gln Arg Leu Lys Phe Leu Cys Glu Arg Asn Asp Lys Val Phe Phe	
1264 1269 1274 1279	
gcc tca gtc cgc tct ggg ggc agc agc caa gtt tac ttc atg act ctg	4069
Ala Ser Val Arg Ser Gly Gly Ser Ser Gln Val Tyr Phe Met Thr Leu	
1280 1285 1290 1295	
aac cgt aac tgc atc atg aac tgg tga cgggg cctgggctg gggctgtccc	4121
Asn Arg Asn Cys Ile Met Asn Trp *	
1296 1301	
acactggacc cagctctccc cctgcagcca ggcttcccgg gccgcccctc tttcccctcc	4181
ctgggctttt gcttttactg gtttgatttc actggagcct gctgggaacg tgacctctga	4241
cccctgatgc tttcgtgac acgtgaccat cctcttcccc aacatgtcct cttcccaaaa	4301
ctgtgcctgt cccagcttc tggggaggga cacagcttcc ccttcccagg aattgagtgg	4361
gcctagcccc tcccccttt tctccatttg agaggagagt gcttggggct tgaaccctt	4421
accccaactgc tgetgactgg gcagggccct ggaccctttt atttgcacgt caggggagcc	4481
ggctcccccc ttgaatgtac cagaccctgg ggggggtcac tgggccctag atttttgggg	4541
ggtcaccagc cactccaggg gcagggacca tttcttcatt ttctgaaagc actttaatga	4601
ttccccttcc cccaaactcc agggaaatgga ggggggaccc cgccagccaa aacattcccc	4661
ccattcccga cccccctctc ctcttctagc ccatgccctt ccccggtgga gggaggagc	4721
agggagccct cactctccac gccccttgct tgcattctgta tatagtgtga gcagcaagta	4781
acccttctcc ccccccccc acccctctc aatgtagtgg ccttgatat cctgtttgtt	4841
aataaagaca attcaaccag ct	4863

<210> 66
 <211> 1223
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (93)..(770)

<400> 66
 gatcgcaaag cggttgatta tcacctcggc aggtggatgg ccttgctgcc ctgcagaaag 60
 gcctggcccc cgccctcttg taccagttcc tg atg aat ggc atc cga ctg ggc 113
 Met Asn Gly Ile Arg Leu Gly
 1 5
 acc tat ggg ctg gct gag gct ggg ggc tac ctg cac aca gcc gaa ggc 161
 Thr Tyr Gly Leu Ala Glu Ala Gly Gly Tyr Leu His Thr Ala Glu Gly
 8 13 18 23
 acc cac agt cct gcc cgc agc gca gca gct ggg gcc atg gct ggg gtc 209
 Thr His Ser Pro Ala Arg Ser Ala Ala Ala Gly Ala Met Ala Gly Val
 24 29 34 39
 atg gga gcc tac ttg ggg agc ccc atc tac atg gtg aag aca cac ctg 257
 Met Gly Ala Tyr Leu Gly Ser Pro Ile Tyr Met Val Lys Thr His Leu
 40 45 50 55
 cag gca cag gca gcc tca gaa att gct gta ggg cac cag tat aag cat 305
 Gln Ala Gln Ala Ala Ser Glu Ile Ala Val Gly His Gln Tyr Lys His
 56 61 66 71
 cag ggc atg ttt cag gcg cta acc gag att ggc cag aaa cat ggt ctg 353
 Gln Gly Met Phe Gln Ala Leu Thr Glu Ile Gly Gln Lys His Gly Leu
 72 77 82 87
 gtg ggg tta tgg cgt ggg gct ctg ggc ggc ctg ccc cga gtt atc gtc 401
 Val Gly Leu Trp Arg Gly Ala Leu Gly Gly Leu Pro Arg Val Ile Val
 88 93 98 103
 ggt tcc tcc acc cag ctg tgc acc ttc tca tcc acc aag gac ctc ctg 449
 Gly Ser Ser Thr Gln Leu Cys Thr Phe Ser Ser Thr Lys Asp Leu Leu
 104 109 114 119
 agc cag tgg gag atc ttt cct ccc cag agc tgg aag ttg gcg ctg gtg 497
 Ser Gln Trp Glu Ile Phe Pro Pro Gln Ser Trp Lys Leu Ala Leu Val
 120 125 130 135
 gct gcc atg atg agt ggc att gca gtt gtc ttg gcc atg gca ccc ttt 545
 Ala Ala Met Met Ser Gly Ile Ala Val Val Leu Ala Met Ala Pro Phe
 136 141 146 151
 gat gtg gcc tgc aca agg ctc tac aac cag ccc aca gat gca cag ggc 593

Asp Val Ala Cys Thr Arg Leu Tyr Asn Gln Pro Thr Asp Ala Gln Gly	
152 157 162 167	
aag ggc ctc atg tac cgg ggg ata ctt gac gct ctg ctg cag aca gct	641
Lys Gly Leu Met Tyr Arg Gly Ile Leu Asp Ala Leu Leu Gln Thr Ala	
168 173 178 183	
cgg acc gag ggc att ttt ggc atg tac aag ggt ata ggt gcc tcc tac	689
Arg Thr Glu Gly Ile Phe Gly Met Tyr Lys Gly Ile Gly Ala Ser Tyr	
184 189 194 199	
ttc cgc ctc ggc ccc cac acc atc ctc tcc ctc ttc ttc tgg gac cag	737
Phe Arg Leu Gly Pro His Thr Ile Leu Ser Leu Phe Phe Trp Asp Gln	
200 205 210 215	
ctg cgc tcc ctc tac tac aca gac act aaa taa cagccgct ttcccagtct	788
Leu Arg Ser Leu Tyr Tyr Thr Asp Thr Lys *	
216 221 226	
ccaccaaag agcactcctt ggccacttgt gcctccacca ctatgtcctg gtgactactg	848
attaggtgac ctttcatcca tccatggggg acagccaacc ccaactcccca tctgtttctca	908
gggttgaatc actacaagag atgagtttcc cttctttcct tgggtgttgc tttaaaccctt	968
ccctacccat tccctgggta actcacaccc ctctctcagg gctgaacgag tcatcccaaa	1028
gtgtatttcc tcccactcac cactgccacc cttgagtccc tccgtgctccc atgcacagtt	1088
ttaaactcct ccctccaaaa ccaaagggaa ttgagagacc caattcccag gcgtctggga	1148
cccaggtgtc ctgttagatt caaaggcaca gagattatat tgattataaa gcaagtttat	1208
tctgaaaaaa aaaaa	1223

<210> 67
 <211> 893
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (309)..(893)

<400> 67	
aaaaattaac ccttgccagc taaaagtaac cctcactaaa gggaataagc ttgcggccgc	60
gcgggagtgag agggggcgcg ggcaggccgg cggggagccc cccggggcgcg acggagcccg	120
cgcgccctcc gggaccctcc cccgtccctg ggccggacct gtgggcgccg ggagtcgggg	180
cagcgttcgg cgcgccgggc cgggggtggcg ggcggccccg ggaccggggc agctggagaa	240
ggagccggag cccggccggg atgagaaggt gacgccgccc ggggcccac tcgctttgtg	300

<210> 68
 <211> 2601
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (93)..(2192)

<400> 68
 cattcgacat tcgaaagctg tacgcctgcg gtaccgggtcc ggaattcccg ggctcgacgat 60
 ttcgtacggg agtgacgcgt attgcctgga gg atg gcg gac gcc ggc att cgc 113
 Met Ala Asp Ala Gly Ile Arg
 1 5
 cgc gtg gtt ccc agc gac ctg tat ccc ctc gtg ctc ggc ttc ctg cgc 161
 Arg Val Val Pro Ser Asp Leu Tyr Pro Leu Val Leu Gly Phe Leu Arg
 8 13 18 23
 gat aac caa ctc tca gag gtg gcc aat aag ttc gcc aaa gcg aca gga 209
 Asp Asn Gln Leu Ser Glu Val Ala Asn Lys Phe Ala Lys Ala Thr Gly
 24 29 34 39
 gct aca cag cag gat gcc aat gcc tct tcc ctc tta gac atc tat agc 257
 Ala Thr Gln Gln Asp Ala Asn Ala Ser Ser Leu Leu Asp Ile Tyr Ser
 40 45 50 55
 ttc tgg ctc aag tct gcc aag gtc cca gag cga aag tta cag gca aat 305
 Phe Trp Leu Lys Ser Ala Lys Val Pro Glu Arg Lys Leu Gln Ala Asn
 56 61 66 71
 gga cca gtg gct aag aaa gct aag aag aag gcc tca tcc agt gac agt 353
 Gly Pro Val Ala Lys Lys Ala Lys Lys Lys Ala Ser Ser Ser Asp Ser
 72 77 82 87
 gag gac agc agc gag gag gag gag gaa gtt caa ggg cct cca gca aag 401
 Glu Asp Ser Ser Glu Glu Glu Glu Glu Val Gln Gly Pro Pro Ala Lys
 88 93 98 103
 aag gct gct gta cct gcc aag cga gtc ggt ctg cct cct ggg aag gct 449
 Lys Ala Ala Val Pro Ala Lys Arg Val Gly Leu Pro Pro Gly Lys Ala
 104 109 114 119
 gca gcc aaa gca tca gag agt agc agc agt gaa gag tcc agt gat gat 497
 Ala Ala Lys Ala Ser Glu Ser Ser Ser Ser Glu Glu Ser Ser Asp Asp
 120 125 130 135
 gat gat gag gag gac caa aag aaa cag cct gtc cag aag gga gtt aag 545
 Asp Asp Glu Glu Asp Gln Lys Lys Gln Pro Val Gln Lys Gly Val Lys
 136 141 146 151
 ccc caa gcc aag gca gcc aaa gct cct cct aag aag gcc aag agc tct 593
 Pro Gln Ala Lys Ala Ala Lys Ala Pro Pro Lys Lys Ala Lys Ser Ser
 152 157 162 167
 gat tct gat tct gac tca agc tcc gag gat gag cca cca aag aac cag 641

Asp Ser Asp Ser Asp Ser Ser Ser Glu Asp Glu Pro Pro Lys Asn Gln	
168 173 178 183	
aag cca aag ata aca cct gtg aca gtt aaa gct cag act aaa gcc cct	689
Lys Pro Lys Ile Thr Pro Val Thr Val Lys Ala Gln Thr Lys Ala Pro	
184 189 194 199	
ccc aaa cca gct cga gca gca cct aaa ata gcc aat ggt aaa gca gcc	737
Pro Lys Pro Ala Arg Ala Ala Pro Lys Ile Ala Asn Gly Lys Ala Ala	
200 205 210 215	
agt agc agc agt agc agc agc agc agt agc agt gat gac tca gag	785
Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Asp Asp Ser Glu	
216 221 226 231	
gag gag aag gca gca gcc acc ccc aag aag act gta cct aaa aag caa	833
Glu Glu Lys Ala Ala Ala Thr Pro Lys Lys Thr Val Pro Lys Lys Gln	
232 237 242 247	
gtt gtg gcc aag gcc cca gtg aaa gca gct acc acc cct acc cgg aag	881
Val Val Ala Lys Ala Pro Val Lys Ala Ala Thr Thr Pro Thr Arg Lys	
248 253 258 263	
agt tct agc agt gag gat tcc tcc agt gac gag gaa gag gag caa aaa	929
Ser Ser Ser Ser Glu Asp Ser Ser Ser Asp Glu Glu Glu Glu Gln Lys	
264 269 274 279	
aaa ccc atg aaa aat aaa cca ggt ccc tac agt tca gtc ccc ccg cct	977
Lys Pro Met Lys Asn Lys Pro Gly Pro Tyr Ser Ser Val Pro Pro Pro	
280 285 290 295	
tct gct ccc cca cca aag aag tct ctg gga acc cag cct ccc aag aag	1025
Ser Ala Pro Pro Pro Lys Lys Ser Leu Gly Thr Gln Pro Pro Lys Lys	
296 301 306 311	
gct gtg gag aag cag cag cct gtg gaa agc agt gaa gac agc agt gat	1073
Ala Val Glu Lys Gln Gln Pro Val Glu Ser Ser Glu Asp Ser Ser Asp	
312 317 322 327	
gag tct gat tca agt tct gaa gaa gag aag aaa ccc cca act aag gca	1121
Glu Ser Asp Ser Ser Ser Glu Glu Glu Lys Lys Pro Pro Thr Lys Ala	
328 333 338 343	
gta gtc tct aaa gca acc act aaa cca cct cca gca aag aaa gca gca	1169
Val Val Ser Lys Ala Thr Thr Lys Pro Pro Pro Ala Lys Lys Ala Ala	
344 349 354 359	
gag agc tct tca gac agc tca gac tct gac agc tct gag gat gat gaa	1217
Glu Ser Ser Ser Asp Ser Ser Asp Ser Asp Ser Ser Glu Asp Asp Glu	
360 365 370 375	
gct cct tct aag cca gct ggt acc acc aag aat tct tca aat aag cca	1265
Ala Pro Ser Lys Pro Ala Gly Thr Thr Lys Asn Ser Ser Asn Lys Pro	
376 381 386 391	
gct gtc acc acc aag tca cct gca gtg aag cca gct gca gcc ccc aag	1313
Ala Val Thr Thr Lys Ser Pro Ala Val Lys Pro Ala Ala Ala Pro Lys	

392	397	402	407	
caa cct gtg ggc ggt ggc cag aag ctt ctg acg aga aag gct gac agc				1361
Gln Pro Val Gly Gly Gly Gln Lys Leu Leu Thr Arg Lys Ala Asp Ser				
408	413	418	423	
agc tcc agc gag gaa gag agc agc tcc agt gag gag gag aag aca aag				1409
Ser Ser Ser Glu Glu Glu Ser Ser Ser Ser Glu Glu Glu Lys Thr Lys				
424	429	434	439	
aag atg gtg gcc acc act aag ccc aag gcg act gcc aaa gca gct cta				1457
Lys Met Val Ala Thr Thr Lys Pro Lys Ala Thr Ala Lys Ala Ala Leu				
440	445	450	455	
tct ctg cct gcc aag cag gct cct cag ggt agt agg gac agc agc tct				1505
Ser Leu Pro Ala Lys Gln Ala Pro Gln Gly Ser Arg Asp Ser Ser Ser				
456	461	466	471	
gat tca gac agc tcc agc agt gag gag gag gaa gag aag aca tct aag				1553
Asp Ser Asp Ser Ser Ser Ser Ser Glu Glu Glu Glu Glu Lys Thr Ser Lys				
472	477	482	487	
tct gca gtt aag aag aag cca cag aag gta gca gga ggt gca gcc cct				1601
Ser Ala Val Lys Lys Lys Pro Gln Lys Val Ala Gly Gly Ala Ala Pro				
488	493	498	503	
tcc aag cca gcc tct gca aag aaa gga aag gct gag agc agc aac agt				1649
Ser Lys Pro Ala Ser Ala Lys Lys Gly Lys Ala Glu Ser Ser Asn Ser				
504	509	514	519	
tct tct tct gat gac tcc agt gag gaa gag gaa gag aag ctc aag ggc				1697
Ser Ser Ser Asp Asp Ser Ser Glu Glu Glu Glu Glu Lys Leu Lys Gly				
520	525	530	535	
aag ggc tct cca aga cca caa gcc ccc aag gcc aat ggc acc tct gca				1745
Lys Gly Ser Pro Arg Pro Gln Ala Pro Lys Ala Asn Gly Thr Ser Ala				
536	541	546	551	
ctg act gcc cag aat gga aaa gca gct aag aac agt gag gag gag gaa				1793
Leu Thr Ala Gln Asn Gly Lys Ala Ala Lys Asn Ser Glu Glu Glu Glu				
552	557	562	567	
gaa gaa aag aaa aag gcg gca gtg gta gtt tcc aaa tca ggt tca tta				1841
Glu Glu Lys Lys Lys Ala Ala Val Val Val Ser Lys Ser Gly Ser Leu				
568	573	578	583	
aag aag cgg aag cag aat gag gct gcc aag gag gca gag act cct cag				1889
Lys Lys Arg Lys Gln Asn Glu Ala Ala Lys Glu Ala Glu Thr Pro Gln				
584	589	594	599	
gcc aag aag ata aag ctt cag acc cct aac aca ttt cca aaa agg aag				1937
Ala Lys Lys Ile Lys Leu Gln Thr Pro Asn Thr Phe Pro Lys Arg Lys				
600	605	610	615	
aaa gga gaa aaa agg gca tca tcc cca ttc cga agg gtc agg gag gag				1985
Lys Gly Glu Lys Arg Ala Ser Ser Pro Phe Arg Arg Val Arg Glu Glu				
616	621	626	631	

gaa att gag gtg gat tca cga gtt gcg gac aac tcc ttt gat gcc aag Glu Ile Glu Val Asp Ser Arg Val Ala Asp Asn Ser Phe Asp Ala Lys 632 637 642 647	2033
cga ggt gca gcc gga gac tgg gga gag cga gcc aat cag gtt ttg aag Arg Gly Ala Ala Gly Asp Trp Gly Glu Arg Ala Asn Gln Val Leu Lys 648 653 658 663	2081
ttc acc aaa ggc aag tcc ttt cgg cat gag aaa acc aag aag aag cgg Phe Thr Lys Gly Lys Ser Phe Arg His Glu Lys Thr Lys Lys Lys Arg 664 669 674 679	2129
ggc agc tac cgg gga ggc tca atc tct gtc cag gtc aat tct att aag Gly Ser Tyr Arg Gly Gly Ser Ile Ser Val Gln Val Asn Ser Ile Lys 680 685 690 695	2177
ttt gac agc gag tga cctgaggcca tcttcggtga agcaaggggtg atgatcggag Phe Asp Ser Glu *	2232
696	
actacttact ttctccagtg gacctgggaa ccctcaggtc tctaggtgag ggtcttgatg	2292
aggacagaag tttagagtag gtcctaagac tttacagtgt aacatcctct ctggtccttt	2352
tctgtgttcc tagttttgta cagacttggt tttgagtgtt gagtagcagg gacaaaataa	2412
gggaatgtta ttttttaaga aaattcattt tcattgttgt ctcttcctt ttctgtgaaa	2472
gtctcctac tgagaaattt gtatatattta tattaaatca cttactattg atttttggtg	2532
tgattttcaa aggtggattc ccacagataa aatcttggct attgccc aaa acataaaaaa	2592
aaaaaaaaa	2601

<210> 69
<211> 8174
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1204)..(6375)

<400> 69 tgtttccagc agtcaaagaa agggacactg ctgattgaga aagaaccacc actgtggctg	60
gattacaaga gtagttttga gcaaaccagg aagcaatcca gggcagcatt gaacctgaag	120
ggagagtact ccttaagtag cagactctgg ggaacagaca atctacagat gaatgtcacc	180
cggactccag agtcatttcc tcccgggaaa ttgttaccaa tttcaccaac atggcctttc	240
acagaagtca ggtcttcctc agcagcagac agaatacaaga ccgtgctggg acagtcctct	300

gacaacacaa gcttgccaca gtcagccga acccctgogt ccaagacaca ccacagaact	360
agggctcacg cggacttctc ttcttccctt taccaaggaa gggacatag cgctccctc	420
gaaccttcca aggattctac cgagtccctg gtccaaccgg ggcctaaagg gggacaagaa	480
gcagccgatg tgtcaggttt gcctctcacc agcatgctcc cctcgttgtc cacagtccca	540
tcaggacat cttcagtgc tgtccccca tcccagccag tatgggcagg gacttcctcc	600
atttcaaagc atcccccaag gtcagacatt cccctactcc tccctctacc tccatcctct	660
tcattggctc ctgactcacc tcattccatc atctctgagc cagcagagca atccccaaa	720
gtgctgtag ttccccaaac agctccagcc gacccctctt taggtcagaa catagcta	780
cccttaatcc cattttctga tgaaatggac cacactgcat cccaaaatgc ccaggatctc	840
ataggcatcc ctcatctagg tgtttctgga tcctcaacaa aatggcattc cgagctgtcc	900
ccaacagagg gtccccattc agcagggttca tccacacctg ggtttttgag ccccatggca	960
gaactgtccc atccgtctcc ccctccccca gcacttgga gtcttcttca gttccagat	1020
ggaagccct catggtcaat gttggaagtg gttcaggtc ctgcatccac ccagcagatc	1080
aaagctgggg tgcttgaag agtgcacaat ggggtgtctt tgccaacttt taagaatata	1140
gaaacagcga cccatgaggc tgagcctcca cttttccaga ctgcagaatc aggggccata	1200
gaa atg acc agc aga aag cta gcc tct gcc act gca aat gac tct gct	1248
Met Thr Ser Arg Lys Leu Ala Ser Ala Thr Ala Asn Asp Ser Ala	
1 5 10	
aac ccg ctg cat ttg tca gca gct cca gag aat tcc aga ggg ccc gcc	1296
Asn Pro Leu His Leu Ser Ala Ala Pro Glu Asn Ser Arg Gly Pro Ala	
16 21 26 31	
ctt tcg gca gaa cac acc tct tct ttg gtg cct tct ctg cat atc acc	1344
Leu Ser Ala Glu His Thr Ser Ser Leu Val Pro Ser Leu His Ile Thr	
32 37 42 47	
aca ctg ggt caa gag caa gcc atc ctt tct ggg gcg gtt ccc gca tca	1392
Thr Leu Gly Gln Glu Gln Ala Ile Leu Ser Gly Ala Val Pro Ala Ser	
48 53 58 63	
cca tca act ggg aca gcc gac ttt ccc tcc ata ctt act ttc ctg cag	1440
Pro Ser Thr Gly Thr Ala Asp Phe Pro Ser Ile Leu Thr Phe Leu Gln	
64 69 74 79	
ccc aca gag aat cat gcc tcc cca tct cct gtg cca gaa atg ccc act	1488
Pro Thr Glu Asn His Ala Ser Pro Ser Pro Val Pro Glu Met Pro Thr	
80 85 90 95	
ctt cca gca gag ggc agt gat ggg tcc cct cct gca act aga gac ttg	1536
Leu Pro Ala Glu Gly Ser Asp Gly Ser Pro Pro Ala Thr Arg Asp Leu	

96	101	106	111	
ctc ctc tca agc aaa gtt cct aat ctt ctt tcc aca tct tgg aca ttt				1584
Leu Leu Ser Ser Lys Val Pro Asn Leu Leu Ser Thr Ser Trp Thr Phe				
112	117	122	127	
ccc cgg tgg aaa aag gac agt gtg aca gcc att tta ggg aag aat gaa				1632
Pro Arg Trp Lys Lys Asp Ser Val Thr Ala Ile Leu Gly Lys Asn Glu				
128	133	138	143	
gag gca aat gtg acg att cct ctc cag gcc ttt cca agg aaa gag gtt				1680
Glu Ala Asn Val Thr Ile Pro Leu Gln Ala Phe Pro Arg Lys Glu Val				
144	149	154	159	
ttg agt ctt cac act gta aat gga ttt gtc tct gat ttc agc acc ggt				1728
Leu Ser Leu His Thr Val Asn Gly Phe Val Ser Asp Phe Ser Thr Gly				
160	165	170	175	
agt gtc tca tct ccc atc att aca gca cca agg acg aat ccc ctt cct				1776
Ser Val Ser Ser Pro Ile Ile Thr Ala Pro Arg Thr Asn Pro Leu Pro				
176	181	186	191	
tca gga cca cct cta cct tcc ata ctc tcc ata caa gcc acc cag act				1824
Ser Gly Pro Pro Leu Pro Ser Ile Leu Ser Ile Gln Ala Thr Gln Thr				
192	197	202	207	
gtt ttc cca tct ctc ttg gct ttt tcc agc acc aag cca gag gtt tat				1872
Val Phe Pro Ser Leu Leu Ala Phe Ser Ser Thr Lys Pro Glu Val Tyr				
208	213	218	223	
gca gct gct gtg gac cat tct ggg ttg cca gct tca gct ccc aaa cag				1920
Ala Ala Ala Val Asp His Ser Gly Leu Pro Ala Ser Ala Pro Lys Gln				
224	229	234	239	
gtg aga gca tcg ccc tcc tcc atg gat gta tat gat tcc tta aca ata				1968
Val Arg Ala Ser Pro Ser Ser Met Asp Val Tyr Asp Ser Leu Thr Ile				
240	245	250	255	
gga gac atg aaa aag cca gca acc aca gat gtt ttc tgg agt tct ctt				2016
Gly Asp Met Lys Lys Pro Ala Thr Thr Asp Val Phe Trp Ser Ser Leu				
256	261	266	271	
tca gca gaa act gga tct ctt tcc aca gaa tca ata ata tct ggc ttg				2064
Ser Ala Glu Thr Gly Ser Leu Ser Thr Glu Ser Ile Ile Ser Gly Leu				
272	277	282	287	
cag cag caa aca aat tat gat tta aat gga cac aca att agc acc aca				2112
Gln Gln Gln Thr Asn Tyr Asp Leu Asn Gly His Thr Ile Ser Thr Thr				
288	293	298	303	
agt tgg gaa act cat tta gct cca aca gct cct ccc aat ggt tta act				2160
Ser Trp Glu Thr His Leu Ala Pro Thr Ala Pro Pro Asn Gly Leu Thr				
304	309	314	319	
tca gct gcc gat gcc ata aaa tct cag gat ttc aaa gat act gct ggg				2208
Ser Ala Ala Asp Ala Ile Lys Ser Gln Asp Phe Lys Asp Thr Ala Gly				
320	325	330	335	

cat His 336	tca Ser 336	gtg Val 336	act Thr 336	gca Ala 341	gaa Glu 341	ggg Gly 341	ttt Phe 341	agt Ser 341	att Ile 341	cag Gln 346	gat Asp 346	cta Leu 346	gtc Val 346	ctc Leu 351	ggg Gly 351	2256
aca Thr 352	agc Ser 352	att Ile 352	gag Glu 357	cag Gln 357	cct Pro 357	gtg Val 357	caa Gln 357	cag Gln 357	tca Ser 362	gac Asp 362	atg Met 362	acc Thr 362	atg Met 362	gtt Val 367	gga Gly 367	2304
agc Ser 368	cat His 368	ata Ile 368	gac Asp 373	ctc Leu 373	tgg Trp 373	ccc Pro 373	aca Thr 373	agc Ser 373	aat Asn 378	aac Asn 378	aac Asn 378	cat His 378	tcc Ser 378	aga Arg 383	gac Asp 383	2352
ttc Phe 384	caa Gln 384	aca Thr 384	gct Ala 389	gaa Glu 389	gtt Val 389	gca Ala 389	tat Tyr 389	tac Tyr 389	tca Ser 394	ccc Pro 394	aca Thr 394	act Thr 394	cga Arg 394	cat His 399	tcc Ser 399	2400
gtg Val 400	tct Ser 400	cat His 400	cct Pro 405	cag Gln 405	cta Leu 405	cag Gln 405	ttg Leu 405	ccc Pro 405	aac Asn 410	cag Gln 410	cca Pro 410	gca Ala 410	cat His 410	cct Pro 415	ctt Leu 415	2448
ttg Leu 416	cta Leu 416	acc Thr 416	tca Ser 421	cca Pro 421	gga Gly 421	cca Pro 421	act Thr 421	tct Ser 421	aca Thr 426	ggg Gly 426	agc Ser 426	ttg Leu 426	cag Gln 426	gaa Glu 431	atg Met 431	2496
ctt Leu 432	tca Ser 432	gat Asp 432	gga Gly 437	aca Thr 437	gat Asp 437	aca Thr 437	ggg Gly 437	tct Ser 437	gaa Glu 442	att Ile 442	tcc Ser 442	agt Ser 442	gac Asp 442	atc Ile 447	aat Asn 447	2544
tca Ser 448	tca Ser 448	cct Pro 448	gag Glu 453	aga Arg 453	aat Asn 453	gct Ala 453	tcc Ser 453	aca Thr 453	cca Pro 458	ttc Phe 458	cag Gln 458	aac Asn 458	atc Ile 458	ttg Leu 463	gga Gly 463	2592
tat Tyr 464	cac His 464	tct Ser 464	gct Ala 469	gct Ala 469	gaa Glu 469	tct Ser 469	tct Ser 469	ata Ile 469	tcg Ser 474	acc Thr 474	agt Ser 474	gtc Val 474	ttt Phe 474	ccc Pro 479	agg Arg 479	2640
acc Thr 480	tcc Ser 480	tcc Ser 480	aga Arg 485	gtg Val 485	ctg Leu 485	cgg Arg 485	gct Ala 485	tct Ser 485	cag Gln 490	cac His 490	ccc Pro 490	aag Lys 490	aaa Lys 490	tgg Trp 495	aca Thr 495	2688
ggg Gly 496	gca Ala 496	gcc Ala 496	act Thr 501	aat Asn 501	gca Ala 501	gcg Ala 501	gac Asp 501	aca Thr 501	gta Val 506	tca Ser 506	tct Ser 506	aag Lys 506	gta Val 506	cag Gln 511	cca Pro 511	2736
aca Thr 512	gca Ala 512	gca Ala 512	gct Ala 517	gcc Ala 517	gtc Val 517	aca Thr 517	ttg Leu 517	ttt Phe 517	ctg Leu 522	agg Arg 522	aaa Lys 522	tca Ser 522	agt Ser 522	cca Pro 527	cct Pro 527	2784
gca Ala 528	ctg Leu 528	tct Ser 528	gca Ala 533	gcc Ala 533	ctg Leu 533	gtt Val 533	gct Ala 533	aag Lys 533	ggc Gly 538	acc Thr 538	agc Ser 538	agc Ser 538	agc Ser 538	cct Pro 543	ttg Leu 543	2832
gcc Ala 544	gtg Val 544	gcc Ala 544	tca Ser 549	gga Gly 549	cca Pro 549	gct Ala 549	aag Lys 549	agc Ser 549	agt Ser 554	tcg Ser 554	atg Met 554	act Thr 554	act Thr 554	ctt Leu 559	gct Ala 559	2880

aaa Lys 560	aat Asn 560	gtc Val 560	aca Thr 560	aac Asn 565	aag Lys 565	gcc Ala 570	gca Ala 570	tct Ser 570	ggc Gly 570	cca Pro 570	aag Lys 575	agg Arg 575	aca Thr 575	cca Pro 575	ggg Gly 575	2928
gca Ala 576	gtc Val 576	cat His 576	aca Thr 576	gcc Ala 581	ttc Phe 581	cca Pro 586	ttc Phe 586	aca Thr 586	cca Pro 586	acc Thr 586	tac Tyr 586	atg Met 586	tat Tyr 586	gca Ala 591	aga Arg 591	2976
aca Thr 592	gga Gly 592	cat His 592	acc Thr 592	acg Thr 597	agc Ser 597	aca Thr 597	cat His 597	aca Thr 597	gcc Ala 602	atg Met 602	caa Gln 602	gga Gly 602	aac Asn 602	atg Met 607	gac Asp 607	3024
act Thr 608	gcc Ala 608	tct Ser 608	ggc Gly 608	ctg Leu 613	ttg Leu 613	tct Ser 613	aca Thr 613	act Thr 613	tac Tyr 613	ctc Leu 618	ccc Pro 618	agg Arg 618	aaa Lys 618	cca Pro 623	caa Gln 623	3072
gcc Ala 624	atg Met 624	cac His 624	acc Thr 624	ggc Gly 629	ctc Leu 629	cca Pro 629	aac Asn 629	ccc Pro 629	acc Thr 634	aac Asn 634	ctg Leu 634	gag Glu 634	atg Met 634	ccc Pro 639	aga Arg 639	3120
gca Ala 640	tcc Ser 640	acg Thr 640	cca Pro 640	cgc Arg 645	cca Pro 645	ctg Leu 645	aca Thr 645	gtc Val 645	acg Thr 645	gcc Ala 650	gcg Ala 650	ctg Leu 650	aca Thr 650	tcc Ser 655	att Ile 655	3168
aca Thr 656	gcc Ala 656	tca Ser 656	gtg Val 656	aag Lys 661	gcc Ala 661	acc Thr 661	cgg Arg 661	ttg Leu 661	cca Pro 666	cca Pro 666	ttg Leu 666	cga Arg 666	gca Ala 666	gaa Glu 671	aac Asn 671	3216
aca Thr 672	gat Asp 672	gct Ala 672	gtc Val 672	ctt Leu 677	cct Pro 677	gct Ala 677	gca Ala 677	tcg Ser 677	gct Ala 682	gca Ala 682	gtg Val 682	gtc Val 682	acg Thr 682	act Thr 687	ggc Gly 687	3264
aaa Lys 688	atg Met 688	gca Ala 688	tcc Ser 688	aac Asn 693	ctg Leu 693	gag Glu 693	tgt Cys 693	cag Gln 693	atg Met 698	tcc Ser 698	agt Ser 698	aag Lys 698	ctc Leu 698	ctg Leu 703	gtg Val 703	3312
aag Lys 704	aca Thr 704	gtt Val 704	ctc Leu 704	ttt Phe 709	ctc Leu 709	acc Thr 709	caa Gln 709	agg Arg 709	aga Arg 714	gtg Val 714	cag Gln 714	atc Ile 714	agt Ser 714	gaa Glu 719	tcc Ser 719	3360
ttg Leu 720	aag Lys 720	ttc Phe 720	agt Ser 720	atc Ile 725	gcc Ala 725	aaa Lys 725	ggg Gly 725	ctc Leu 725	aca Thr 730	cag Gln 730	gca Ala 730	ttg Leu 730	cgg Arg 730	aag Lys 735	gct Ala 735	3408
ttc Phe 736	cac His 736	cag Gln 736	aac Asn 736	gat Asp 741	gtc Val 741	tca Ser 741	gct Ala 741	cac His 741	gtg Val 746	gac Asp 746	att Ile 746	ctg Leu 746	gaa Glu 746	tat Tyr 751	tct Ser 751	3456
cat His 752	aat Asn 752	gtc Val 752	aca Thr 752	gtt Val 757	ggg Gly 757	tat Tyr 757	tat Tyr 757	gct Ala 757	acc Thr 762	aaa Lys 762	ggg Gly 762	aag Lys 762	ttg Leu 762	gtg Val 767	tat Tyr 767	3504
ttg Leu 768	cct Pro 768	gct Ala 768	gtg Val 768	gtg Val 773	atc Ile 773	gaa Glu 773	atg Met 773	ctg Leu 773	ggg Gly 778	gtg Val 778	tat Tyr 778	gga Gly 778	gtc Val 778	agc Ser 783	aac Asn 783	3552
gtc Leu 3600	act Thr 3600	gca Ala 3600	gac Thr 3600	ctg Leu 3600	aag Lys 3600	caa Gln 3600	cac His 3600	acc Thr 3600	cca Pro 3600	cac His 3600	tta Leu 3600	cag Gln 3600	tct Ser 3600	gtg Val 3600	gca Ala 3600	

Val Thr Ala Asp Leu Lys Gln His Thr Pro His Leu Gln Ser Val Ala	
784 789 794 799	
gta ctt gcc tcc cca tgg aat ccc cag cct gca ggc tac ttc cag cta	3648
Val Leu Ala Ser Pro Trp Asn Pro Gln Pro Ala Gly Tyr Phe Gln Leu	
800 805 810 815	
aaa aca gtg ctg cag ttt gtg agc caa gcg gac aac ata cag tcc tgc	3696
Lys Thr Val Leu Gln Phe Val Ser Gln Ala Asp Asn Ile Gln Ser Cys	
816 821 826 831	
aag ttt gct cag aca atg gaa cag agg ctg cag aag gca ttc cag gat	3744
Lys Phe Ala Gln Thr Met Glu Gln Arg Leu Gln Lys Ala Phe Gln Asp	
832 837 842 847	
gcc gag agg aaa gtc ctg aat acc aaa agc aac ttg aca att cag att	3792
Ala Glu Arg Lys Val Leu Asn Thr Lys Ser Asn Leu Thr Ile Gln Ile	
848 853 858 863	
gtg agc acg tcc aat gcc tcc cag gca gtc acc ttg gtg tac gtc gtg	3840
Val Ser Thr Ser Asn Ala Ser Gln Ala Val Thr Leu Val Tyr Val Val	
864 869 874 879	
ggc aat cag agc aca ttc ctc aac ggc acc gtc gcc agc agc ctc ctc	3888
Gly Asn Gln Ser Thr Phe Leu Asn Gly Thr Val Ala Ser Ser Leu Leu	
880 885 890 895	
agc cag ctc tcg gct gag ctg gtg gga ttc tac ctc acc tat ccg ccg	3936
Ser Gln Leu Ser Ala Glu Leu Val Gly Phe Tyr Leu Thr Tyr Pro Pro	
896 901 906 911	
cta acc att gct gaa cca ctg gaa tat ccc aac ctt gac ata tca gaa	3984
Leu Thr Ile Ala Glu Pro Leu Glu Tyr Pro Asn Leu Asp Ile Ser Glu	
912 917 922 927	
aca acc aga gac tat tgg gta att aca gtg ctg cag ggt gtg gac aat	4032
Thr Thr Arg Asp Tyr Trp Val Ile Thr Val Leu Gln Gly Val Asp Asn	
928 933 938 943	
tcg ctg gtg ggc ctg cac aac cag agc ttt gcc cgg gtc atg gag cag	4080
Ser Leu Val Gly Leu His Asn Gln Ser Phe Ala Arg Val Met Glu Gln	
944 949 954 959	
cgc ctg gcc cag cta ttc atg atg tcc cag caa caa ggc cgg cgg ttt	4128
Arg Leu Ala Gln Leu Phe Met Met Ser Gln Gln Gln Gly Arg Arg Phe	
960 965 970 975	
aaa cgg gcc acc acc ctg gga agc tac act gtg cag atg gtg aag atg	4176
Lys Arg Ala Thr Thr Leu Gly Ser Tyr Thr Val Gln Met Val Lys Met	
976 981 986 991	
cag cgt gtc cca ggc ccg aag gac cca gcg gag ctg act tac tat acc	4224
Gln Arg Val Pro Gly Pro Lys Asp Pro Ala Glu Leu Thr Tyr Tyr Thr	
992 997 1002 1007	
ctg tac aac ggg aag cct ttg ttg ggg acc gta gct gcc aag atc ctg	4272
Leu Tyr Asn Gly Lys Pro Leu Leu Gly Thr Val Ala Ala Lys Ile Leu	

1008	1013	1018	1023	
agc acc att gat tcc caa agg atg gcc ttg acc ctt cat cac gtt gtc				4320
Ser Thr Ile Asp Ser Gln Arg Met Ala Leu Thr Leu His His Val Val				
1024	1029	1034	1039	
ctt ctg caa gct gac ccc gtg gtg aag aac ccg ccc aat aac ctg tgg				4368
Leu Leu Gln Ala Asp Pro Val Val Lys Asn Pro Pro Asn Asn Leu Trp				
1040	1045	1050	1055	
atc atc gct gca gtg ctg gcg ccc att gcc gtg gtc acg gtc atc atc				4416
Ile Ile Ala Ala Val Leu Ala Pro Ile Ala Val Val Thr Val Ile Ile				
1056	1061	1066	1071	
atc atc atc act gcc gtg ctc tgc agg aag aac aag aac gac ttc aag				4464
Ile Ile Ile Thr Ala Val Leu Cys Arg Lys Asn Lys Asn Asp Phe Lys				
1072	1077	1082	1087	
cct gac acc atg ata aac ctg ccg cag aga gca aag cct gtg caa ggc				4512
Pro Asp Thr Met Ile Asn Leu Pro Gln Arg Ala Lys Pro Val Gln Gly				
1088	1093	1098	1103	
ttt gat tat gcc aag caa cac ctg ggc cag caa ggg gca gat gag gag				4560
Phe Asp Tyr Ala Lys Gln His Leu Gly Gln Gln Gly Ala Asp Glu Glu				
1104	1109	1114	1119	
gtc atc cct gtg act cag gag aca gtg gtt ctc cca ctg ccc att aga				4608
Val Ile Pro Val Thr Gln Glu Thr Val Val Leu Pro Leu Pro Ile Arg				
1120	1125	1130	1135	
gat gct cct cag gaa aga gac gtc gct cag gat gga agc acc atc aag				4656
Asp Ala Pro Gln Glu Arg Asp Val Ala Gln Asp Gly Ser Thr Ile Lys				
1136	1141	1146	1151	
acc gcc aaa tcc act gaa acc agg aag agc agg tcg ccc agt gag aat				4704
Thr Ala Lys Ser Thr Glu Thr Arg Lys Ser Arg Ser Pro Ser Glu Asn				
1152	1157	1162	1167	
ggc tct gtc atc agc aac gaa tca ggg aag ccc agc tca ggg aga cgc				4752
Gly Ser Val Ile Ser Asn Glu Ser Gly Lys Pro Ser Ser Gly Arg Arg				
1168	1173	1178	1183	
tca ccc cag aat gta atg gca cag cag aaa gtg aca aag gag gag gca				4800
Ser Pro Gln Asn Val Met Ala Gln Gln Lys Val Thr Lys Glu Glu Ala				
1184	1189	1194	1199	
agg aag aga aat gtg cca gcg agt gac gaa gag gag gga gcg gtt cta				4848
Arg Lys Arg Asn Val Pro Ala Ser Asp Glu Glu Glu Gly Ala Val Leu				
1200	1205	1210	1215	
ttt gac aac tcc agc aag gtg gcc gct gaa ccc ttt gac aca tct tct				4896
Phe Asp Asn Ser Ser Lys Val Ala Ala Glu Pro Phe Asp Thr Ser Ser				
1216	1221	1226	1231	
ggg tct gtg cag ctc att gcc ata aaa ccc aca gcc ctc ccc atg gtg				4944
Gly Ser Val Gln Leu Ile Ala Ile Lys Pro Thr Ala Leu Pro Met Val				
1232	1237	1242	1247	

ccc ccc acc tcg gac agg agc cag gag tca tcg gca gtc ctc aac ggc	4992
Pro Pro Thr Ser Asp Arg Ser Gln Glu Ser Ser Ala Val Leu Asn Gly	
1248 1253 1258 1263	
 gag gtg aac aaa gcc ctg aag cag aag tca gac atc gag cac tat cgg	5040
Glu Val Asn Lys Ala Leu Lys Gln Lys Ser Asp Ile Glu His Tyr Arg	
1264 1269 1274 1279	
 aac aag ctg cgc ctc aaa gcc aag agg aag gga tat tac gac ttc cct	5088
Asn Lys Leu Arg Leu Lys Ala Lys Arg Lys Gly Tyr Tyr Asp Phe Pro	
1280 1285 1290 1295	
 gca gtg gag acg agc aag ggt ctg acc gaa aga aag aag atg tat gaa	5136
Ala Val Glu Thr Ser Lys Gly Leu Thr Glu Arg Lys Lys Met Tyr Glu	
1296 1301 1306 1311	
 aaa gcc ccg aag gaa atg gag cat gtt ttg gat cca gat tca gaa ctc	5184
Lys Ala Pro Lys Glu Met Glu His Val Leu Asp Pro Asp Ser Glu Leu	
1312 1317 1322 1327	
 tgt gct cca ttc acc gag tct aaa aac agg caa cag atg aag aac tct	5232
Cys Ala Pro Phe Thr Glu Ser Lys Asn Arg Gln Gln Met Lys Asn Ser	
1328 1333 1338 1343	
 gtc tac aga agc cgg cag tct ctg aac agc ccg agt cca ggg gaa acc	5280
Val Tyr Arg Ser Arg Gln Ser Leu Asn Ser Pro Ser Pro Gly Glu Thr	
1344 1349 1354 1359	
 gag atg gac ctt ctg gtg act cgg gag cga ccc cgg cgt gga atc cgc	5328
Glu Met Asp Leu Leu Val Thr Arg Glu Arg Pro Arg Arg Gly Ile Arg	
1360 1365 1370 1375	
 aac agc gga tac gat act gag cct gaa atc ata gag gaa acc aac att	5376
Asn Ser Gly Tyr Asp Thr Glu Pro Glu Ile Ile Glu Glu Thr Asn Ile	
1376 1381 1386 1391	
 gac aga gtt cct gag ccc cgg ggc tat tcc agg tct cga cag gtg aaa	5424
Asp Arg Val Pro Glu Pro Arg Gly Tyr Ser Arg Ser Arg Gln Val Lys	
1392 1397 1402 1407	
 ggc cac tcg gag acc tcc aca ctg agc tcc cag cca tcc atc gac gag	5472
Gly His Ser Glu Thr Ser Thr Leu Ser Ser Gln Pro Ser Ile Asp Glu	
1408 1413 1418 1423	
 gtc agg cag cag atg cac atg ctg ctg gag gag gcc ttc agc ctg gca	5520
Val Arg Gln Gln Met His Met Leu Leu Glu Glu Ala Phe Ser Leu Ala	
1424 1429 1434 1439	
 tcc gcg ggc cac gca ggc cag agc cgg cac caa gag gcc tac ggc tca	5568
Ser Ala Gly His Ala Gly Gln Ser Arg His Gln Glu Ala Tyr Gly Ser	
1440 1445 1450 1455	
 gcc cag cac ctg ccc tat tcg gag gtg gtg acc agc gct ccg ggg acc	5616
Ala Gln His Leu Pro Tyr Ser Glu Val Val Thr Ser Ala Pro Gly Thr	
1456 1461 1466 1471	

atg acg cgg ccc agg gcc ggg gtg cag tgg gtg ccg acc tac cgc cca	5664
Met Thr Arg Pro Arg Ala Gly Val Gln Trp Val Pro Thr Tyr Arg Pro	
1472 1477 1482 1487	
gaa atg tat cag tac agt ctg ccc cgg ccg gct tac agg ttt tcc cag	5712
Glu Met Tyr Gln Tyr Ser Leu Pro Arg Pro Ala Tyr Arg Phe Ser Gln	
1488 1493 1498 1503	
ctt cct gag atg gtc atg ggc tca ccg cct cca ccc gta cct ccc cgg	5760
Leu Pro Glu Met Val Met Gly Ser Pro Pro Pro Pro Val Pro Pro Arg	
1504 1509 1514 1519	
act ggt cct gtg gct gtc gct tct ctc agg cga tcc acc tca gac atc	5808
Thr Gly Pro Val Ala Val Ala Ser Leu Arg Arg Ser Thr Ser Asp Ile	
1520 1525 1530 1535	
ggc agc aag acc aga atg gcc gag tct aca ggg ccc gag ccg gcc cag	5856
Gly Ser Lys Thr Arg Met Ala Glu Ser Thr Gly Pro Glu Pro Ala Gln	
1536 1541 1546 1551	
ctg cac gac agc gcc tcc ttc acg cag atg tcc aga ggc cct gtg tcc	5904
Leu His Asp Ser Ala Ser Phe Thr Gln Met Ser Arg Gly Pro Val Ser	
1552 1557 1562 1567	
gtg acg cag ttg gat cag tcg gct tta aat tac tca ggt aat acg gtg	5952
Val Thr Gln Leu Asp Gln Ser Ala Leu Asn Tyr Ser Gly Asn Thr Val	
1568 1573 1578 1583	
cca gca gtg ttc gcc atc cca gct gcc aac aga cct ggc ttc acc ggc	6000
Pro Ala Val Phe Ala Ile Pro Ala Ala Asn Arg Pro Gly Phe Thr Gly	
1584 1589 1594 1599	
tac ttc atc cca acg cct ccc tca tcc tat agg aac cag gcc tgg atg	6048
Tyr Phe Ile Pro Thr Pro Pro Ser Ser Tyr Arg Asn Gln Ala Trp Met	
1600 1605 1610 1615	
tcc tat gca gga gag aat gag ctc ccg agc cag tgg gca gat tcg gtg	6096
Ser Tyr Ala Gly Glu Asn Glu Leu Pro Ser Gln Trp Ala Asp Ser Val	
1616 1621 1626 1631	
ccc ctc cca ggg tac atc gag gcc tac ccc cga tca ccg tac ccc cag	6144
Pro Leu Pro Gly Tyr Ile Glu Ala Tyr Pro Arg Ser Arg Tyr Pro Gln	
1632 1637 1642 1647	
agc tct ccc tcc agg ctt cct cgt cag tac agc cag cca gcc aac ctg	6192
Ser Ser Pro Ser Arg Leu Pro Arg Gln Tyr Ser Gln Pro Ala Asn Leu	
1648 1653 1658 1663	
cac ccc agc ctg gag cag gcc ccg gcg ccc tcc aca gcg gcc tcg cag	6240
His Pro Ser Leu Glu Gln Ala Pro Ala Pro Ser Thr Ala Ala Ser Gln	
1664 1669 1674 1679	
cag agc ctg gca gaa aac gac ccg tct gac gct ccc ctg acc aac atc	6288
Gln Ser Leu Ala Glu Asn Asp Pro Ser Asp Ala Pro Leu Thr Asn Ile	
1680 1685 1690 1695	
tcc act gcg gcc ctt gtg aag gcc atc cgg gag gag gtg gcc aag ctg	6336

Ser Thr Ala Ala Leu Val Lys Ala Ile Arg Glu Glu Val Ala Lys Leu	
1696	1701 1706 1711
gcc aaa aaa cag aca gac atg ttt gag ttc cag gtc taa cgccttagcc	6385
Ala Lys Lys Gln Thr Asp Met Phe Glu Phe Gln Val *	
1712	1717 1722
ccgtgggact ctggacttcc aaactctgag gactcagcct ttgggtttcc catgcctacg	6445
tgtaggact tgagacatag caatgggtga gtctttctca ccctccattt ctgaaaagggt	6505
gaactatggg gcttctggga acaggaaact cttgaacgac tagattcttg gctcatccaa	6565
ctgattgtgg gtcaagtccc tggcttgggg ccttatgttt gatactctct catgtcaa	6625
gtttgaactt tgggcatgtg ccctatggaa gcttagtcac aagaggcact agctaata	6685
cagattccta tccaatgcc cattttaata aatcaccgga agcgggagaa tgtagctctt	6745
atcttcgggtg acctctgcat gttaactctg tttctgtgtt aaaggcaatg caggagtgtg	6805
gattaagcac cagactgtat tctcattcaa ccatgaccgt gcgcattaaa atcagtttgt	6865
aaggagagaca ctgactccag ccaagaaacc tgagcccctt ttttttaggt tcatattcaa	6925
agtcaaatga actggatgaa agtcagtacc aatggctgtg cctataaata gacctgattc	6985
tttgtttccc tcgtcaatta aacaaaggcc aagaaagaga gaagatgaga gggaatgggtg	7045
gatttgcggt gacagatttt ttaaaagggt ttgccatttt ggaaataaaa gtcccctaca	7105
agttaggatc taactgaaag agaatcgggt ctaagagctt ttaggatcct acaaaagaaa	7165
cacagttatt tgtgaagggt tttctttgcc ttgttttgaa ggtggcctga gaatggagct	7225
tctctttttc ttgggataat agatacatca acttttataa gaaaatctct gtctcttcaa	7285
caatgatgtc cagtgtgtgc tgctgagtgg taaaaagga aatagtactt gattcctgtt	7345
agaaacagga gtggtagaac cacagtcttc ccaggccgca gcctctgttt atagaagctt	7405
ctgaatgtag aaaagctgtt gaatttcatt taaatgtaaa taacctttta aaaagcgtat	7465
ggagttagcc agttccccct agttaatgga cataggaaga catttgctga aatggtaggg	7525
tggccacttt gtgaccatga tgttgcaagt tgccctccct ggcatgggtga gttggcttcc	7585
agagctgtgg gtagaggaca tcgcctcacg gcaactgagge accagccgct gcctacccat	7645
caatgcaagc aaaacagcta ctgactttgt gtagcagggg gattggggac tctggttccc	7705
tcgccaagtg tggcagcctg tgcagtgttg ggggcttact tggatatctgt tggagaatga	7765
ggctctgtcc tgctttcacc catgacccat ctagcttcag ctgtatccat tttcttctga	7825
gcccattctc cattgtcctc aacgagtttc tttggtcttt actgaaagaa gatagtagaa	7885

121	126	131	136	
gat cga aaa cag aag	gaa gaa ttg aaa gaa	gac cgc aag cca aga gaa		485
Asp Arg Lys Gln Lys	Glu Glu Leu Lys Glu	Asp Arg Lys Pro Arg Glu		
137	142	147	152	
aag gac aag gac aag	gag aag gcc aag gag	aat ggc gga aac aga cac		533
Lys Asp Lys Asp Lys	Glu Lys Ala Lys Glu	Asn Gly Gly Asn Arg His		
153	158	163	168	
aga gaa ggg gag aga	gag aga gcc aaa gcc	cgg gcc agg cca gac aac		581
Arg Glu Gly Glu Arg	Glu Arg Ala Lys Ala	Arg Ala Arg Pro Asp Asn		
169	174	179	184	
gag cga cag aaa gac	aga ggc aac agg gag	cgg gac aga gac tcc gag		629
Glu Arg Gln Lys Asp	Arg Gly Asn Arg Glu	Arg Asp Arg Asp Ser Glu		
185	190	195	200	
cgc aag aag gag aca	gag aga aag agt gag	ggg ggg aaa gag aag gag		677
Arg Lys Lys Glu Thr	Glu Arg Lys Ser Glu	Gly Gly Lys Glu Lys Glu		
201	206	211	216	
aga ctg aga gac agg	gac cga gag cgc gac	cgg gac aaa ggg aag gac		725
Arg Leu Arg Asp Arg	Asp Arg Glu Arg Asp	Arg Asp Lys Gly Lys Asp		
217	222	227	232	
agg gac aga cgg aga	gtg aaa aac ggg gag	cac tcc tgg gac ctg gac		773
Arg Asp Arg Arg Arg	Val Lys Asn Gly Glu	His Ser Trp Asp Leu Asp		
233	238	243	248	
agg gag aat aac aga	gag cat gac aaa cct	gag aaa aag tca gca agc		821
Arg Glu Asn Asn Arg	Glu His Asp Lys Pro	Glu Lys Lys Ser Ala Ser		
249	254	259	264	
tca ggg gag atg tct	aaa aag tta tca gat	gga act ttt aaa gac tcc		869
Ser Gly Glu Met Ser	Lys Lys Leu Ser Asp	Gly Thr Phe Lys Asp Ser		
265	270	275	280	
aag gct gaa aca gag	act gag att tcc act	aga gct tcc aag tca ttg		917
Lys Ala Glu Thr Glu	Thr Glu Ile Ser Thr	Arg Ala Ser Lys Ser Leu		
281	286	291	296	
aca aca aaa aca tca	aaa cgg cga tcc aaa	aat tca gtg gaa ggt gac		965
Thr Thr Lys Thr Ser	Lys Arg Arg Ser Lys	Asn Ser Val Glu Gly Asp		
297	302	307	312	
tcc acc agt gat gca	gaa gga gat gct gga	cct gct ggc caa gat aag		1013
Ser Thr Ser Asp Ala	Glu Gly Asp Ala Gly	Pro Ala Gly Gln Asp Lys		
313	318	323	328	
tct gag gtg cca gag	act cca gaa att cct	aat gag ctt tca tcc aac		1061
Ser Glu Val Pro Glu	Thr Pro Glu Ile Pro	Asn Glu Leu Ser Ser Asn		
329	334	339	344	
atc aga aga att cct	cgg cct ggg agt gca	aga cca gcc cct ccc cgg		1109
Ile Arg Arg Ile Pro	Arg Pro Gly Ser Ala	Arg Pro Ala Pro Pro Arg		
345	350	355	360	

gtc aaa cgg caa gac agc atg gag gcg cta caa atg gat agg tca ggg Val Lys Arg Gln Asp Ser Met Glu Ala Leu Gln Met Asp Arg Ser Gly 361 366 371 376	1157
agt ggt aaa acc gtt tca aat gtg att aca gag tca cac aat tct gac Ser Gly Lys Thr Val Ser Asn Val Ile Thr Glu Ser His Asn Ser Asp 377 382 387 392	1205
aat gaa gag gat gat caa ttt gtg gtg gaa gct gcc cct cag ctc tct Asn Glu Glu Asp Asp Gln Phe Val Val Glu Ala Ala Pro Gln Leu Ser 393 398 403 408	1253
gaa atg tca gaa att gaa atg gta aca gca gtg gaa cta gaa gaa gag Glu Met Ser Glu Ile Glu Met Val Thr Ala Val Glu Leu Glu Glu Glu 409 414 419 424	1301
gag aag cat ggt gga ctt gtg aaa aaa att ttg gag acg aag aaa gat Glu Lys His Gly Gly Leu Val Lys Lys Ile Leu Glu Thr Lys Lys Asp 425 430 435 440	1349
tat gag aaa ttg cag cag tca ccc aaa cct ggg gag aag gag cga tct Tyr Glu Lys Leu Gln Gln Ser Pro Lys Pro Gly Glu Lys Glu Arg Ser 441 446 451 456	1397
ctc ttt gag tcg gca tgg aag aag gag aag gac atc gtt tcc aag gag Leu Phe Glu Ser Ala Trp Lys Lys Glu Lys Asp Ile Val Ser Lys Glu 457 462 467 472	1445
ata gag aag ctc cgc acg tcc atc cag acc ctg tgc aag agc gca ctt Ile Glu Lys Leu Arg Thr Ser Ile Gln Thr Leu Cys Lys Ser Ala Leu 473 478 483 488	1493
ccc ctg ggg aag atc atg gac tac atc cag gaa gac gtg gat gcc atg Pro Leu Gly Lys Ile Met Asp Tyr Ile Gln Glu Asp Val Asp Ala Met 489 494 499 504	1541
cag aat gag ctg cag atg tgg cac agc gag aac agg cag cac gcc gag Gln Asn Glu Leu Gln Met Trp His Ser Glu Asn Arg Gln His Ala Glu 505 510 515 520	1589
gcc ctg cag cag gag cag agg atc aca gac tgt gcc gtg gag ccc tta Ala Leu Gln Gln Glu Gln Arg Ile Thr Asp Cys Ala Val Glu Pro Leu 521 526 531 536	1637
aag gct gag ctc gcg gag ctg gag cag ctg atc aaa gac cag caa gac Lys Ala Glu Leu Ala Glu Leu Glu Gln Leu Ile Lys Asp Gln Gln Asp 537 542 547 552	1685
aag atc tgt gct gtg aag gcc aac atc ctc aag aat gaa gaa aaa atc Lys Ile Cys Ala Val Lys Ala Asn Ile Leu Lys Asn Glu Glu Lys Ile 553 558 563 568	1733
cag aaa atg gta tat agt atc aat ttg act tcg aga agg tga acactca Gln Lys Met Val Tyr Ser Ile Asn Leu Thr Ser Arg Arg *	1782
569 574 579	

```

aaagtttcag agatgaaaag tcacctcagt ttaaaagcaa aaaggaagat agaaaatcat 1842
tactctttta agttccagtt tgctaagaaa atgaacagtt tacaatgtta ttatccagct 1902
aattttcaga gctttaaaac tgtaagcatg ttaagtgtat taaaaaaacc atgttttctt 1962
acctccttcc agatggaata ctggctagtt ataaatagcg cttccaaaca aaaaaaaaaa 2022
aaa 2025

```

```

<210> 71
<211> 5069
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (1)..(4359)

```

```

<400> 71
atg agg aca ctt ggg act tgc ctg gcg act ttg gcc gga ctt ttg cta 48
Met Arg Thr Leu Gly Thr Cys Leu Ala Thr Leu Ala Gly Leu Leu Leu
1 5 10

act gcg gcg ggc gag acg ttc tca ggt ggc tgc ctc ttt gat gag ccg 96
Thr Ala Ala Gly Glu Thr Phe Ser Gly Gly Cys Leu Phe Asp Glu Pro
17 22 27 32

tat agc aca tgt gga tat agt caa tct gaa ggt gat gac ttc aat tgg 144
Tyr Ser Thr Cys Gly Tyr Ser Gln Ser Glu Gly Asp Asp Phe Asn Trp
33 38 43 48

gag caa gtg aac acc ttg act aaa ccg act tct gat cca tgg atg cca 192
Glu Gln Val Asn Thr Leu Thr Lys Pro Thr Ser Asp Pro Trp Met Pro
49 54 59 64

tca ggt tct ttc atg ctg gtg aat gcc tct ggg aga cct gag ggg cag 240
Ser Gly Ser Phe Met Leu Val Asn Ala Ser Gly Arg Pro Glu Gly Gln
65 70 75 80

aga gcc cac ctg ctc tta ccc caa ctt aaa gaa aat gac acc cac tgc 288
Arg Ala His Leu Leu Pro Gln Leu Lys Glu Asn Asp Thr His Cys
81 86 91 96

atc gat ttt cac tat ttt gtg tcc agc aag agt aat tct cct ccg ggg 336
Ile Asp Phe His Tyr Phe Val Ser Ser Lys Ser Asn Ser Pro Pro Gly
97 102 107 112

tta ctc aat gtc tac gtg aag gtc aat aac ggg cca ctg ggg aat cct 384
Leu Leu Asn Val Tyr Val Lys Val Asn Asn Gly Pro Leu Gly Asn Pro
113 118 123 128

atc tgg aat ata tct gga gac cca aca cgt aca tgg aac agg gca gaa 432
Ile Trp Asn Ile Ser Gly Asp Pro Thr Arg Thr Trp Asn Arg Ala Glu

```

129	134	139	144	
ctg gcc att agt act ttc tgg cct aac ttt tat cag gtg att ttt gaa				480
Leu Ala Ile Ser Thr Phe Trp Pro Asn Phe Tyr Gln Val Ile Phe Glu				
145	150	155	160	
gtg ata act tct gga cat caa ggc tat ctc gct atc gat gag gtg aag				528
Val Ile Thr Ser Gly His Gln Gly Tyr Leu Ala Ile Asp Glu Val Lys				
161	166	171	176	
gtg tta gga cat cca tgt acc agg act cct cac ttc ctg cgg att cag				576
Val Leu Gly His Pro Cys Thr Arg Thr Pro His Phe Leu Arg Ile Gln				
177	182	187	192	
aat gtg gaa gtt aat gct ggc cag ttt gct acc ttc cag tgc agt gcc				624
Asn Val Glu Val Asn Ala Gly Gln Phe Ala Thr Phe Gln Cys Ser Ala				
193	198	203	208	
atc ggc agg acc gtg gca gga gac agg ctc tgg tta cag ggc att gat				672
Ile Gly Arg Thr Val Ala Gly Asp Arg Leu Trp Leu Gln Gly Ile Asp				
209	214	219	224	
gtg cga gat gct cct ctg aag gaa atc aag gtg acc agc tcc cga cgc				720
Val Arg Asp Ala Pro Leu Lys Glu Ile Lys Val Thr Ser Ser Arg Arg				
225	230	235	240	
ttc att gct tca ttt aat gtt gtg aat acc acc aaa cga gat gct gga				768
Phe Ile Ala Ser Phe Asn Val Val Asn Thr Thr Lys Arg Asp Ala Gly				
241	246	251	256	
aag tac cgc tgc atg att cgc act gaa gga ggt gtt gga ata tca aac				816
Lys Tyr Arg Cys Met Ile Arg Thr Glu Gly Gly Val Gly Ile Ser Asn				
257	262	267	272	
tat gca gag ttg gta gtt aaa gaa cca ccc gtt cct att gcc cca cct				864
Tyr Ala Glu Leu Val Val Lys Glu Pro Pro Val Pro Ile Ala Pro Pro				
273	278	283	288	
cag ctc gcc tct gta gga gcc acc tac ctg tgg ata cag ctc aac gcc				912
Gln Leu Ala Ser Val Gly Ala Thr Tyr Leu Trp Ile Gln Leu Asn Ala				
289	294	299	304	
aac tcc atc aat ggg gat ggg ccc att gtg gcc cga gag gtg gag tac				960
Asn Ser Ile Asn Gly Asp Gly Pro Ile Val Ala Arg Glu Val Glu Tyr				
305	310	315	320	
tgc acg gcc agt ggg agc tgg aat gac cgg cag cca gtc gat tcc acg				1008
Cys Thr Ala Ser Gly Ser Trp Asn Asp Arg Gln Pro Val Asp Ser Thr				
321	326	331	336	
agc tat aaa att gga cac ctt gac cca gat aca gaa tat gag att agt				1056
Ser Tyr Lys Ile Gly His Leu Asp Pro Asp Thr Glu Tyr Glu Ile Ser				
337	342	347	352	
gtg ctc ctg acc agg cca ggg gag ggt ggc act ggc tct cct ggt cca				1104
Val Leu Leu Thr Arg Pro Gly Glu Gly Gly Thr Gly Ser Pro Gly Pro				
353	358	363	368	

gct ctc agg aca aga aca aag tgt gct gat ccc atg cga ggc cca aga	1152
Ala Leu Arg Thr Arg Thr Lys Cys Ala Asp Pro Met Arg Gly Pro Arg	
369 374 379 384	
aaa cta gaa gta gtg gag gtc aaa tct cgg caa atc act atc cgc tgg	1200
Lys Leu Glu Val Val Glu Val Lys Ser Arg Gln Ile Thr Ile Arg Trp	
385 390 395 400	
gag cca ttt gga tat aat gta act cgt tgc cac agt tat aat ctc act	1248
Glu Pro Phe Gly Tyr Asn Val Thr Arg Cys His Ser Tyr Asn Leu Thr	
401 406 411 416	
gtc cac tac tgt tac caa gtt gga gga caa gaa caa gtg cga gaa gaa	1296
Val His Tyr Cys Tyr Gln Val Gly Gly Gln Glu Gln Val Arg Glu Glu	
417 422 427 432	
gta agc tgg gat aca gaa aat tca cac cct caa cac acg atc act aac	1344
Val Ser Trp Asp Thr Glu Asn Ser His Pro Gln His Thr Ile Thr Asn	
433 438 443 448	
ctg tca cca tac acc aat gtc agt gtg aaa ctg atc ctc atg aac cca	1392
Leu Ser Pro Tyr Thr Asn Val Ser Val Lys Leu Ile Leu Met Asn Pro	
449 454 459 464	
gag ggc cgg aag gaa agc caa gaa ctc ata gtg cag aca gat gaa gac	1440
Glu Gly Arg Lys Glu Ser Gln Glu Leu Ile Val Gln Thr Asp Glu Asp	
465 470 475 480	
ctc cca ggt gct gtt ccc act gaa tcc ata caa gga agt acc ttt gaa	1488
Leu Pro Gly Ala Val Pro Thr Glu Ser Ile Gln Gly Ser Thr Phe Glu	
481 486 491 496	
gag aag ata ttt ctt cag tgg aga gaa cca act caa aca tat ggt gta	1536
Glu Lys Ile Phe Leu Gln Trp Arg Glu Pro Thr Gln Thr Tyr Gly Val	
497 502 507 512	
atc act tta tat gag atc acc tac aaa gca gtc agt tcc ttt gac cca	1584
Ile Thr Leu Tyr Glu Ile Thr Tyr Lys Ala Val Ser Ser Phe Asp Pro	
513 518 523 528	
gaa ata gat tta tcc aat cag agt gga aga gtt tca aag ctg gga aat	1632
Glu Ile Asp Leu Ser Asn Gln Ser Gly Arg Val Ser Lys Leu Gly Asn	
529 534 539 544	
gaa acc cat ttt ctg ttt ttt gga ctg tat ccg ggg acc aca tac tcc	1680
Glu Thr His Phe Leu Phe Phe Gly Leu Tyr Pro Gly Thr Thr Tyr Ser	
545 550 555 560	
ttt acc atc cga gct agc aca gct aag ggt ttt ggg cct cca gca aca	1728
Phe Thr Ile Arg Ala Ser Thr Ala Lys Gly Phe Gly Pro Pro Ala Thr	
561 566 571 576	
aac cag ttc acc acc aaa ata tca gca ccc tct atg cca gct tat gaa	1776
Asn Gln Phe Thr Thr Lys Ile Ser Ala Pro Ser Met Pro Ala Tyr Glu	
577 582 587 592	

ctt gag aca cct ttg aat caa act gac aat acc gtg aca gtc atg ctg	1824
Leu Glu Thr Pro Leu Asn Gln Thr Asp Asn Thr Val Thr Val Met Leu	
593 598 603 608	
aaa cct gcc cac agc aga gga gca cct gtc agt gtc tat caa ata gtt	1872
Lys Pro Ala His Ser Arg Gly Ala Pro Val Ser Val Tyr Gln Ile Val	
609 614 619 624	
gtt gag gaa gaa cgt cct cga aga act aaa aag acg aca gaa atc tta	1920
Val Glu Glu Glu Arg Pro Arg Arg Thr Lys Lys Thr Thr Glu Ile Leu	
625 630 635 640	
aag tgc tac cca gtg cca att cac ttc cag aat gct tct ctg ctg aac	1968
Lys Cys Tyr Pro Val Pro Ile His Phe Gln Asn Ala Ser Leu Leu Asn	
641 646 651 656	
tca cag tac tac ttt gct gca gaa ttt cct gca gac agc ctc caa gct	2016
Ser Gln Tyr Tyr Phe Ala Ala Glu Phe Pro Ala Asp Ser Leu Gln Ala	
657 662 667 672	
gcg cag cct ttt aca att ggt gat aat aag aca tat aat gga tac tgg	2064
Ala Gln Pro Phe Thr Ile Gly Asp Asn Lys Thr Tyr Asn Gly Tyr Trp	
673 678 683 688	
aac act ccc ctt ctc ccc tat aaa agc tac aga att tat ttc caa gct	2112
Asn Thr Pro Leu Leu Pro Tyr Lys Ser Tyr Arg Ile Tyr Phe Gln Ala	
689 694 699 704	
gct agt aga gcc aat ggg gaa acc aaa ata gac tgt gtc caa gtg gcc	2160
Ala Ser Arg Ala Asn Gly Glu Thr Lys Ile Asp Cys Val Gln Val Ala	
705 710 715 720	
aca aaa gga gct gcc act ccg aaa cca gtc cca gaa ccc gag aaa cag	2208
Thr Lys Gly Ala Ala Thr Pro Lys Pro Val Pro Glu Pro Glu Lys Gln	
721 726 731 736	
aca gac cat aca gtt aaa att gct gga gtc atc gcg ggc atc ttg ctg	2256
Thr Asp His Thr Val Lys Ile Ala Gly Val Ile Ala Gly Ile Leu Leu	
737 742 747 752	
ttc gtg att ata ttt ctt gga gtt gtg ttg gta atg aag aaa agg aaa	2304
Phe Val Ile Ile Phe Leu Gly Val Val Leu Val Met Lys Lys Arg Lys	
753 758 763 768	
ctg gcc aag aag cgg aaa gag acc atg agc agc acc cga cag gag atg	2352
Leu Ala Lys Lys Arg Lys Glu Thr Met Ser Ser Thr Arg Gln Glu Met	
769 774 779 784	
act gtg atg gtg aac tca atg gac aag agc tat gct gag cag ggc aca	2400
Thr Val Met Val Asn Ser Met Asp Lys Ser Tyr Ala Glu Gln Gly Thr	
785 790 795 800	
aac tgc gac gag gct ttc tca ttc atg gac acg cac aat ctg aat ggg	2448
Asn Cys Asp Glu Ala Phe Ser Phe Met Asp Thr His Asn Leu Asn Gly	
801 806 811 816	
aga tct gtg tct tca cca tcg tcc ttc aca atg aaa aca aat aca ctg	2496

Arg Ser Val Ser Ser Pro Ser Ser Phe Thr Met Lys Thr Asn Thr Leu	
817	822 827 832
agc aca tcg gtg cct aat tcc tat tac cca gat gaa acc cac aca atg	2544
Ser Thr Ser Val Pro Asn Ser Tyr Tyr Pro Asp Glu Thr His Thr Met	
833	838 843 848
gcc agc gat acc agc agc ctg gtg cag tcc cat act tac aag aag cga	2592
Ala Ser Asp Thr Ser Ser Leu Val Gln Ser His Thr Tyr Lys Lys Arg	
849	854 859 864
gag ccg gcc gac gtg ccc tat cag act ggg cag ctc cac ccc gcc atc	2640
Glu Pro Ala Asp Val Pro Tyr Gln Thr Gly Gln Leu His Pro Ala Ile	
865	870 875 880
cgg gtg gca gac ctc ctt cag cac atc aca cag atg aag tgt gcg gag	2688
Arg Val Ala Asp Leu Leu Gln His Ile Thr Gln Met Lys Cys Ala Glu	
881	886 891 896
ggc tac ggc ttc aag gag gaa tac gag agc ttc ttt gaa ggg cag tct	2736
Gly Tyr Gly Phe Lys Glu Glu Tyr Glu Ser Phe Phe Glu Gly Gln Ser	
897	902 907 912
gca cca tgg gac tcg gct aag aaa gat gag aac aga atg aag aac aga	2784
Ala Pro Trp Asp Ser Ala Lys Lys Asp Glu Asn Arg Met Lys Asn Arg	
913	918 923 928
tac ggg aat atc att gca tac gat cat tcc cga gtg agg ctg cag aca	2832
Tyr Gly Asn Ile Ile Ala Tyr Asp His Ser Arg Val Arg Leu Gln Thr	
929	934 939 944
ata gaa gga gac aca aac tca gac tat atc aat ggc aat tat atc gat	2880
Ile Glu Gly Asp Thr Asn Ser Asp Tyr Ile Asn Gly Asn Tyr Ile Asp	
945	950 955 960
ggt tat cat cga ccc aat cat tac att gct acc caa ggg cca atg cag	2928
Gly Tyr His Arg Pro Asn His Tyr Ile Ala Thr Gln Gly Pro Met Gln	
961	966 971 976
gaa acc atc tat gac ttc tgg agg atg gtg tgg cac gaa aac act gca	2976
Glu Thr Ile Tyr Asp Phe Trp Arg Met Val Trp His Glu Asn Thr Ala	
977	982 987 992
agt atc atc atg gtg acc aat ctt gtg gaa gtg gga agg gtc aaa tgc	3024
Ser Ile Ile Met Val Thr Asn Leu Val Glu Val Gly Arg Val Lys Cys	
993	998 1003 1008
tgc aaa tac tgg cca gat gac aca gag ata tat aaa gac att aaa gtt	3072
Cys Lys Tyr Trp Pro Asp Asp Thr Glu Ile Tyr Lys Asp Ile Lys Val	
1009	1014 1019 1024
acc cta ata gaa aca gaa cta ctg gca gaa tat gtg ata aga aca ttt	3120
Thr Leu Ile Glu Thr Glu Leu Leu Ala Glu Tyr Val Ile Arg Thr Phe	
1025	1030 1035 1040
gct gtt gaa aag aga ggt gtg cat gaa atc cga gag atc aga cag ttt	3168
Ala Val Glu Lys Arg Gly Val His Glu Ile Arg Glu Ile Arg Gln Phe	

1041	1046	1051	1056	
cac ttc act ggc tgg ccg gat cat ggg gtc ccc tac cat gcc acc ggc				3216
His Phe Thr Gly Trp Pro Asp His Gly Val Pro Tyr His Ala Thr Gly				
1057	1062	1067	1072	
ctg ctg gga ttc gtg cgg caa gtc aag tcc aag agc ccg ccc agt gca				3264
Leu Leu Gly Phe Val Arg Gln Val Lys Ser Lys Ser Pro Pro Ser Ala				
1073	1078	1083	1088	
ggc cca ctg gtg gtg cac tgc agt gct ggt gca ggg agg act ggc tgt				3312
Gly Pro Leu Val Val His Cys Ser Ala Gly Ala Gly Arg Thr Gly Cys				
1089	1094	1099	1104	
ttc atc gtc att gat atc atg ttg gac atg gcc gaa agg gaa ggg gtc				3360
Phe Ile Val Ile Asp Ile Met Leu Asp Met Ala Glu Arg Glu Gly Val				
1105	1110	1115	1120	
gta gac atc tac aac tgc gtc agg gag ctg cgg tca cgg agg gtg aac				3408
Val Asp Ile Tyr Asn Cys Val Arg Glu Leu Arg Ser Arg Arg Val Asn				
1121	1126	1131	1136	
atg gtg caa aca gag gag cag tat gtg ttt atc cac gat gcg atc ctg				3456
Met Val Gln Thr Glu Glu Gln Tyr Val Phe Ile His Asp Ala Ile Leu				
1137	1142	1147	1152	
gaa gcc tgt ctt tgt ggg gac acc tct gtg cct gct tcc caa gtt agg				3504
Glu Ala Cys Leu Cys Gly Asp Thr Ser Val Pro Ala Ser Gln Val Arg				
1153	1158	1163	1168	
tct ctg tat tat gac atg aac aaa ctg gat cca cag aca aac tca agc				3552
Ser Leu Tyr Tyr Asp Met Asn Lys Leu Asp Pro Gln Thr Asn Ser Ser				
1169	1174	1179	1184	
cag att aaa gag gaa ttc cgg acg cta aac atg gtg aca cca acg ctg				3600
Gln Ile Lys Glu Glu Phe Arg Thr Leu Asn Met Val Thr Pro Thr Leu				
1185	1190	1195	1200	
cga gta gag gac tgc agc atc gca ctg ttg ccc cgg aac cat gag aaa				3648
Arg Val Glu Asp Cys Ser Ile Ala Leu Leu Pro Arg Asn His Glu Lys				
1201	1206	1211	1216	
aac cgg tgc atg gac atc ctg ccc cca gac cgc tgc ctg ccc ttc ctc				3696
Asn Arg Cys Met Asp Ile Leu Pro Pro Asp Arg Cys Leu Pro Phe Leu				
1217	1222	1227	1232	
atc acc atc gat ggg gag agc agc aac tac atc aat gct gcc ctc atg				3744
Ile Thr Ile Asp Gly Glu Ser Ser Asn Tyr Ile Asn Ala Ala Leu Met				
1233	1238	1243	1248	
gac agc tat aaa cag cct tca gct ttt ata gtc acc cag cat cct ttg				3792
Asp Ser Tyr Lys Gln Pro Ser Ala Phe Ile Val Thr Gln His Pro Leu				
1249	1254	1259	1264	
cca aac aca gtg aaa gac ttt tgg aga ctg gtc ctg gat tat cac tgc				3840
Pro Asn Thr Val Lys Asp Phe Trp Arg Leu Val Leu Asp Tyr His Cys				
1265	1270	1275	1280	

aca tcc gta gtt atg cta aat gat gtg gat cct gcc cag ttg tgt cca	3888
Thr Ser Val Val Met Leu Asn Asp Val Asp Pro Ala Gln Leu Cys Pro	
1281 1286 1291 1296	
cag tac tgg cca gaa aac gga gta cac aga cac ggc ccc atc cag gtg	3936
Gln Tyr Trp Pro Glu Asn Gly Val His Arg His Gly Pro Ile Gln Val	
1297 1302 1307 1312	
gaa ttt gtc tct gct gac ctg gaa gag gac atc atc agc agg ata ttc	3984
Glu Phe Val Ser Ala Asp Leu Glu Glu Asp Ile Ile Ser Arg Ile Phe	
1313 1318 1323 1328	
cgc att tac aat gcc gcc aga ccc caa gat gga tat cgg atg gtg cag	4032
Arg Ile Tyr Asn Ala Ala Arg Pro Gln Asp Gly Tyr Arg Met Val Gln	
1329 1334 1339 1344	
caa ttc cag ttc ctg ggc tgg ccg atg tac agg gac aca cca gtg tct	4080
Gln Phe Gln Phe Leu Gly Trp Pro Met Tyr Arg Asp Thr Pro Val Ser	
1345 1350 1355 1360	
aag cgc tcc ttc ttg aag ctc att cgc cag gtg gac aag tgg caa gag	4128
Lys Arg Ser Phe Leu Lys Leu Ile Arg Gln Val Asp Lys Trp Gln Glu	
1361 1366 1371 1376	
gaa tac aat ggc ggg gaa ggc cgc acc gtt gtg cac tgc ttg aac ggg	4176
Glu Tyr Asn Gly Gly Glu Gly Arg Thr Val Val His Cys Leu Asn Gly	
1377 1382 1387 1392	
gga ggc cgc agt ggg acg ttc tgc gcc atc agc atc gta tgt gag atg	4224
Gly Gly Arg Ser Gly Thr Phe Cys Ala Ile Ser Ile Val Cys Glu Met	
1393 1398 1403 1408	
ctc cgg cac cag aga acc gtg gat gtc ttt cac gct gtg aag aca ctg	4272
Leu Arg His Gln Arg Thr Val Asp Val Phe His Ala Val Lys Thr Leu	
1409 1414 1419 1424	
agg aac aac aag ccc aac atg gtc gac ctc ctg gat cag tac aag ttc	4320
Arg Asn Asn Lys Pro Asn Met Val Asp Leu Leu Asp Gln Tyr Lys Phe	
1425 1430 1435 1440	
tgc tac gag gtg gcc ctg gaa tac ttg aat tct ggc tga tgggtgtaa	4369
Cys Tyr Glu Val Ala Leu Glu Tyr Leu Asn Ser Gly *	
1441 1446 1451	
agctctgcaa acaatccctt tcataccaca aagccaagac gttccatggt atttgtgcaa	4429
aagagatgaa gactttctcaa tatgcttatt ttgctttgca taattggctc tttttaagag	4489
cccaagaaag tgttttctaaa attgcttgca ctgcccatac ccagtaatgc tgctgcctga	4549
cagaaacaca cacacagcca cagttgccaa atcccgtact ccttgccacc ggcttcctag	4609
agcagcgtag acagctggta aactgaagag cacaactata ttcttatgaa ggaatttgta	4669
cctttgggggt attattttgt ggcccgtgac cctcgttatt gttacagctg agtgtatgtt	4729

```

tttgttctgt ggagaatgct atctggcatt atggtaatat attattttag gtaatatattg 4789
tactttaaca tgttgcataa tatatgctta tgtagctttc caggactaac agataaatgt 4849
gtaatgaaca aagatatggt gtatgagtcg tcgtttctgt cagatttgta ttgtttccaa 4909
gggaaaagct tgggggagga ctcaagttcac aaaatgcaaa actcaacgat cagattcacg 4969
gacccagagc ttttccatgt gtttatattg taaatatttt tgatttcac c aaattattta 5029
ttcattaataa gaaatttttg tgaaaaaaaa aaaaaaaaaa 5069

```

```

<210> 72
<211> 6278
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (16) .. (5634)

```

```

<400> 72
tccaaactgt tcaaa atg atg aac gaa gat gca gct cag aaa agc gac agt 51
          Met Met Asn Glu Asp Ala Ala Gln Lys Ser Asp Ser
          1              5              10

gga gag aag ttc aac ggc agt agt cag agg aga aaa aga ccc aag aag 99
Gly Glu Lys Phe Asn Gly Ser Ser Gln Arg Arg Lys Arg Pro Lys Lys
 13              18              23              28

tct gac agc aat gca agc ttc ctc cgt gct gcc aga gca ggc aac ctg 147
Ser Asp Ser Asn Ala Ser Phe Leu Arg Ala Ala Arg Ala Gly Asn Leu
 29              34              39              44

gac aaa gtt gtg gaa tat ctg aag ggg ggc ata gac atc aat acc tgc 195
Asp Lys Val Val Glu Tyr Leu Lys Gly Gly Ile Asp Ile Asn Thr Cys
 45              50              55              60

aat cag aat gga ctc aac gct ctc cat ctg gct gcc aag gaa ggc cac 243
Asn Gln Asn Gly Leu Asn Ala Leu His Leu Ala Ala Lys Glu Gly His
 61              66              71              76

gtg ggg ctg gtg cag gag ctg ctg gga aga ggg tcc tct gtg gat tct 291
Val Gly Leu Val Gln Glu Leu Leu Gly Arg Gly Ser Ser Val Asp Ser
 77              82              87              92

gcc act aag aag gga aat acc gct ctt cac att gca tct ttg gct gga 339
Ala Thr Lys Lys Gly Asn Thr Ala Leu His Ile Ala Ser Leu Ala Gly
 93              98              103              108

caa gca gaa gtt gtc aaa gtt ctt gtt aag gaa gga gcc aat att aat 387
Gln Ala Glu Val Val Lys Val Leu Val Lys Glu Gly Ala Asn Ile Asn
109              114              119              124

```

gca cag tct cag aat ggc ttt act cct tta tac atg gct gcc caa gag	435
Ala Gln Ser Gln Asn Gly Phe Thr Pro Leu Tyr Met Ala Ala Gln Glu	
125 130 135 140	
aat cac att gat gtt gta aaa tat ttg ctg gaa aat gga gct aat cag	483
Asn His Ile Asp Val Val Lys Tyr Leu Leu Glu Asn Gly Ala Asn Gln	
141 146 151 156	
agc act gct aca gag gat ggc ttt act cct cta gct gtg gca ctc cag	531
Ser Thr Ala Thr Glu Asp Gly Phe Thr Pro Leu Ala Val Ala Leu Gln	
157 162 167 172	
caa gga cac aac cag gcg gtg gcc atc ctc ttg gag aat gac acc aaa	579
Gln Gly His Asn Gln Ala Val Ala Ile Leu Leu Glu Asn Asp Thr Lys	
173 178 183 188	
ggg aaa gtg agg ctg cca gct ctg cat att gcc gct agg aaa gac gac	627
Gly Lys Val Arg Leu Pro Ala Leu His Ile Ala Ala Arg Lys Asp Asp	
189 194 199 204	
acc aaa tct gcc gca ctt ctg ctt cag aat gac cac aat gct gac gta	675
Thr Lys Ser Ala Ala Leu Leu Leu Gln Asn Asp His Asn Ala Asp Val	
205 210 215 220	
caa tcc aag atg atg gtg aat agg aca act gag agt ggt ttt acc cct	723
Gln Ser Lys Met Met Val Asn Arg Thr Thr Glu Ser Gly Phe Thr Pro	
221 226 231 236	
ttg cac ata gct gca cat tac gga aat gtc aac gtg gca act ctt ctt	771
Leu His Ile Ala Ala His Tyr Gly Asn Val Asn Val Ala Thr Leu Leu	
237 242 247 252	
cta aac cgg gga gct gct gtg gac ttc aca gcc agg aat gga atc act	819
Leu Asn Arg Gly Ala Ala Val Asp Phe Thr Ala Arg Asn Gly Ile Thr	
253 258 263 268	
cct ctg cat gtg gct tcc aaa aga gga aat aca aac atg gtg aag ctc	867
Pro Leu His Val Ala Ser Lys Arg Gly Asn Thr Asn Met Val Lys Leu	
269 274 279 284	
tta ctg gat cga ggc ggt cag atc gat gcc aaa act agg gat ggg ttg	915
Leu Leu Asp Arg Gly Gly Gln Ile Asp Ala Lys Thr Arg Asp Gly Leu	
285 290 295 300	
aca cca ctt cac tgt gct gca cga agt ggg cat gac caa gtg gtg gaa	963
Thr Pro Leu His Cys Ala Ala Arg Ser Gly His Asp Gln Val Val Glu	
301 306 311 316	
ctt ctg ttg gaa cgg ggt gcc ccc ttg ctg gca agg act aag aat ggg	1011
Leu Leu Leu Glu Arg Gly Ala Pro Leu Leu Ala Arg Thr Lys Asn Gly	
317 322 327 332	
ctg tct cca cta cac atg gct gcc cag gga gac cac gtg gaa tgt gtg	1059
Leu Ser Pro Leu His Met Ala Ala Gln Gly Asp His Val Glu Cys Val	
333 338 343 348	
aag cac ctg tta cag cac aag gca cct gtt gat gat gtc acc cta gac	1107

Lys His Leu Leu Gln His Lys Ala Pro Val Asp Asp Val Thr Leu Asp 349 354 359 364	
tac ctg aca gcc ctc cac gtt gct gcg cac tgt ggc cac tac cgt gta Tyr Leu Thr Ala Leu His Val Ala Ala His Cys Gly His Tyr Arg Val 365 370 375 380	1155
acc aaa ctc ctt tta gac aag aga gcc aat ccg aac gcc aga gcc ctg Thr Lys Leu Leu Leu Asp Lys Arg Ala Asn Pro Asn Ala Arg Ala Leu 381 386 391 396	1203
aat ggt ttt act cca ctg cac att gcc tgc aag aaa aac cgc atc aaa Asn Gly Phe Thr Pro Leu His Ile Ala Cys Lys Lys Asn Arg Ile Lys 397 402 407 412	1251
gtc atg gaa ctg ctg gtg aaa tat ggg gct tca atc caa gct ata aca Val Met Glu Leu Leu Val Lys Tyr Gly Ala Ser Ile Gln Ala Ile Thr 413 418 423 428	1299
gag tct ggc ctc aca cca ata cat gtg gct gcc ttc atg ggc cac ttg Glu Ser Gly Leu Thr Pro Ile His Val Ala Ala Phe Met Gly His Leu 429 434 439 444	1347
aac att gtc ctc ctt ctg ctg cag aac gga gcc tct cca gat gtc act Asn Ile Val Leu Leu Leu Leu Gln Asn Gly Ala Ser Pro Asp Val Thr 445 450 455 460	1395
aac att cgt ggt gag acg gca cta cac atg gca gcc cga gcc ggg cag Asn Ile Arg Gly Glu Thr Ala Leu His Met Ala Ala Arg Ala Gly Gln 461 466 471 476	1443
gtg gaa gtg gtc cga tgc ctc ctg aga aat ggt gcc ctt gtt gat gcc Val Glu Val Val Arg Cys Leu Leu Arg Asn Gly Ala Leu Val Asp Ala 477 482 487 492	1491
aga gcc agg gag gaa cag aca cct tta cat att gcc tcc cgc ctg ggt Arg Ala Arg Glu Glu Gln Thr Pro Leu His Ile Ala Ser Arg Leu Gly 493 498 503 508	1539
aag aca gaa att gtc cag ctg ctt cta caa cat atg gct cat cca gat Lys Thr Glu Ile Val Gln Leu Leu Leu Gln His Met Ala His Pro Asp 509 514 519 524	1587
gcg gcc act aca aat ggg tac aca cca ctg cac atc tct gcc cgg gag Ala Ala Thr Thr Asn Gly Tyr Thr Pro Leu His Ile Ser Ala Arg Glu 525 530 535 540	1635
ggc cag gtg gat gtg gca tca gtc cta ttg gaa gca gga gca gcc cac Gly Gln Val Asp Val Ala Ser Val Leu Leu Glu Ala Gly Ala Ala His 541 546 551 556	1683
tcc tta gct acc aag aag ggt ttt act ccc ctg cat gta gca gcc aag Ser Leu Ala Thr Lys Lys Gly Phe Thr Pro Leu His Val Ala Ala Lys 557 562 567 572	1731
tat gga agc ctg gat gtg gca aaa ctt ctc ttg caa cgc cgt gct gcc Tyr Gly Ser Leu Asp Val Ala Lys Leu Leu Leu Gln Arg Arg Ala Ala 573 578 583 588	1779

573	578	583	588	
gca gat tct gca ggg aag aac ggc ctt acc ccg ctc cat gtt gct gct				1827
Ala Asp Ser Ala Gly Lys Asn Gly Leu Thr Pro Leu His Val Ala Ala				
589	594	599	604	
cat tat gac aac cag aag gtg gcg ctg ctg tta ctg gag aag ggt gct				1875
His Tyr Asp Asn Gln Lys Val Ala Leu Leu Leu Leu Glu Lys Gly Ala				
605	610	615	620	
tcc cct cat gcc act gcc aag aat ggc tat act ccg tta cat att gct				1923
Ser Pro His Ala Thr Ala Lys Asn Gly Tyr Thr Pro Leu His Ile Ala				
621	626	631	636	
gcc aag aag aat caa atg cag ata gct tcc aca ctc ctg aac tat gga				1971
Ala Lys Lys Asn Gln Met Gln Ile Ala Ser Thr Leu Leu Asn Tyr Gly				
637	642	647	652	
gca gag aca aac att gtg aca aag caa gga gta act cca ctc cat ctg				2019
Ala Glu Thr Asn Ile Val Thr Lys Gln Gly Val Thr Pro Leu His Leu				
653	658	663	668	
gcc tcg cag gag ggg cac aca gat atg gtt acc ttg ctt ctg gat aag				2067
Ala Ser Gln Glu Gly His Thr Asp Met Val Thr Leu Leu Leu Asp Lys				
669	674	679	684	
gga gcc aat atc cac atg tca act aag agt gga ctc aca tcc tta cac				2115
Gly Ala Asn Ile His Met Ser Thr Lys Ser Gly Leu Thr Ser Leu His				
685	690	695	700	
ctt gca gcc cag gaa gat aaa gtg aat gtt gct gat att ctc acc aag				2163
Leu Ala Ala Gln Glu Asp Lys Val Asn Val Ala Asp Ile Leu Thr Lys				
701	706	711	716	
cat gga gct gat cag gat gct cat aca aag ctt ggt tac aca cct tta				2211
His Gly Ala Asp Gln Asp Ala His Thr Lys Leu Gly Tyr Thr Pro Leu				
717	722	727	732	
att gtg gcc tgt cac tat gga aat gtg aaa atg gtc aac ttt ctt ctg				2259
Ile Val Ala Cys His Tyr Gly Asn Val Lys Met Val Asn Phe Leu Leu				
733	738	743	748	
aag cag gga gca aat gtt aac gca aaa acc aag aac ggc tac acg cct				2307
Lys Gln Gly Ala Asn Val Asn Ala Lys Thr Lys Asn Gly Tyr Thr Pro				
749	754	759	764	
ttg cac cag gcc gct cag cag ggt cac acg cac atc atc aac gtc ctg				2355
Leu His Gln Ala Ala Gln Gln Gly His Thr His Ile Ile Asn Val Leu				
765	770	775	780	
ctc cag cat ggg gcc aag ccc aac gcc acc act gcg aat ggc aac act				2403
Leu Gln His Gly Ala Lys Pro Asn Ala Thr Thr Ala Asn Gly Asn Thr				
781	786	791	796	
gcc ttg gcg att gct aag cgt ctg ggc tac atc tcc gtg gtc gac acc				2451
Ala Leu Ala Ile Ala Lys Arg Leu Gly Tyr Ile Ser Val Val Asp Thr				
797	802	807	812	

ctg aag gtt gtg act gag gag gtc acc acc acc acc aca act att aca	2499
Leu Lys Val Val Thr Glu Glu Val Thr Thr Thr Thr Thr Thr Ile Thr	
813 818 823 828	
gaa aaa cac aaa cta aat gta cct gag acg atg act gag gtt ctt gat	2547
Glu Lys His Lys Leu Asn Val Pro Glu Thr Met Thr Glu Val Leu Asp	
829 834 839 844	
gtt tct gat gaa gag ggt gat gac aca atg act ggt gat ggg gga gaa	2595
Val Ser Asp Glu Glu Gly Asp Asp Thr Met Thr Gly Asp Gly Gly Glu	
845 850 855 860	
tac ctt agg cct gag gac cta aaa gaa ctg ggt gat gac tca cta ccc	2643
Tyr Leu Arg Pro Glu Asp Leu Lys Glu Leu Gly Asp Asp Ser Leu Pro	
861 866 871 876	
agc agt cag ttc ctg gat ggt atg aat tac ctg cga tac agc ttg gag	2691
Ser Ser Gln Phe Leu Asp Gly Met Asn Tyr Leu Arg Tyr Ser Leu Glu	
877 882 887 892	
gga gga cga tct gac agc ctt cga tcc ttc agt tcc gac agg tct cac	2739
Gly Gly Arg Ser Asp Ser Leu Arg Ser Phe Ser Ser Asp Arg Ser His	
893 898 903 908	
act ctg agc cat gcc tcc tac ctg agg gac agt gcc gtg atg gat gac	2787
Thr Leu Ser His Ala Ser Tyr Leu Arg Asp Ser Ala Val Met Asp Asp	
909 914 919 924	
tca gtt gtg att ccc agt cac cag gtg tca act cta gcc aag gag gca	2835
Ser Val Val Ile Pro Ser His Gln Val Ser Thr Leu Ala Lys Glu Ala	
925 930 935 940	
gaa agg aat tct tat cgc cta agc tgg ggc act gag aac tta gac aac	2883
Glu Arg Asn Ser Tyr Arg Leu Ser Trp Gly Thr Glu Asn Leu Asp Asn	
941 946 951 956	
gtg gct ctt tct tct agt cct att cat tca ggt ttc ctg gtt agt ttt	2931
Val Ala Leu Ser Ser Ser Pro Ile His Ser Gly Phe Leu Val Ser Phe	
957 962 967 972	
atg gtg gat gcc cga ggt ggt gct atg cga gga tgc aga cac aat ggg	2979
Met Val Asp Ala Arg Gly Gly Ala Met Arg Gly Cys Arg His Asn Gly	
973 978 983 988	
ctc cga atc att att cca cct cgg aaa tgt act gct cca acg cga gtc	3027
Leu Arg Ile Ile Ile Pro Pro Arg Lys Cys Thr Ala Pro Thr Arg Val	
989 994 999 1004	
acc tgc cga ctg gtc aag cgc cac aga ctg gca aca atg cct cca atg	3075
Thr Cys Arg Leu Val Lys Arg His Arg Leu Ala Thr Met Pro Pro Met	
1005 1010 1015 1020	
gtg gaa gga gaa ggc ctg gcc agt cgc ctg atc gaa gtt gga cct tct	3123
Val Glu Gly Glu Gly Leu Ala Ser Arg Leu Ile Glu Val Gly Pro Ser	
1021 1026 1031 1036	

ggt gct cag ttc ctt ggt aaa ctt cac ctg cca acg gct cct ccc cca	3171
Gly Ala Gln Phe Leu Gly Lys Leu His Leu Pro Thr Ala Pro Pro Pro	
1037 1042 1047 1052	
ctt aat gag gga gaa agt ttg gtc agc cgc att ctt cag ctg ggg cct	3219
Leu Asn Glu Gly Glu Ser Leu Val Ser Arg Ile Leu Gln Leu Gly Pro	
1053 1058 1063 1068	
cct gga acc aaa ttc ctt ggg cct gtg atc gtg gag atc cct cac ttt	3267
Pro Gly Thr Lys Phe Leu Gly Pro Val Ile Val Glu Ile Pro His Phe	
1069 1074 1079 1084	
gcg gcc ctt cga gga aag gaa agg gaa ctg gtg gtc ctg cgc agt gag	3315
Ala Ala Leu Arg Gly Lys Glu Arg Glu Leu Val Val Leu Arg Ser Glu	
1085 1090 1095 1100	
aat ggg gac agc tgg aaa gag cat ttc tgt gac tac act gaa gat gaa	3363
Asn Gly Asp Ser Trp Lys Glu His Phe Cys Asp Tyr Thr Glu Asp Glu	
1101 1106 1111 1116	
ttg aat gaa att ctt aac ggc atg gat gaa gta ctg gat agc cca gaa	3411
Leu Asn Glu Ile Leu Asn Gly Met Asp Glu Val Leu Asp Ser Pro Glu	
1117 1122 1127 1132	
gac cta gaa aag aaa cga atc tgc cgc atc atc acc cga gac ttc cca	3459
Asp Leu Glu Lys Lys Arg Ile Cys Arg Ile Ile Thr Arg Asp Phe Pro	
1133 1138 1143 1148	
cag tac ttt gca gtg gtg tct cgt atc aaa cag gac agc aat ctg att	3507
Gln Tyr Phe Ala Val Val Ser Arg Ile Lys Gln Asp Ser Asn Leu Ile	
1149 1154 1159 1164	
ggc cca gaa gga ggt gta ctg agc agc aca gtg gtg ccc cag gtg cag	3555
Gly Pro Glu Gly Gly Val Leu Ser Ser Thr Val Val Pro Gln Val Gln	
1165 1170 1175 1180	
gcc gtc ttc cca gag ggg gca ctc acc aag cgg atc cgt gta ggc ctg	3603
Ala Val Phe Pro Glu Gly Ala Leu Thr Lys Arg Ile Arg Val Gly Leu	
1181 1186 1191 1196	
cag gct caa cct atg cac agt gag ctg gtt aag aag atc cta ggc aac	3651
Gln Ala Gln Pro Met His Ser Glu Leu Val Lys Lys Ile Leu Gly Asn	
1197 1202 1207 1212	
aaa gct acc ttc agc cct ata gtc act ttg gaa cct aga aga aga aaa	3699
Lys Ala Thr Phe Ser Pro Ile Val Thr Leu Glu Pro Arg Arg Arg Lys	
1213 1218 1223 1228	
ttc cac aaa cca att acc atg acc att cct gtc ccc aaa gct tca agt	3747
Phe His Lys Pro Ile Thr Met Thr Ile Pro Val Pro Lys Ala Ser Ser	
1229 1234 1239 1244	
gat gtc atg ttg aat ggt ttt ggg gga gat gca cca acc tta aga tta	3795
Asp Val Met Leu Asn Gly Phe Gly Gly Asp Ala Pro Thr Leu Arg Leu	
1245 1250 1255 1260	
cta tgc agc ata aca ggt gga acc acc cct gcc cag tgg gaa gat att	3843

Leu Cys Ser Ile Thr Gly Gly Thr Thr Pro Ala Gln Trp Glu Asp Ile	
1261	1266 1271 1276
aca gga act acg cca tta aca ttt gtc aat gaa tgt gtt tcc ttt aca	3891
Thr Gly Thr Thr Pro Leu Thr Phe Val Asn Glu Cys Val Ser Phe Thr	
1277	1282 1287 1292
aca aac gtg tct gcc agg ttc tgg ctg ata gat tgt cga cag atc cag	3939
Thr Asn Val Ser Ala Arg Phe Trp Leu Ile Asp Cys Arg Gln Ile Gln	
1293	1298 1303 1308
gaa tcc gtt act ttt gca tca caa gta tac aga gaa att atc tgc gta	3987
Glu Ser Val Thr Phe Ala Ser Gln Val Tyr Arg Glu Ile Ile Cys Val	
1309	1314 1319 1324
cct tat atg gcc aaa ttt gta gtg ttt gcc aaa tca cat gac ccc att	4035
Pro Tyr Met Ala Lys Phe Val Val Phe Ala Lys Ser His Asp Pro Ile	
1325	1330 1335 1340
gaa gcc agg ttg agg tgt ttc tgc atg act gat gat aaa gtg gat aag	4083
Glu Ala Arg Leu Arg Cys Phe Cys Met Thr Asp Asp Lys Val Asp Lys	
1341	1346 1351 1356
acc ctt gaa caa caa gaa aat ttt gct gag gtg gcc aga agc agg gat	4131
Thr Leu Glu Gln Gln Glu Asn Phe Ala Glu Val Ala Arg Ser Arg Asp	
1357	1362 1367 1372
gtg gag gtg tta gaa gga aaa ccc atc tac gtt gat tgt ttc ggc aac	4179
Val Glu Val Leu Glu Gly Lys Pro Ile Tyr Val Asp Cys Phe Gly Asn	
1373	1378 1383 1388
ttg gta cca tta act aaa agt ggc cag cat cat ata ttc agt ttt ttt	4227
Leu Val Pro Leu Thr Lys Ser Gly Gln His His Ile Phe Ser Phe Phe	
1389	1394 1399 1404
gcc ttc aaa gaa aat aga ctt cct cta ttt gtc aag gta cgc gat acg	4275
Ala Phe Lys Glu Asn Arg Leu Pro Leu Phe Val Lys Val Arg Asp Thr	
1405	1410 1415 1420
act cag gaa cct tgc gga cga cta tca ttt atg aag gag cca aaa tcc	4323
Thr Gln Glu Pro Cys Gly Arg Leu Ser Phe Met Lys Glu Pro Lys Ser	
1421	1426 1431 1436
acg aga ggc ctg gtg cat caa gct att tgc aac tta aac atc act ttg	4371
Thr Arg Gly Leu Val His Gln Ala Ile Cys Asn Leu Asn Ile Thr Leu	
1437	1442 1447 1452
ccg att tat aca aag gaa tca gag tca gat caa gaa cag gag gaa gag	4419
Pro Ile Tyr Thr Lys Glu Ser Glu Ser Asp Gln Glu Gln Glu Glu Glu	
1453	1458 1463 1468
atc gat atg aca tca gaa aaa aat cca cag gat gag cag gaa cgg atc	4467
Ile Asp Met Thr Ser Glu Lys Asn Pro Gln Asp Glu Gln Glu Arg Ile	
1469	1474 1479 1484
gag gaa agg ctg gct tat att gct gat cac ctt ggc ttc agc tgg aca	4515
Glu Glu Arg Leu Ala Tyr Ile Ala Asp His Leu Gly Phe Ser Trp Thr	

1485	1490	1495	1500	
gaa tta gca aga gaa ctg gat ttc act gag gag caa att cat caa att				4563
Glu Leu Ala Arg Glu Leu Asp Phe Thr Glu Glu Gln Ile His Gln Ile				
1501	1506	1511	1516	
cga att gaa aat ccc aac tct ctt caa gac cag agt cat gca ctg ttg				4611
Arg Ile Glu Asn Pro Asn Ser Leu Gln Asp Gln Ser His Ala Leu Leu				
1517	1522	1527	1532	
aag tac tgg cta gag agg gat ggg aaa cat gct aca gat acc aac ctc				4659
Lys Tyr Trp Leu Glu Arg Asp Gly Lys His Ala Thr Asp Thr Asn Leu				
1533	1538	1543	1548	
gtt gaa tgt ctc acc aag atc aac cga atg gat att gtt cat ctc atg				4707
Val Glu Cys Leu Thr Lys Ile Asn Arg Met Asp Ile Val His Leu Met				
1549	1554	1559	1564	
gag acc aac aca gaa cct ctc cag gag cgc atc agt cat agt tat gca				4755
Glu Thr Asn Thr Glu Pro Leu Gln Glu Arg Ile Ser His Ser Tyr Ala				
1565	1570	1575	1580	
gaa att gaa cag acc att aca ctg gat cat agt gaa ggg ttc tcg gta				4803
Glu Ile Glu Gln Thr Ile Thr Leu Asp His Ser Glu Gly Phe Ser Val				
1581	1586	1591	1596	
ctt caa gag gag tta tgc act gca cag cac aag cag aaa gag gag caa				4851
Leu Gln Glu Glu Leu Cys Thr Ala Gln His Lys Gln Lys Glu Glu Gln				
1597	1602	1607	1612	
gct gtt tct aaa gaa agt gag acc tgc gat cac cct cct atc gtc tca				4899
Ala Val Ser Lys Glu Ser Glu Thr Cys Asp His Pro Pro Ile Val Ser				
1613	1618	1623	1628	
gag gaa gac att tct gtt ggt tat tcc act ttt cag gat ggc gtc ccc				4947
Glu Glu Asp Ile Ser Val Gly Tyr Ser Thr Phe Gln Asp Gly Val Pro				
1629	1634	1639	1644	
aaa act gag ggg gac agc tca tca aca gca ctc ttt ccc caa act cac				4995
Lys Thr Glu Gly Asp Ser Ser Ser Thr Ala Leu Phe Pro Gln Thr His				
1645	1650	1655	1660	
aag gag caa gtt caa cag gat ttc tca ggg aaa atg caa gac ctg cct				5043
Lys Glu Gln Val Gln Gln Asp Phe Ser Gly Lys Met Gln Asp Leu Pro				
1661	1666	1671	1676	
gaa gag tca tct ctg gaa tat cag cag gaa tat ttt gtg aca act cca				5091
Glu Glu Ser Ser Leu Glu Tyr Gln Gln Glu Tyr Phe Val Thr Thr Pro				
1677	1682	1687	1692	
gga aca gaa aca tca gag act cag aag gct atg ata gta ccc agc tct				5139
Gly Thr Glu Thr Ser Glu Thr Gln Lys Ala Met Ile Val Pro Ser Ser				
1693	1698	1703	1708	
ccc agc aag aca cct gag gaa gtt agc acc cct gca gag gag gag aag				5187
Pro Ser Lys Thr Pro Glu Glu Val Ser Thr Pro Ala Glu Glu Glu Lys				
1709	1714	1719	1724	

ctg tac ctc cag acc cca aca tcc agc gag cgg gga ggc tct ccc atc	5235
Leu Tyr Leu Gln Thr Pro Thr Ser Ser Glu Arg Gly Gly Ser Pro Ile	
1725 1730 1735 1740	
ata caa gaa ccc gaa gag ccc tca gag cac aga gag gag agc tct ccg	5283
Ile Gln Glu Pro Glu Glu Pro Ser Glu His Arg Glu Glu Ser Ser Pro	
1741 1746 1751 1756	
cgg aaa acc agc ctc gta ata gtg gag tct gcc gat aac cag cct gag	5331
Arg Lys Thr Ser Leu Val Ile Val Glu Ser Ala Asp Asn Gln Pro Glu	
1757 1762 1767 1772	
acc tgt gaa aga ctc gat gaa gat gca gct ttt gaa aag gga gac gat	5379
Thr Cys Glu Arg Leu Asp Glu Asp Ala Ala Phe Glu Lys Gly Asp Asp	
1773 1778 1783 1788	
atg cct gaa ata ccc cca gaa aca gtc aca gaa gaa gaa tac att gat	5427
Met Pro Glu Ile Pro Pro Glu Thr Val Thr Glu Glu Glu Tyr Ile Asp	
1789 1794 1799 1804	
gag cat gga cac acc gtg gta aag aag gtt act agg aaa atc att agg	5475
Glu His Gly His Thr Val Val Lys Lys Val Thr Arg Lys Ile Ile Arg	
1805 1810 1815 1820	
cgg tat gta tcc tct gaa ggc aca gag aaa gaa gag att atg gtg cag	5523
Arg Tyr Val Ser Ser Glu Gly Thr Glu Lys Glu Glu Ile Met Val Gln	
1821 1826 1831 1836	
gga atg cca cag gaa cct gtc aac atc gag gaa ggg gat ggc tat tcc	5571
Gly Met Pro Gln Glu Pro Val Asn Ile Glu Glu Gly Asp Gly Tyr Ser	
1837 1842 1847 1852	
aaa gtt ata aag cgt gtt gta ttg aag agt gac acc gag cag tca gag	5619
Lys Val Ile Lys Arg Val Val Leu Lys Ser Asp Thr Glu Gln Ser Glu	
1853 1858 1863 1868	
gac aac aat gag taa agccatcaca cagaagaggg ctgtggtgaa ggaccagcat	5674
Asp Asn Asn Glu *	
1869	
ggaaaacgca ttgacttgga gcacctggag gatgtaccag aagcactaga ccaggacgac	5734
ctccagcgcg atctccagca gctccttcgg catttctgca aggaggactt gaagcaagag	5794
gccaagtgag ggactgcca gttctcacac cagaaaccac acattcactc aatatgcagc	5854
ttcctgtttc agtaggggag tgacctaaact ggccctaatta atgggatacc ccgacatttc	5914
cactgttagc aaatatacgg cattttgctt tagttttccc ccatactctt taactataaa	5974
gctaatttgt gaccaaagat ggcatacttc atactggatg ctgtatccaa tactttgttg	6034
tgtctgtgct aacctgggaa ctggccacct ccattgttct ttgcttctgc acaagatcca	6094
tgaaaatcca ttgatcagaa gaacttcacc tgcagacctc ttcaagtgac actatgtagg	6154

aatccttcca aggaatatct atgtacaatg tatatagctg aaatgctcag atgaacaaca 6214
tattaaaatt aaaaccactg cctattgttaa ctacactggg catcagaata aaaggcctct 6274
aaaa 6278

<210> 73
<211> 9412
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (68)..(8890)

<400> 73
cattgaccaa ctcaagtcatt ctttaaacia attggaaact gagggaaact tgagaatttg 60
tgctgtt atg gga tgc ata atg aca gaa gca tta gag aat aaa agt gta 109
Met Gly Cys Ile Met Thr Glu Ala Leu Glu Asn Lys Ser Val
1 5 10
cat ttt ccc cta aga agt aaa tac aac agg ctt aca aaa gtt gct cgc 157
His Phe Pro Leu Arg Ser Lys Tyr Asn Arg Leu Thr Lys Val Ala Arg
15 20 25 30
ttt ctc caa gaa aat cct tca tgt tta cta tgt aat ata cta cac cac 205
Phe Leu Gln Glu Asn Pro Ser Cys Leu Leu Cys Asn Ile Leu His His
31 36 41 46
tat ctg cac cag gca aat tac tcc atc att gat gat gct aca atg agc 253
Tyr Leu His Gln Ala Asn Tyr Ser Ile Ile Asp Asp Ala Thr Met Ser
47 52 57 62
gat gga ctt cct gct ttg gta act ttg aag aaa ggt tta gtt gca ctg 301
Asp Gly Leu Pro Ala Leu Val Thr Leu Lys Lys Gly Leu Val Ala Leu
63 68 73 78
gca agg cag tgg atg aag ttt att gtg gtg aca cca gcc ttt aaa gga 349
Ala Arg Gln Trp Met Lys Phe Ile Val Val Thr Pro Ala Phe Lys Gly
79 84 89 94
gtt agc tta cat aga cca gct cag cct ctg aaa cct caa ata gct atg 397
Val Ser Leu His Arg Pro Ala Gln Pro Leu Lys Pro Gln Ile Ala Met
95 100 105 110
gac cat gaa cat gaa gat gga ctt gga ttg gac aat ggg ggt ggt ctt 445
Asp His Glu His Glu Asp Gly Leu Gly Leu Asp Asn Gly Gly Gly Leu
111 116 121 126
caa agt gat acc agt gct gat gga gca gaa ttt gag ttc gat gca gcc 493
Gln Ser Asp Thr Ser Ala Asp Gly Ala Glu Phe Glu Phe Asp Ala Ala
127 132 137 142

aca gtc agt gaa cac	aca atg cta tta gaa gga	aca gct aac cgg cct	541
Thr Val Ser Glu His	Thr Met Leu Leu Glu Gly	Thr Ala Asn Arg Pro	
143	148	153	158
cca cct ggt agc tct	gga cct gta act gga gct	gag ata atg agg aaa	589
Pro Pro Gly Ser Ser	Gly Pro Val Thr Gly	Ala Glu Ile Met Arg Lys	
159	164	169	174
ctt tct aaa act cat	acc cat agt gac tct	gca tta aaa ata aag ggc	637
Leu Ser Lys Thr His	Thr His Ser Asp Ser	Ala Leu Lys Ile Lys Gly	
175	180	185	190
att cac cca tat cat	tct ctg agc tat acc	agt gga gac act gcc act	685
Ile His Pro Tyr His	Ser Leu Ser Tyr Thr	Ser Gly Asp Thr Ala Thr	
191	196	201	206
gat tct cca gtg cat	gtt gga cgt gct ggg	atg cca gta aag gac agt	733
Asp Ser Pro Val His	Val Gly Arg Ala Gly	Met Pro Val Lys Asp Ser	
207	212	217	222
cca agg aag gag agc	cta ctc agc tac ctg	act gga agc ttc cca agc	781
Pro Arg Lys Glu Ser	Leu Leu Ser Tyr Leu	Thr Gly Ser Phe Pro Ser	
223	228	233	238
ctg cac aac ctc ctg	gaa ggt act cct cag	aga agc agt gct gct gtg	829
Leu His Asn Leu Leu	Glu Gly Thr Pro Gln	Arg Ser Ser Ala Ala Val	
239	244	249	254
aaa agt agc tcc cta	acg aga aca gga aat	aca gta gcc act gat atg	877
Lys Ser Ser Ser Leu	Thr Arg Thr Gly Asn	Thr Val Ala Thr Asp Met	
255	260	265	270
tta tct gaa cat ccc	ttg cta tct gag cca	tca tct gtg agt ttc tat	925
Leu Ser Glu His Pro	Leu Leu Ser Glu Pro	Ser Ser Val Ser Phe Tyr	
271	276	281	286
aat tgg atg tca aat	gct gtg ggt aat cga	gga agt gtg tta caa gaa	973
Asn Trp Met Ser Asn	Ala Val Gly Asn Arg	Gly Ser Val Leu Gln Glu	
287	292	297	302
tct cct gtt aca aaa	tca gga cac aat agt	ctt ccc aca ggt gtt gca	1021
Ser Pro Val Thr Lys	Ser Gly His Asn Ser	Leu Pro Thr Gly Val Ala	
303	308	313	318
ccc aat ctt cca aca	ata ccc tca gcc tca	gat ttc aac act gtc ttg	1069
Pro Asn Leu Pro Thr	Ile Pro Ser Ala Ser	Asp Phe Asn Thr Val Leu	
319	324	329	334
tct agt gac caa aat	act ttg gat ggg aca	cat tct cag cat agc acc	1117
Ser Ser Asp Gln Asn	Thr Leu Asp Gly Thr	His Ser Gln His Ser Thr	
335	340	345	350
agt cag gat gat gtg	gca ggt gta gaa gaa	gca aac caa ggg ttt cct	1165
Ser Gln Asp Asp Val	Ala Gly Val Glu Glu	Ala Asn Gln Gly Phe Pro	
351	356	361	366
gct gtt cag ctt gct	gat gca cag gtt gtt	ttc aag cct ctt ctg agt	1213

Ala Val Gln Leu Ala Asp Ala Gln Val Val Phe Lys Pro Leu Leu Ser	
367 372 377 382	
cat aca ggg atc cag tca cag gat aca atg cca ttc tgc tac cga atg	1261
His Thr Gly Ile Gln Ser Gln Asp Thr Met Pro Phe Cys Tyr Arg Met	
383 388 393 398	
tac ttt gga gaa cac ctt tca ttt tca ggg act ttg gac tgc ctc aga	1309
Tyr Phe Gly Glu His Leu Ser Phe Ser Gly Thr Leu Asp Cys Leu Arg	
399 404 409 414	
gca gat att gtg gat tca gac aca gcc aaa gag aga aaa ggc aaa aga	1357
Ala Asp Ile Val Asp Ser Asp Thr Ala Lys Glu Arg Lys Gly Lys Arg	
415 420 425 430	
gca aga agg caa ggc cat gtg aat ctt cct cca ctt gag ttc aaa cca	1405
Ala Arg Arg Gln Gly His Val Asn Leu Pro Pro Leu Glu Phe Lys Pro	
431 436 441 446	
gca tta atg ttg gga acc ttt agc atc agt gct gtt gta atg gaa aag	1453
Ala Leu Met Leu Gly Thr Phe Ser Ile Ser Ala Val Val Met Glu Lys	
447 452 457 462	
tcc gtg tgc acc cct cag aac tct acc agt gcc ctt tct ttt cat gat	1501
Ser Val Cys Thr Pro Gln Asn Ser Thr Ser Ala Leu Ser Phe His Asp	
463 468 473 478	
ctc agc aag cgg tat tat aac acc ttt cac tgc aac ttt act att tcc	1549
Leu Ser Lys Arg Tyr Tyr Asn Thr Phe His Cys Asn Phe Thr Ile Ser	
479 484 489 494	
tgt cag tca ata agc cag cat gta gac atg gct ttg gtt cgt ctt att	1597
Cys Gln Ser Ile Ser Gln His Val Asp Met Ala Leu Val Arg Leu Ile	
495 500 505 510	
cat cag ttt agc aca atg ata gat gac atc aaa gca act cag act gat	1645
His Gln Phe Ser Thr Met Ile Asp Asp Ile Lys Ala Thr Gln Thr Asp	
511 516 521 526	
att aaa ctt agc aga tat aca gcc gga tct gct tcc cca aca cct acc	1693
Ile Lys Leu Ser Arg Tyr Thr Ala Gly Ser Ala Ser Pro Thr Pro Thr	
527 532 537 542	
ttc aaa acc aga aaa cat cgg gac ttt cgt tca tct gac ttt agc cgc	1741
Phe Lys Thr Arg Lys His Arg Asp Phe Arg Ser Ser Asp Phe Ser Arg	
543 548 553 558	
agt tct aga gga agt ctt aat ggt ggc aat aga gta aat aat gca aag	1789
Ser Ser Arg Gly Ser Leu Asn Gly Gly Asn Arg Val Asn Asn Ala Lys	
559 564 569 574	
aac aaa cgg acc aac aat gag aat aac aaa aag gaa tct cga aac aag	1837
Asn Lys Arg Thr Asn Asn Glu Asn Asn Lys Lys Glu Ser Arg Asn Lys	
575 580 585 590	
aat tca tta gga aga tct gaa aga aga aca tca aaa gtg tct agg aaa	1885
Asn Ser Leu Gly Arg Ser Glu Arg Arg Thr Ser Lys Val Ser Arg Lys	

591	596	601	606	
ggt tca aaa gat gtg gtg gat cac atg act att cat atg gat gac tct				1933
Gly Ser Lys Asp Val Val Asp His Met Thr Ile His Met Asp Asp Ser				
607	612	617	622	
gat tca att aca gtg tca gaa caa agt gag cct tca gct gag tgc tgg				1981
Asp Ser Ile Thr Val Ser Glu Gln Ser Glu Pro Ser Ala Glu Cys Trp				
623	628	633	638	
cag aat atg tat aaa ttg ctt aac ttc tat tca ctt atc tcc gat cca				2029
Gln Asn Met Tyr Lys Leu Leu Asn Phe Tyr Ser Leu Ile Ser Asp Pro				
639	644	649	654	
aca gga ata ttg gaa aag tct tca gaa aca ttt gga cca gca gga gtt				2077
Thr Gly Ile Leu Glu Lys Ser Ser Glu Thr Phe Gly Pro Ala Gly Val				
655	660	665	670	
cgg agc cct aca gag cca aca tgt aaa gtt gtg ttt gag aat gaa caa				2125
Arg Ser Pro Thr Glu Pro Thr Cys Lys Val Val Phe Glu Asn Glu Gln				
671	676	681	686	
gac aac agc agt ttg act aag act cag agg aaa cgt agc ttg gta act				2173
Asp Asn Ser Ser Leu Thr Lys Thr Gln Arg Lys Arg Ser Leu Val Thr				
687	692	697	702	
tct gaa cct cag cat gtt act cta ata gtg ttt ggg att ggc atg gtg				2221
Ser Glu Pro Gln His Val Thr Leu Ile Val Phe Gly Ile Gly Met Val				
703	708	713	718	
aac cgc aca cac cta gag gca gat att ggt gga cta aca atg gaa tca				2269
Asn Arg Thr His Leu Glu Ala Asp Ile Gly Gly Leu Thr Met Glu Ser				
719	724	729	734	
gaa ctg aag agg atc cat ggc agt ttt act ctt aag gaa aaa atg aaa				2317
Glu Leu Lys Arg Ile His Gly Ser Phe Thr Leu Lys Glu Lys Met Lys				
735	740	745	750	
gat gtt tta cat caa aag atg act gag act tgt gct act gct cat att				2365
Asp Val Leu His Gln Lys Met Thr Glu Thr Cys Ala Thr Ala His Ile				
751	756	761	766	
ggt ggg gtt aat att gtg ctg ctt gaa ggg att aca cca aat ata caa				2413
Gly Gly Val Asn Ile Val Leu Leu Glu Gly Ile Thr Pro Asn Ile Gln				
767	772	777	782	
ctg gag gat ttt cct aca tct cct aca agt aca gcc aaa caa gag ttt				2461
Leu Glu Asp Phe Pro Thr Ser Pro Thr Ser Thr Ala Lys Gln Glu Phe				
783	788	793	798	
cta act gta gtg aaa tgt agt att gcc aag tcc caa gcc ctc tac agt				2509
Leu Thr Val Val Lys Cys Ser Ile Ala Lys Ser Gln Ala Leu Tyr Ser				
799	804	809	814	
gcc caa aga ggg ctg aag aca aac aat gct gct gtg ttc aaa gta gga				2557
Ala Gln Arg Gly Leu Lys Thr Asn Asn Ala Ala Val Phe Lys Val Gly				
815	820	825	830	

gct atc agt atc aac att cct cag cac cct gcc acc tta cat agc atg	2605
Ala Ile Ser Ile Asn Ile Pro Gln His Pro Ala Thr Leu His Ser Met	
831 836 841 846	
atg gtt cga agt tct cac caa cta tct aaa caa atc tca gac cta atc	2653
Met Val Arg Ser Ser His Gln Leu Ser Lys Gln Ile Ser Asp Leu Ile	
847 852 857 862	
aga cag cct tct aca gcc cca cag cct gta aaa gaa gat att gca acc	2701
Arg Gln Pro Ser Thr Ala Pro Gln Pro Val Lys Glu Asp Ile Ala Thr	
863 868 873 878	
cca cta cct tct gaa aaa acc cca aca agt gtt aat caa act cct gtt	2749
Pro Leu Pro Ser Glu Lys Thr Pro Thr Ser Val Asn Gln Thr Pro Val	
879 884 889 894	
gaa aca aat gaa ttt cct cag cta cca gaa ggc tta gaa aag aag cct	2797
Glu Thr Asn Glu Phe Pro Gln Leu Pro Glu Gly Leu Glu Lys Lys Pro	
895 900 905 910	
att gtt ctt aaa ttc agt gcc atg tta gat ggt ata gcc att gga gca	2845
Ile Val Leu Lys Phe Ser Ala Met Leu Asp Gly Ile Ala Ile Gly Ala	
911 916 921 926	
gca ctt tta cca tct ctg aaa gca gaa tac aag atg gga aga atg aga	2893
Ala Leu Leu Pro Ser Leu Lys Ala Glu Tyr Lys Met Gly Arg Met Arg	
927 932 937 942	
agt cat gga atg aca ggt gca cag aca aga ttt aca ttt gag ctg cca	2941
Ser His Gly Met Thr Gly Ala Gln Thr Arg Phe Thr Phe Glu Leu Pro	
943 948 953 958	
aat cac aga ttg cgt ttt act tca aaa gtt tct gcc aca gat atg tca	2989
Asn His Arg Leu Arg Phe Thr Ser Lys Val Ser Ala Thr Asp Met Ser	
959 964 969 974	
acc att cct cct tct gcc agt ctt aac ctt ccc cct gtt acc atg tca	3037
Thr Ile Pro Pro Ser Ala Ser Leu Asn Leu Pro Pro Val Thr Met Ser	
975 980 985 990	
ggg aaa tat ata atg gaa gaa cat gat agt tat tcg gat cag gtg tgg	3085
Gly Lys Tyr Ile Met Glu Glu His Asp Ser Tyr Ser Asp Gln Val Trp	
991 996 1001 1006	
agt ata gat gaa ctg cct tct aaa caa ggt tac tat tta cag gga aat	3133
Ser Ile Asp Glu Leu Pro Ser Lys Gln Gly Tyr Tyr Leu Gln Gly Asn	
1007 1012 1017 1022	
tat ctg cgt tgt gtg gca gaa gtt ggt tcc ttt gaa cat aat ctt aca	3181
Tyr Leu Arg Cys Val Ala Glu Val Gly Ser Phe Glu His Asn Leu Thr	
1023 1028 1033 1038	
act gat ctt cta aac cac ttg gta ttt gta cag aaa gtg ttc atg aag	3229
Thr Asp Leu Leu Asn His Leu Val Phe Val Gln Lys Val Phe Met Lys	
1039 1044 1049 1054	

gaa gtt aat gaa gta ata caa aaa gtt tct ggt ggg gag cag cct att	3277
Glu Val Asn Glu Val Ile Gln Lys Val Ser Gly Gly Glu Gln Pro Ile	
1055 1060 1065 1070	
cct ctc tgg aac gaa cat gat gga aca gca gat gga gat aaa cct aaa	3325
Pro Leu Trp Asn Glu His Asp Gly Thr Ala Asp Gly Asp Lys Pro Lys	
1071 1076 1081 1086	
att ctc ctc tat tcc cta aac ttg cag ttc aag ggt att caa gta acg	3373
Ile Leu Leu Tyr Ser Leu Asn Leu Gln Phe Lys Gly Ile Gln Val Thr	
1087 1092 1097 1102	
gcc act act cca tca atg aga gct gta aga ttt gaa act gga ttg att	3421
Ala Thr Thr Pro Ser Met Arg Ala Val Arg Phe Glu Thr Gly Leu Ile	
1103 1108 1113 1118	
gaa ctg gaa ctt tct aac cga ctt caa acc aaa gct tca cca gga agt	3469
Glu Leu Glu Leu Ser Asn Arg Leu Gln Thr Lys Ala Ser Pro Gly Ser	
1119 1124 1129 1134	
agc agc tat ctg aaa ctg ttt ggc aaa tgc cag gtg gat tta aat ctg	3517
Ser Ser Tyr Leu Lys Leu Phe Gly Lys Cys Gln Val Asp Leu Asn Leu	
1135 1140 1145 1150	
gca tta gga caa att gtc aaa cat cag gtt tat gag gaa gct ggt tct	3565
Ala Leu Gly Gln Ile Val Lys His Gln Val Tyr Glu Glu Ala Gly Ser	
1151 1156 1161 1166	
gat ttt cat caa gtt gcc tat ttt aaa acc aga att gga tta aga aat	3613
Asp Phe His Gln Val Ala Tyr Phe Lys Thr Arg Ile Gly Leu Arg Asn	
1167 1172 1177 1182	
gcc ctc cga gaa gaa atc agt ggt tct tca gat agg gaa gct gtg ctt	3661
Ala Leu Arg Glu Glu Ile Ser Gly Ser Ser Asp Arg Glu Ala Val Leu	
1183 1188 1193 1198	
att act ttg aat aga cca att gtt tat gca cag cct gtg gcc ttt gat	3709
Ile Thr Leu Asn Arg Pro Ile Val Tyr Ala Gln Pro Val Ala Phe Asp	
1199 1204 1209 1214	
aga gct gtg ctg ttt tgg ctg aat tat aag gct gcc tat gac aac tgg	3757
Arg Ala Val Leu Phe Trp Leu Asn Tyr Lys Ala Ala Tyr Asp Asn Trp	
1215 1220 1225 1230	
aat gaa caa cga atg gct tta cat aag gat att cat atg gct aca aag	3805
Asn Glu Gln Arg Met Ala Leu His Lys Asp Ile His Met Ala Thr Lys	
1231 1236 1241 1246	
gaa gta gta gat atg cta cct ggt atc cag caa aca tca gcc cag gcc	3853
Glu Val Val Asp Met Leu Pro Gly Ile Gln Gln Thr Ser Ala Gln Ala	
1247 1252 1257 1262	
ttt ggg act ctt ttt ctc cag ctc act gtc aat gat ctg gga att tgc	3901
Phe Gly Thr Leu Phe Leu Gln Leu Thr Val Asn Asp Leu Gly Ile Cys	
1263 1268 1273 1278	
cta cct atc aca aat act gca cag tct aat cat act gga gac ctt gac	3949

Leu Pro Ile Thr Asn Thr Ala Gln Ser Asn His Thr Gly Asp Leu Asp	
1279 1284 1289 1294	
act ggt tct gct ttg gta tta acc att gaa agt act ctc atc act gca	3997
Thr Gly Ser Ala Leu Val Leu Thr Ile Glu Ser Thr Leu Ile Thr Ala	
1295 1300 1305 1310	
tgc tct tca gag tct ctg gtt agc aaa ggg cat ttc aaa aac ttt tgt	4045
Cys Ser Ser Glu Ser Leu Val Ser Lys Gly His Phe Lys Asn Phe Cys	
1311 1316 1321 1326	
atc cgt ttt gct gat gga ttt gag aca tca tgg gat gac tgg aaa cca	4093
Ile Arg Phe Ala Asp Gly Phe Glu Thr Ser Trp Asp Asp Trp Lys Pro	
1327 1332 1337 1342	
gaa att cat ggg gat tta gtg atg aat gcc tgt gta gtt cca gat ggc	4141
Glu Ile His Gly Asp Leu Val Met Asn Ala Cys Val Val Pro Asp Gly	
1343 1348 1353 1358	
acc tat gaa gta tgt tca aga act aca gga caa gca gca gct gaa agc	4189
Thr Tyr Glu Val Cys Ser Arg Thr Thr Gly Gln Ala Ala Ala Glu Ser	
1359 1364 1369 1374	
agt agt gct gga acc tgg aca ctc aac gta ttg tgg aaa atg tgt ggg	4237
Ser Ser Ala Gly Thr Trp Thr Leu Asn Val Leu Trp Lys Met Cys Gly	
1375 1380 1385 1390	
att gat gtt cac atg gat cct aac att ggc aaa agg ctt aat gct ctg	4285
Ile Asp Val His Met Asp Pro Asn Ile Gly Lys Arg Leu Asn Ala Leu	
1391 1396 1401 1406	
ggc aat act ctt aca aca ctg aca gga gag gaa gac ata gat gac att	4333
Gly Asn Thr Leu Thr Thr Leu Thr Gly Glu Glu Asp Ile Asp Asp Ile	
1407 1412 1417 1422	
gct gac tta aat tca gtg aac ata gct gac ctg tca gat gag gat gaa	4381
Ala Asp Leu Asn Ser Val Asn Ile Ala Asp Leu Ser Asp Glu Asp Glu	
1423 1428 1433 1438	
gtt gat act atg tct ccc act atc cat act gaa gcc aca gat tat cga	4429
Val Asp Thr Met Ser Pro Thr Ile His Thr Glu Ala Thr Asp Tyr Arg	
1439 1444 1449 1454	
aga cag gca gca tct gct agc cag ccg gga gaa ctt aga gga aga aaa	4477
Arg Gln Ala Ala Ser Ala Ser Gln Pro Gly Glu Leu Arg Gly Arg Lys	
1455 1460 1465 1470	
att atg aag cgt ata gtg gat atc aga gaa ctg aat gaa cag gcc aaa	4525
Ile Met Lys Arg Ile Val Asp Ile Arg Glu Leu Asn Glu Gln Ala Lys	
1471 1476 1481 1486	
gta ata gat gat ctg aaa aaa tta ggt gca agt gaa gga acc ata aac	4573
Val Ile Asp Asp Leu Lys Lys Leu Gly Ala Ser Glu Gly Thr Ile Asn	
1487 1492 1497 1502	
cag gaa att caa cgt tac caa cag tta gaa tct gtg gct gtg aat gac	4621
Gln Glu Ile Gln Arg Tyr Gln Gln Leu Glu Ser Val Ala Val Asn Asp	

1503	1508	1513	1518	
att aga aga gat gtt cgt aaa aaa tta cgg agg tcc agt atg cgg gct				4669
Ile Arg Arg Asp Val Arg Lys Lys Leu Arg Arg Ser Ser Met Arg Ala				
1519	1524	1529	1534	
gct tcc cta aag gat aag tgg ggt ttg agt tac aaa cca agt tac agc				4717
Ala Ser Leu Lys Asp Lys Trp Gly Leu Ser Tyr Lys Pro Ser Tyr Ser				
1535	1540	1545	1550	
cga tca aaa agc att tct gct tct gga aga cca cct ctt aag cga atg				4765
Arg Ser Lys Ser Ile Ser Ala Ser Gly Arg Pro Pro Leu Lys Arg Met				
1551	1556	1561	1566	
gaa agg gca agt tct cga gta gga gaa act gaa gag ctc cca gaa atc				4813
Glu Arg Ala Ser Ser Arg Val Gly Glu Thr Glu Glu Leu Pro Glu Ile				
1567	1572	1577	1582	
cgt gtg gat gca gca tct cct gga cct aga gta act ttt aat atc cag				4861
Arg Val Asp Ala Ala Ser Pro Gly Pro Arg Val Thr Phe Asn Ile Gln				
1583	1588	1593	1598	
gat aca ttt cca gag gag aca gaa ctg gac ctt ttg tca gta acc att				4909
Asp Thr Phe Pro Glu Glu Thr Glu Leu Asp Leu Leu Ser Val Thr Ile				
1599	1604	1609	1614	
gaa ggt cca tcc cat tat tca tca aat agt gaa gga tca tgt tct gtg				4957
Glu Gly Pro Ser His Tyr Ser Ser Asn Ser Glu Gly Ser Cys Ser Val				
1615	1620	1625	1630	
ttc agt tct ccc aaa act cca gga ggc ttt tca cca ggc att cct ttc				5005
Phe Ser Ser Pro Lys Thr Pro Gly Gly Phe Ser Pro Gly Ile Pro Phe				
1631	1636	1641	1646	
caa act gaa gag ggc cga cgg gat gac agt ttg tct tct acc agt gaa				5053
Gln Thr Glu Glu Gly Arg Arg Asp Asp Ser Leu Ser Ser Thr Ser Glu				
1647	1652	1657	1662	
gat tcc gag aag gat gaa aaa gat gaa gac cat gag agg gaa agg ttt				5101
Asp Ser Glu Lys Asp Glu Lys Asp Glu Asp His Glu Arg Glu Arg Phe				
1663	1668	1673	1678	
tat att tac agg aaa ccc tca cat acg tct cgt aaa aaa gca aca ggc				5149
Tyr Ile Tyr Arg Lys Pro Ser His Thr Ser Arg Lys Lys Ala Thr Gly				
1679	1684	1689	1694	
ttt gct gct gtt cat cag cta ttt aca gaa cgc tgg cca aca aca cca				5197
Phe Ala Ala Val His Gln Leu Phe Thr Glu Arg Trp Pro Thr Thr Pro				
1695	1700	1705	1710	
gtc aat aga agt ctt agt ggc aca gct aca gag aga aat att gac ttt				5245
Val Asn Arg Ser Leu Ser Gly Thr Ala Thr Glu Arg Asn Ile Asp Phe				
1711	1716	1721	1726	
gaa ctt gat ata cgg gtt gaa att gat agt gga aaa tgt gta ctc cac				5293
Glu Leu Asp Ile Arg Val Glu Ile Asp Ser Gly Lys Cys Val Leu His				
1727	1732	1737	1742	

cca acc acc ctt cta caa gaa cat gat gat ata agt ttg aga agg agt	5341
Pro Thr Thr Leu Leu Gln Glu His Asp Asp Ile Ser Leu Arg Arg Ser	
1743 1748 1753 1758	
tat gat cga agt tcc agg agc tta gat caa gat tca cct tca aaa aag	5389
Tyr Asp Arg Ser Ser Arg Ser Leu Asp Gln Asp Ser Pro Ser Lys Lys	
1759 1764 1769 1774	
aag aag ttt caa act aat tat gct tct acc acc cat tta atg acc ggc	5437
Lys Lys Phe Gln Thr Asn Tyr Ala Ser Thr Thr His Leu Met Thr Gly	
1775 1780 1785 1790	
aag aaa gtg cca tca tct cta cag aca aag cct agt gac tta gaa aca	5485
Lys Lys Val Pro Ser Ser Leu Gln Thr Lys Pro Ser Asp Leu Glu Thr	
1791 1796 1801 1806	
aca gta ttt tac att ccc gga gtt gat gta aag ttg cat tac aat tcc	5533
Thr Val Phe Tyr Ile Pro Gly Val Asp Val Lys Leu His Tyr Asn Ser	
1807 1812 1817 1822	
aag acg cta aag act gaa tca cct aat gcc tcc agg gga tct tcc ttg	5581
Lys Thr Leu Lys Thr Glu Ser Pro Asn Ala Ser Arg Gly Ser Ser Leu	
1823 1828 1833 1838	
cca aga aca ctg tcc aaa gag tcc aag ctg tat ggt atg aaa gat agt	5629
Pro Arg Thr Leu Ser Lys Glu Ser Lys Leu Tyr Gly Met Lys Asp Ser	
1839 1844 1849 1854	
gca aca tct cct cct tct cct cct tta cct tcc act gtc cag agc aag	5677
Ala Thr Ser Pro Pro Ser Pro Pro Leu Pro Ser Thr Val Gln Ser Lys	
1855 1860 1865 1870	
act aac acc tta ctt cct ccc cag ccc cca cct att cct gca gcc aaa	5725
Thr Asn Thr Leu Leu Pro Pro Gln Pro Pro Pro Ile Pro Ala Ala Lys	
1871 1876 1881 1886	
gga aaa gga agt gga gga gta aaa aca gcc aag tta tat gcc tgg gta	5773
Gly Lys Gly Ser Gly Gly Val Lys Thr Ala Lys Leu Tyr Ala Trp Val	
1887 1892 1897 1902	
gca ctt cag tca ttg cca gaa gaa atg gtt att agt ccc tgc cta tta	5821
Ala Leu Gln Ser Leu Pro Glu Glu Met Val Ile Ser Pro Cys Leu Leu	
1903 1908 1913 1918	
gac ttt ctg gaa aaa gct ctg gaa act atc cca att aca cca gtt gaa	5869
Asp Phe Leu Glu Lys Ala Leu Glu Thr Ile Pro Ile Thr Pro Val Glu	
1919 1924 1929 1934	
agg aat tat aca gct gtc agc tca caa gat gaa gat atg gga cat ttt	5917
Arg Asn Tyr Thr Ala Val Ser Ser Gln Asp Glu Asp Met Gly His Phe	
1935 1940 1945 1950	
gaa ata cca gat cct atg gaa gaa tca aca aca tca cta gtg tcg tct	5965
Glu Ile Pro Asp Pro Met Glu Glu Ser Thr Thr Ser Leu Val Ser Ser	
1951 1956 1961 1966	

tca aca tct gct tac tct tcc ttc cct gta gat gtt gtg gtt tat gta Ser Thr Ser Ala Tyr Ser Ser Phe Pro Val Asp Val Val Val Tyr Val 1967 1972 1977 1982	6013
cga gtt cag ccc tca cag atc aaa ttt agc tgt tta cca gta tca aga Arg Val Gln Pro Ser Gln Ile Lys Phe Ser Cys Leu Pro Val Ser Arg 1983 1988 1993 1998	6061
gta gaa tgc atg tta aag ctg cca tcc ctg gat ttg gtg ttt tct tca Val Glu Cys Met Leu Lys Leu Pro Ser Leu Asp Leu Val Phe Ser Ser 1999 2004 2009 2014	6109
aac cga gga gaa ctg gag act tta ggg act aca tat cct gca gag act Asn Arg Gly Glu Leu Glu Thr Leu Gly Thr Thr Tyr Pro Ala Glu Thr 2015 2020 2025 2030	6157
tta tcc cct gga ggt aat gct act cag agt gga aca aag act tct gct Leu Ser Pro Gly Gly Asn Ala Thr Gln Ser Gly Thr Lys Thr Ser Ala 2031 2036 2041 2046	6205
agc aaa act gga ata cca ggt tca tgc gga tta ggc agc cct ctt ggc Ser Lys Thr Gly Ile Pro Gly Ser Ser Gly Leu Gly Ser Pro Leu Gly 2047 2052 2057 2062	6253
cga agt cga cat agt agt agt cag tca gac ctg acc agt tcc agc agt Arg Ser Arg His Ser Ser Ser Gln Ser Asp Leu Thr Ser Ser Ser Ser 2063 2068 2073 2078	6301
agt tca tct ggc ttg agc ttc act gca tgc atg tct gac ttt tcc ctt Ser Ser Ser Gly Leu Ser Phe Thr Ala Cys Met Ser Asp Phe Ser Leu 2079 2084 2089 2094	6349
tat gta ttt cat cca tat gga gca ggg aaa caa aaa act gct gtt tct Tyr Val Phe His Pro Tyr Gly Ala Gly Lys Gln Lys Thr Ala Val Ser 2095 2100 2105 2110	6397
ggc ctc aca cct gga tca gga gga tta ggg aat gtg gat gag gag ccc Gly Leu Thr Pro Gly Ser Gly Gly Leu Gly Asn Val Asp Glu Glu Pro 2111 2116 2121 2126	6445
act tca gtc act ggt cga aaa gat tca ctc agt ata aac ctt gag ttt Thr Ser Val Thr Gly Arg Lys Asp Ser Leu Ser Ile Asn Leu Glu Phe 2127 2132 2137 2142	6493
gta aaa gtg agt ttg tca cgg atc agg cgt tca gga ggt gcc tca ttt Val Lys Val Ser Leu Ser Arg Ile Arg Arg Ser Gly Gly Ala Ser Phe 2143 2148 2153 2158	6541
ttt gaa agt cag tct gta agc aag tct gca agc aaa atg gat act acg Phe Glu Ser Gln Ser Val Ser Lys Ser Ala Ser Lys Met Asp Thr Thr 2159 2164 2169 2174	6589
tta ata aat ata tct gct gtt tgt gat ata ggg tct gcc tcc ttt aaa Leu Ile Asn Ile Ser Ala Val Cys Asp Ile Gly Ser Ala Ser Phe Lys 2175 2180 2185 2190	6637
tat gat atg cgc cga ctc agt gaa att ctg gca ttt cca aga gca tgg	6685

Tyr Asp Met Arg Arg Leu Ser Glu Ile Leu Ala Phe Pro Arg Ala Trp	
2191	2196 2201 2206
tat aga aga agt att gca aga cgt cta ttc ctt gga gac caa act ata	6733
Tyr Arg Arg Ser Ile Ala Arg Arg Leu Phe Leu Gly Asp Gln Thr Ile	
2207	2212 2217 2222
aat ttg cca aca tct ggc cca ggg aca cct gat tcc att gaa ggg gta	6781
Asn Leu Pro Thr Ser Gly Pro Gly Thr Pro Asp Ser Ile Glu Gly Val	
2223	2228 2233 2238
agc caa cac ctt tcc cct gaa tca tca aga aaa gct tac tgc aag acc	6829
Ser Gln His Leu Ser Pro Glu Ser Ser Arg Lys Ala Tyr Cys Lys Thr	
2239	2244 2249 2254
tgg gag cag cca agt cag tca gcc tcc ttc acc cac atg cct cag tca	6877
Trp Glu Gln Pro Ser Gln Ser Ala Ser Phe Thr His Met Pro Gln Ser	
2255	2260 2265 2270
cct aat gtg ttc aat gag cat atg aca aac agc acc atg tca cca ggg	6925
Pro Asn Val Phe Asn Glu His Met Thr Asn Ser Thr Met Ser Pro Gly	
2271	2276 2281 2286
aca gta gga cag agc cta aaa tcc cca gct tcc ata aga tca agg agt	6973
Thr Val Gly Gln Ser Leu Lys Ser Pro Ala Ser Ile Arg Ser Arg Ser	
2287	2292 2297 2302
gta tct gat tct tca gtt cct cga aga gat tca ctt tca aaa aca tca	7021
Val Ser Asp Ser Ser Val Pro Arg Arg Asp Ser Leu Ser Lys Thr Ser	
2303	2308 2313 2318
act cct ttt aac aaa tca aac aaa gca gca agc caa caa ggg acc cca	7069
Thr Pro Phe Asn Lys Ser Asn Lys Ala Ala Ser Gln Gln Gly Thr Pro	
2319	2324 2329 2334
tgg gaa aca ctt gtc gtg ttt gct atc aac ttg aag caa tta aac gtt	7117
Trp Glu Thr Leu Val Val Phe Ala Ile Asn Leu Lys Gln Leu Asn Val	
2335	2340 2345 2350
caa atg aat atg agt aat gta atg gga aat aca act tgg aca act agt	7165
Gln Met Asn Met Ser Asn Val Met Gly Asn Thr Thr Trp Thr Thr Ser	
2351	2356 2361 2366
ggg ttg aag agc cag ggc cgt ctg tca gta gga agt aat cgt gat cga	7213
Gly Leu Lys Ser Gln Gly Arg Leu Ser Val Gly Ser Asn Arg Asp Arg	
2367	2372 2377 2382
gag atc agc atg tct gtt ggt ctg gga aga tca caa tta gat tct aaa	7261
Glu Ile Ser Met Ser Val Gly Leu Gly Arg Ser Gln Leu Asp Ser Lys	
2383	2388 2393 2398
gga gga gta gtt gga ggg acc ata gat gtc aat gct ttg gag atg gtt	7309
Gly Gly Val Val Gly Gly Thr Ile Asp Val Asn Ala Leu Glu Met Val	
2399	2404 2409 2414
gct cat att tct gaa cat cca aat cag caa ccc agt cac aaa att cag	7357
Ala His Ile Ser Glu His Pro Asn Gln Gln Pro Ser His Lys Ile Gln	

2415	2420	2425	2430	
att act atg ggt tct act gaa gct cgt gtt gat tac atg ggc tca agt				7405
Ile Thr Met Gly Ser Thr Glu Ala Arg Val Asp Tyr Met Gly Ser Ser				
2431	2436	2441	2446	
atc ctc atg ggc atc ttc agt aat gct gat ctt aag ctt cag gat gaa				7453
Ile Leu Met Gly Ile Phe Ser Asn Ala Asp Leu Lys Leu Gln Asp Glu				
2447	2452	2457	2462	
tgg aaa gta aac ttg tat aat aca ttg gat tca agc ata act gat aaa				7501
Trp Lys Val Asn Leu Tyr Asn Thr Leu Asp Ser Ser Ile Thr Asp Lys				
2463	2468	2473	2478	
agt gag att ttc gtc cat gga gat ttg aag tgg gat att ttc caa gta				7549
Ser Glu Ile Phe Val His Gly Asp Leu Lys Trp Asp Ile Phe Gln Val				
2479	2484	2489	2494	
atg ata tca agg tca acc aca cca gat ctg ata aaa ata gga atg aag				7597
Met Ile Ser Arg Ser Thr Thr Pro Asp Leu Ile Lys Ile Gly Met Lys				
2495	2500	2505	2510	
ctc cag gaa ttt ttc aca caa caa ttt gat acc agc aaa cga gct ctg				7645
Leu Gln Glu Phe Phe Thr Gln Gln Phe Asp Thr Ser Lys Arg Ala Leu				
2511	2516	2521	2526	
tct acc tgg gga cca gtt cct tac ctt ccg cca aag aca atg act agc				7693
Ser Thr Trp Gly Pro Val Pro Tyr Leu Pro Pro Lys Thr Met Thr Ser				
2527	2532	2537	2542	
aac cta gaa aaa agt tca caa gaa caa tta ctt gat gca gca cat cat				7741
Asn Leu Glu Lys Ser Ser Gln Glu Gln Leu Leu Asp Ala Ala His His				
2543	2548	2553	2558	
cga cac tgg cct gga gta ttg aag gtg gta tca gga tgc cac ata tcc				7789
Arg His Trp Pro Gly Val Leu Lys Val Val Ser Gly Cys His Ile Ser				
2559	2564	2569	2574	
tta ttt cag att cca tta cca gaa gat gga atg caa ttt gga gga tca				7837
Leu Phe Gln Ile Pro Leu Pro Glu Asp Gly Met Gln Phe Gly Gly Ser				
2575	2580	2585	2590	
atg agc tta cat gga aat cat atg aca ctg gca tgt ttt cat ggt cca				7885
Met Ser Leu His Gly Asn His Met Thr Leu Ala Cys Phe His Gly Pro				
2591	2596	2601	2606	
aat ttt cgt tca aaa tct tgg gcc ctt ttt cat tta gaa gaa cca aat				7933
Asn Phe Arg Ser Lys Ser Trp Ala Leu Phe His Leu Glu Glu Pro Asn				
2607	2612	2617	2622	
att gct ttt tgg act gaa gct cag aaa atc tgg gaa gat ggc tcc agt				7981
Ile Ala Phe Trp Thr Glu Ala Gln Lys Ile Trp Glu Asp Gly Ser Ser				
2623	2628	2633	2638	
gat cat tct aca tat att gta caa aca cta gat ttt cac ctg ggt cat				8029
Asp His Ser Thr Tyr Ile Val Gln Thr Leu Asp Phe His Leu Gly His				
2639	2644	2649	2654	

aat Asn	act Thr	atg Met	gtt Val	acc Thr	aaa Lys	cca Pro	tgt Cys	ggt Gly	gct Ala	ttg Leu	gaa Glu	agt Ser	cct Pro	atg Met	gca Ala	8077
2655				2660						2665					2670	
aca Thr	ata Ile	acc Thr	aag Lys	ata Ile	aca Thr	agg Arg	cgt Arg	cgc Arg	cat His	gaa Glu	aat Asn	cca Pro	ccc Pro	cat His	gga Gly	8125
2671				2676						2681					2686	
gta Val	gca Ala	agt Ser	gtg Val	aaa Lys	gaa Glu	tgg Trp	ttc Phe	aat Asn	tat Tyr	gtt Val	aca Thr	gct Ala	aca Thr	agg Arg	aat Asn	8173
2687				2692						2697					2702	
gaa Glu	gag Glu	cta Leu	aat Asn	ctg Leu	ctt Leu	cgt Arg	aat Asn	gtt Val	gat Asp	gct Ala	aac Asn	aac Asn	act Thr	gag Glu	aat Asn	8221
2703				2708						2713					2718	
agc Ser	act Thr	act Thr	gtg Val	aag Lys	aat Asn	tct Ser	agt Ser	ttg Leu	ttg Leu	agt Ser	gga Gly	ttc Phe	aga Arg	gga Gly	ggt Gly	8269
2719				2724						2729					2734	
tct Ser	agc Ser	tac Tyr	aac Asn	cat His	gaa Glu	aca Thr	gag Glu	act Thr	atc Ile	ttt Phe	gca Ala	tta Leu	cca Pro	agg Arg	atg Met	8317
2735				2740						2745					2750	
cag Gln	ctt Leu	gac Asp	ttt Phe	aaa Lys	tcc Ser	att Ile	cat His	gtt Val	caa Gln	gaa Glu	cca Pro	cag Gln	gag Glu	cct Pro	tca Ser	8365
2751				2756						2761					2766	
tta Leu	cag Gln	gat Asp	gcc Ala	agc Ser	ctg Leu	aag Lys	cca Pro	aaa Lys	gta Val	gaa Glu	tgt Cys	agt Ser	gtg Val	gtg Val	aca Thr	8413
2767				2772						2777					2782	
gag Glu	ttc Phe	act Thr	gac Asp	cac His	att Ile	tgt Cys	gtg Val	act Thr	atg Met	gat Asp	gct Ala	gag Glu	ctc Leu	atc Ile	atg Met	8461
2783				2788						2793					2798	
ttt Phe	ctt Leu	cat His	gat Asp	tta Leu	gta Val	tca Ser	gct Ala	tat Tyr	ctt Leu	aaa Lys	gaa Glu	aaa Lys	gaa Glu	aaa Lys	gcc Ala	8509
2799				2804						2809					2814	
atc Ile	ttt Phe	cca Pro	cct Pro	cgg Arg	att Ile	tta Leu	tct Ser	act Thr	cga Arg	cca Pro	gga Gly	caa Gln	aaa Lys	agt Ser	cca Pro	8557
2815				2820						2825					2830	
att Ile	att Ile	ata Ile	cat His	gac Asp	gac Asp	aat Asn	tcc Ser	tct Ser	gat Asp	aaa Lys	gat Asp	aga Arg	gaa Glu	gat Asp	agc Ser	8605
2831				2836						2841					2846	
atc Ile	act Thr	tat Tyr	act Thr	act Thr	gtg Val	gac Asp	tgg Trp	aga Arg	gat Asp	ttt Phe	atg Met	tgc Cys	aat Asn	aca Thr	tgg Trp	8653
2847				2852						2857					2862	
cat His	cta Leu	gaa Glu	cct Pro	act Thr	ctt Leu	aga Arg	tta Leu	att Ile	tct Ser	tgg Trp	act Thr	gga Gly	aga Arg	aag Lys	att Ile	8701
2863				2868						2873					2878	

gat cca gta ggt gtt gat tat att ctt caa aaa ttg ggc ttt cat cat	8749
Asp Pro Val Gly Val Asp Tyr Ile Leu Gln Lys Leu Gly Phe His His	
2879 2884 2889 2894	
gct agg act act att cct aaa tgg ctt caa aga gga gtc atg gat cca	8797
Ala Arg Thr Thr Ile Pro Lys Trp Leu Gln Arg Gly Val Met Asp Pro	
2895 2900 2905 2910	
ctg gac aag gtt ctg tca gtt ctt atc aaa aag ctc ggt act gca cta	8845
Leu Asp Lys Val Leu Ser Val Leu Ile Lys Lys Leu Gly Thr Ala Leu	
2911 2916 2921 2926	
cag gat gaa aag gaa aag aaa ggc aaa gac aaa gaa gaa cac taa aaa	8893
Gln Asp Glu Lys Glu Lys Lys Gly Lys Asp Lys Glu Glu His *	
2927 2932 2937	
agtaatttga tctgtgaaca aattatgatt gtgtctgttt tattacactg gagtgttttt	8953
ttagtataat aatttgaaat ataacttta aataattcta aatttgtggc tataattaaa	9013
agtttgtaag ttaacctggt ctagttccat cattctgtgt acagtgaagt attgcatgat	9073
aatgtaaatt ttgtgaaaaa ctagattaaa atatataact gcttgttatg gtttataatt	9133
atataatgtg caatacaatt cctgcatctt taaaatgtct gcagaataac tgtgaatttt	9193
tttgttattg gattggccgt aactttttaga aaaaaatctt gttgatgata atgtgatttt	9253
ggggaggtca ttaattgctt tttctttttt aaatgtagac ttatataaat acctgtttgt	9313
atatagcttg agtaattgtg atatgattgt ataccactaa aatattgtta actattataa	9373
taaagtcaca gtaatggttt aaaaaaaaaa aaaaaaaaaa	9412

```
<210> 74
<211> 621
<212> DNA
<213> Homo sapiens
```

<400> 74																								
atttggccct cgaggccaag aattcggcac gagggcgaa										atg gag ggg tgt gtg					54									
										Met Glu Gly Cys Val														
										1														
tct aac cta atg gtc tgc aac ctg gcc tac agc ggg aag ctg gaa gag										102														
Ser Asn Leu Met Val Cys Asn Leu Ala Tyr Ser Gly Lys Leu Glu Glu																								
6										11					16					21				
ttg aag gag agt att ctg gcc gat aaa tcc ctg gct act aga act gac										150														
Leu Lys Glu Ser Ile Leu Ala Asp Lys Ser Leu Ala Thr Arg Thr Asp																								

22	27	32	37	
cag gca ggt tgg tct cct ctt cat att gcg gct tct gct ggc cgg gat				198
Gln Ala Gly Trp Ser Pro Leu His Ile Ala Ala Ser Ala Gly Arg Asp				
38	43	48	53	
gag att gta aaa gcc ctt ctg gga aaa ggt gct caa gtg aat gct gtc				246
Glu Ile Val Lys Ala Leu Leu Gly Lys Gly Ala Gln Val Asn Ala Val				
54	59	64	69	
aat caa aat ggc tgt act ccc tta cat tat gca gct tcg aaa aac agg				294
Asn Gln Asn Gly Cys Thr Pro Leu His Tyr Ala Ala Ser Lys Asn Arg				
70	75	80	85	
cat gag atc gct gtc atg tta ctg gaa ggc ggg gct aat cca gat gct				342
His Glu Ile Ala Val Met Leu Leu Glu Gly Gly Ala Asn Pro Asp Ala				
86	91	96	101	
aag gac cat tat gag gct aca gca atg cac cgg gca gca gcc aag ggt				390
Lys Asp His Tyr Glu Ala Thr Ala Met His Arg Ala Ala Ala Lys Gly				
102	107	112	117	
aac ttg aag atg att cat atc ctt ctg tac tac aaa gca tcc aca aac				438
Asn Leu Lys Met Ile His Ile Leu Leu Tyr Tyr Lys Ala Ser Thr Asn				
118	123	128	133	
atc caa gac act gag ggt aac act cct cta cac tta gcc tgt gat gag				486
Ile Gln Asp Thr Glu Gly Asn Thr Pro Leu His Leu Ala Cys Asp Glu				
134	139	144	149	
gag aga gtg gaa gaa gca aaa ctg ctg gtg tcc caa gga gca agt att				534
Glu Arg Val Glu Glu Ala Lys Leu Leu Val Ser Gln Gly Ala Ser Ile				
150	155	160	165	
tac att gag aat aaa gaa gaa aag aca ccc ctg caa gtg gcc aaa ggt				582
Tyr Ile Glu Asn Lys Glu Glu Lys Thr Pro Leu Gln Val Ala Lys Gly				
166	171	176	181	
ggc ctg ggt tta ata ctc aag aga atg gtg gaa ggt taa				621
Gly Leu Gly Leu Ile Leu Lys Arg Met Val Glu Gly *				
182	187	192		

<210> 75
 <211> 1128
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (389) .. (1036)

<400> 75
 ccggtccggt attccccgggt ggcgctgcgg aggggggacg tggtaaaagt actcagcaag 60


```

169              174              179              184
cag gcc act aac agc aac aac aga gag gct gga gct ctg cct gcg tgc      988
Gln Ala Thr Asn Ser Asn Asn Arg Glu Ala Gly Ala Leu Pro Ala Cys
185              190              195              200

ggg cca agg gct aaa cct tgg aca ggt tct ttc act tac tcc gcc tga      1036
Gly Pro Arg Ala Lys Pro Trp Thr Gly Ser Phe Thr Tyr Ser Ala  *
201              206              211              216

caaccctgcg acgtgatacc attatcccca cttcgcagat caaataaacg gagtcttggt      1096

gagattgagg tgaatttggc taacctgtaa aa                                  1128

```

```

<210> 76
<211> 911
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (90)..(665)

```

```

<220>
<221> misc_feature
<222> (1)...(911)
<223> n = a,t,c or g

```

```

<400> 76
ttcctgcact atagaataca agctacttgt tcttttttgca ggatcccatc gattcgaatt      60

```

```

cggcagcagc agccatcagg taagccaag  atg ggt gca tac aag tac atc cag      113
          Met Gly Ala Tyr Lys Tyr Ile Gln
                   1                   5

```

```

gag cta tgg aga aag aag cag tct gat gtc atg cgc ttt ctt ctg agg      161
Glu Leu Trp Arg Lys Lys Gln Ser Asp Val Met Arg Phe Leu Leu Arg
  9              14              19              24

```

```

gtc cgc tgc tgg cag tac cgc cag ctc tct gct ctc cac agg gct ccc      209
Val Arg Cys Trp Gln Tyr Arg Gln Leu Ser Ala Leu His Arg Ala Pro
 25              30              35              40

```

```

cgc ccc acc cgg cct gat aaa gcg cgc cga ctg ggc tac aag gcc aag      257
Arg Pro Thr Arg Pro Asp Lys Ala Arg Arg Leu Gly Tyr Lys Ala Lys
 41              46              51              56

```

```

caa ggt tac gtt ata tat agg att cgt gtt cgc cgt ggt ggc cga aaa      305
Gln Gly Tyr Val Ile Tyr Arg Ile Arg Val Arg Arg Gly Gly Arg Lys
 57              62              67              72

```

```

cgc cca gtt cct aag ggt gca act tac ggc aag cct gtc cat cat ggt      353
Arg Pro Val Pro Lys Gly Ala Thr Tyr Gly Lys Pro Val His His Gly
 73              78              83              88

```


aca aaa cca gtg tat cca gtc atg gaa aag aag gag gaa gat ggc acc	217
Thr Lys Pro Val Tyr Pro Val Met Glu Lys Lys Glu Glu Asp Gly Thr	
14 19 24 29	
ctg gag cgg ggg cac tgg aac aac aag atg gag ttt gtg ctg tca gtg	265
Leu Glu Arg Gly His Trp Asn Asn Lys Met Glu Phe Val Leu Ser Val	
30 35 40 45	
gct ggg gag atc att ggc tta ggc aac gtc tgg agg ttt ccc tat ctc	313
Ala Gly Glu Ile Ile Gly Leu Gly Asn Val Trp Arg Phe Pro Tyr Leu	
46 51 56 61	
tgc tac aaa aat ggg gga ggt gcc ttc ttc atc ccc tac ctc gtc ttc	361
Cys Tyr Lys Asn Gly Gly Gly Ala Phe Phe Ile Pro Tyr Leu Val Phe	
62 67 72 77	
ctc ttt acc tgt ggc att cct gtc ttc ctt ctg gag aca gca cta ggc	409
Leu Phe Thr Cys Gly Ile Pro Val Phe Leu Leu Glu Thr Ala Leu Gly	
78 83 88 93	
cag tac act agc cag gga ggc gtc aca gcc tgg agg aag atc tgc ccc	457
Gln Tyr Thr Ser Gln Gly Gly Val Thr Ala Trp Arg Lys Ile Cys Pro	
94 99 104 109	
atc ttt gag ggc att ggc tat gcc tcc cag atg atc gtc atc ctc ctc	505
Ile Phe Glu Gly Ile Gly Tyr Ala Ser Gln Met Ile Val Ile Leu Leu	
110 115 120 125	
aac gtc tac tac atc att gtg ttg gcc tgg gcc ctg ttc tac ctc ttc	553
Asn Val Tyr Tyr Ile Ile Val Leu Ala Trp Ala Leu Phe Tyr Leu Phe	
126 131 136 141	
agc agc ttc acc atc gac ctg ccc tgg ggc ggc tgc tac cat gag tgg	601
Ser Ser Phe Thr Ile Asp Leu Pro Trp Gly Gly Cys Tyr His Glu Trp	
142 147 152 157	
aac aca gaa cac tgt atg gag ttc cag aag acc aac ggc tcc ctg aat	649
Asn Thr Glu His Cys Met Glu Phe Gln Lys Thr Asn Gly Ser Leu Asn	
158 163 168 173	
ggt acc tct gag aat gcc acc tct cct gtc atc gag ttc tgg gag cgg	697
Gly Thr Ser Glu Asn Ala Thr Ser Pro Val Ile Glu Phe Trp Glu Arg	
174 179 184 189	
cgg gtc ttg aag atc tct gat ggg atc cag cac ctg ggg gcc ctg cgc	745
Arg Val Leu Lys Ile Ser Asp Gly Ile Gln His Leu Gly Ala Leu Arg	
190 195 200 205	
tgg gag ctg gct ctg tgc ctc ctg ctg gcc tgg gtc atc tgc tac ttc	793
Trp Glu Leu Ala Leu Cys Leu Leu Leu Ala Trp Val Ile Cys Tyr Phe	
206 211 216 221	
tgc atc tgg aag ggg gtg aag tcc aca ggc aag gtg gtg tac ttc acg	841
Cys Ile Trp Lys Gly Val Lys Ser Thr Gly Lys Val Val Tyr Phe Thr	
222 227 232 237	

gcc aca ttt cct tac ctc atg ctg gtg gtc ctg tta att cga ggg gtg	889
Ala Thr Phe Pro Tyr Leu Met Leu Val Val Leu Leu Ile Arg Gly Val	
238 243 248 253	
acg ttg cct ggg gca gcc caa gga att cag ttt tac ctg tac cca aac	937
Thr Leu Pro Gly Ala Ala Gln Gly Ile Gln Phe Tyr Leu Tyr Pro Asn	
254 259 264 269	
ctc acg cgt ctg tgg gat ccc cag gtg tgg atg gat gca ggc acc cag	985
Leu Thr Arg Leu Trp Asp Pro Gln Val Trp Met Asp Ala Gly Thr Gln	
270 275 280 285	
ata ttc ttc tcc ttc gcc atc tgt ctt ggg tgc ctg aca gcc ctg ggc	1033
Ile Phe Phe Ser Phe Ala Ile Cys Leu Gly Cys Leu Thr Ala Leu Gly	
286 291 296 301	
agc tac aac aag tac cac aac aac tgc tac agc ggc acc agc ttt gtg	1081
Ser Tyr Asn Lys Tyr His Asn Asn Cys Tyr Ser Gly Thr Ser Phe Val	
302 307 312 317	
gcc ggc ttt gcc atc ttc tcc atc ctg ggc ttc atg tct cag gag cag	1129
Ala Gly Phe Ala Ile Phe Ser Ile Leu Gly Phe Met Ser Gln Glu Gln	
318 323 328 333	
ggg gtg ccc att tct gag gtg gcc gag tca ggc cct ggc ctg gct ttc	1177
Gly Val Pro Ile Ser Glu Val Ala Glu Ser Gly Pro Gly Leu Ala Phe	
334 339 344 349	
atc gct tac ccg cgg gct gtg gtg atg ctg ccc ttc tct cct ctc tgg	1225
Ile Ala Tyr Pro Arg Ala Val Val Met Leu Pro Phe Ser Pro Leu Trp	
350 355 360 365	
gcc tgc tgt ttc ttc ttc atg gtc gtt ctc ctg gga ctg gat agc cag	1273
Ala Cys Cys Phe Phe Phe Met Val Val Leu Leu Gly Leu Asp Ser Gln	
366 371 376 381	
ttt gtg tgt gta gaa agc ctg gtg aca gcg ctg gtg gac atg tac cct	1321
Phe Val Cys Val Glu Ser Leu Val Thr Ala Leu Val Asp Met Tyr Pro	
382 387 392 397	
cac gtg ttc cgc aag aag aac cgg agg gaa gtc ctc atc ctt gga gta	1369
His Val Phe Arg Lys Lys Asn Arg Arg Glu Val Leu Ile Leu Gly Val	
398 403 408 413	
tct gtc gtc tcc ttc cct gtg ggg ctg atc atg ctc aca gag ggc gga	1417
Ser Val Val Ser Phe Pro Val Gly Leu Ile Met Leu Thr Glu Gly Gly	
414 419 424 429	
atg tac gtg ttc cag ctc ttt gac tac tat gcg gcc agt ggc atg tgc	1465
Met Tyr Val Phe Gln Leu Phe Asp Tyr Tyr Ala Ala Ser Gly Met Cys	
430 435 440 445	
ctc ctg ttc gtg gcc atc ttc gag tcc ctc tgt gtg gct tgg gtt tac	1513
Leu Leu Phe Val Ala Ile Phe Glu Ser Leu Cys Val Ala Trp Val Tyr	
446 451 456 461	
gga gcc aag cgc ttc tac gac aac atc gaa gac atg att ggg tac agg	1561

Gly	Ala	Lys	Arg	Phe	Tyr	Asp	Asn	Ile	Glu	Asp	Met	Ile	Gly	Tyr	Arg	
462					467					472					477	
cca	tgg	cct	ctt	atc	aaa	tac	tgt	tgg	ctc	ttc	ctc	aca	cca	gct	gtg	1609
Pro	Trp	Pro	Leu	Ile	Lys	Tyr	Cys	Trp	Leu	Phe	Leu	Thr	Pro	Ala	Val	
478					483					488					493	
tgc	aca	gcc	acc	ttt	ctc	ttc	tcc	ctg	ata	aag	tac	act	ccg	ctg	acc	1657
Cys	Thr	Ala	Thr	Phe	Leu	Phe	Ser	Leu	Ile	Lys	Tyr	Thr	Pro	Leu	Thr	
494					499					504					509	
tac	aac	aag	aag	tac	acg	tac	ccg	tgg	tgg	ggc	gat	gcc	ctg	ggc	tgg	1705
Tyr	Asn	Lys	Lys	Tyr	Thr	Tyr	Pro	Trp	Trp	Gly	Asp	Ala	Leu	Gly	Trp	
510					515					520					525	
ctc	ctg	gct	ctg	tcc	tcc	tgg	tct	gca	ttc	ctg	cct	gga	gcc	tct	aca	1753
Leu	Leu	Ala	Leu	Ser	Ser	Trp	Ser	Ala	Phe	Leu	Pro	Gly	Ala	Ser	Thr	
526					531					536					541	
gac	tcg	gaa	ccc	tca	agg	gcc	cct	tca	gag	aga	gaa	tcc	gtc	agc	tca	1801
Asp	Ser	Glu	Pro	Ser	Arg	Ala	Pro	Ser	Glu	Arg	Glu	Ser	Val	Ser	Ser	
542					547					552					557	
tgt	gcc	cag	ccg	agg	acc	tgc	ccc	agc	gga	acc	cag	cag	gac	cct	cgg	1849
Cys	Ala	Gln	Pro	Arg	Thr	Cys	Pro	Ser	Gly	Thr	Gln	Gln	Asp	Pro	Arg	
558					563					568					573	
ctc	ccg	cca	ccc	cca	gga	cct	cac	tgc	tca	gac	tca	cag	agc	tag	agt	1897
Leu	Pro	Pro	Pro	Pro	Gly	Pro	His	Cys	Ser	Asp	Ser	Gln	Ser	*		
574					579					584						
ctcactgcta	gggggcaggc	ccttgatgg	tgcctgtgtg	cctggccttg	gggatggctg											1957
tggaggggaac	gtggcagaag	cagcccatg	tgttccctgc	ccccgacctg	gagtggataa											2017
gacaagaggg	gtatttttga	gtccacctgc	tgagctggag	gcctcccact	gcaacttttc											2077
agctcagggg	ttgttgaaca	gatgtgaaaa	ggccagtgcc	aagagtgtcc	ctcggagacc											2137
cttgaaggc																2146

<210> 78
 <211> 930
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (39) .. (593)

<400> 78																
gaaagcctgc	cagcacctat	tccacctccc	agcccagc													
				atg	gca	ccc	ctg	ctg								53
				Met	Ala	Pro	Leu	Leu								

ccc atc cgg acc ttg ccc ttg atc ctg att ctg ctg gct ctg ctg tcc	101
Pro Ile Arg Thr Leu Pro Leu Ile Leu Ile Leu Leu Ala Leu Leu Ser	
6 11 16 21	
cca ggg gct gca gac ttc aac atc tca agc ctc tct ggt ctg ctg tcc	149
Pro Gly Ala Ala Asp Phe Asn Ile Ser Ser Leu Ser Gly Leu Leu Ser	
22 27 32 37	
ccg gcg cta acg gag agc ctg ctg gtt gcc ttg ccc ccc tgt cac ctc	197
Pro Ala Leu Thr Glu Ser Leu Leu Val Ala Leu Pro Pro Cys His Leu	
38 43 48 53	
aca gga ggc aat gcc aca ctg atg gtc cgg aga gcc aat gac agc aaa	245
Thr Gly Gly Asn Ala Thr Leu Met Val Arg Arg Ala Asn Asp Ser Lys	
54 59 64 69	
gtg gtg acg tcc agc ttt gtg gtg cct ccg tgc cgt ggg cgc agg gaa	293
Val Val Thr Ser Ser Phe Val Val Pro Pro Cys Arg Gly Arg Arg Glu	
70 75 80 85	
ctg gtg agt gtg gtg gac agt ggt gct ggc ttc aca gtc act cgg ctc	341
Leu Val Ser Val Val Asp Ser Gly Ala Gly Phe Thr Val Thr Arg Leu	
86 91 96 101	
agt gca tac cag gtg aca aac ctc gtg cca gga acc aaa ttc tac att	389
Ser Ala Tyr Gln Val Thr Asn Leu Val Pro Gly Thr Lys Phe Tyr Ile	
102 107 112 117	
tcc tac cta gtg aag aag ggg aca gcc act gag tcc agc aga gag atc	437
Ser Tyr Leu Val Lys Lys Gly Thr Ala Thr Glu Ser Ser Arg Glu Ile	
118 123 128 133	
cca atg tcc aca ctc cct cga agg aac atg gaa tcc att ggg ctg ggt	485
Pro Met Ser Thr Leu Pro Arg Arg Asn Met Glu Ser Ile Gly Leu Gly	
134 139 144 149	
atg gcc cgc aca ggg ggc atg gtg gtc atc acg gtg ctg ctc tct gtc	533
Met Ala Arg Thr Gly Gly Met Val Val Ile Thr Val Leu Leu Ser Val	
150 155 160 165	
gcc atg ttc ctg ctg gtg ctg ggc ttc atc att gcc ctg gca ctg ggc	581
Ala Met Phe Leu Leu Val Leu Gly Phe Ile Ile Ala Leu Ala Leu Gly	
166 171 176 181	
tcc cgc aag taa gga ggtctgcccc gagcagcagc ttctccagga agcccagggc	636
Ser Arg Lys *	
182	
accatccagc tccccagccc acctgtctccc aggccccagg cctgtggctc ccttggtgcc	696
ctgcctcct cctcctgccc tctctctccc tagagccctc tctccctct gtccctctcc	756
ttgccccag tgcctcacct tccaacactc cattattcct ctaccccac tctgtcaga	816
gttgactttc ctcccatttt accactttaa acacccccat aacaattccc ccatacttca	876

gtgaactaag tccctataat aaaggctgag gctgcatctg ccaaaaaaaaa aaaa

930

<210> 79
<211> 2153
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (68)..(1645)

<400> 79

tgaaaaaaatt tgaaagcggtt ggcggcgctg taccgggtccg gaattcccgg gtcgacccac 60

gcgtccg atg gcg gct gtg gtg ctg gcg gcg acg cgg ttg ctg cgg ggc 109
Met Ala Ala Val Val Leu Ala Ala Thr Arg Leu Leu Arg Gly
1 5 10

tcg ggt tct tgg ggc tgt tcg cgg ctg agg ttt gga cct cct gcg tat 157
Ser Gly Ser Trp Gly Cys Ser Arg Leu Arg Phe Gly Pro Pro Ala Tyr
15 20 25 30

aga cgg ttt agt agt ggt ggt gcc tat ccc aac atc ccc ctc tct tct 205
Arg Arg Phe Ser Ser Gly Gly Ala Tyr Pro Asn Ile Pro Leu Ser Ser
31 36 41 46

ccc tta cct gga gta ccc aag cct gtt ttt gct aca gtt gat gga cag 253
Pro Leu Pro Gly Val Pro Lys Pro Val Phe Ala Thr Val Asp Gly Gln
47 52 57 62

gaa aag ttt gaa acc aaa gta acc aca ttg gat aat ggg ctt cgc gtg 301
Glu Lys Phe Glu Thr Lys Val Thr Thr Leu Asp Asn Gly Leu Arg Val
63 68 73 78

gca tct cag aat aag ttt gga cag ttt tgt aca gta gga att ctt atc 349
Ala Ser Gln Asn Lys Phe Gly Gln Phe Cys Thr Val Gly Ile Leu Ile
79 84 89 94

aat tca gga tcg aga tat gaa gcg aaa tac ctt agt gga att gct cac 397
Asn Ser Gly Ser Arg Tyr Glu Ala Lys Tyr Leu Ser Gly Ile Ala His
95 100 105 110

ttt ttg gaa aaa ttg gca ttt tcg tct act gct cga ttt gac agc aaa 445
Phe Leu Glu Lys Leu Ala Phe Ser Ser Thr Ala Arg Phe Asp Ser Lys
111 116 121 126

gat gaa att ctg ctt acg ttg gaa aag cat ggg ggt atc tgt gac tgc 493
Asp Glu Ile Leu Leu Thr Leu Glu Lys His Gly Gly Ile Cys Asp Cys
127 132 137 142

cag aca tca aga gac acc acc atg tat gct gtg tct gct gat agc aaa 541
Gln Thr Ser Arg Asp Thr Thr Met Tyr Ala Val Ser Ala Asp Ser Lys
143 148 153 158

ggc ttg gac acg gtg gtt gcc tta ctg gct gat gtg gtt ctg cag ccc Gly Leu Asp Thr Val Val Ala Leu Leu Ala Asp Val Val Leu Gln Pro 159 164 169 174	589
cgg cta aca gat gaa gaa gtc gag atg acg cgg atg gcg gtc cag ttt Arg Leu Thr Asp Glu Glu Val Glu Met Thr Arg Met Ala Val Gln Phe 175 180 185 190	637
gag ctg gag gac ctg aac ctg cgg cct gac cca gag cca ctt ctc acc Glu Leu Glu Asp Leu Asn Leu Arg Pro Asp Pro Glu Pro Leu Leu Thr 191 196 201 206	685
gag atg att cat gaa gcg gct tac agg gag aac aca gtt ggc ctc cac Glu Met Ile His Glu Ala Ala Tyr Arg Glu Asn Thr Val Gly Leu His 207 212 217 222	733
cgt ttc tgc ccc aca gaa aac gta gca aag atc aat cga gag gtg ctg Arg Phe Cys Pro Thr Glu Asn Val Ala Lys Ile Asn Arg Glu Val Leu 223 228 233 238	781
cat tcc tac ctg agg aac tac tac act ccc gac cgc atg gtg ctg gcc His Ser Tyr Leu Arg Asn Tyr Tyr Thr Pro Asp Arg Met Val Leu Ala 239 244 249 254	829
ggc gtg ggc gtg gag cac gag cat ctg gtg gac tgt gcc cgg aag tac Gly Val Gly Val Glu His Glu His Leu Val Asp Cys Ala Arg Lys Tyr 255 260 265 270	877
ctc ctg ggg gtc cag ccg gcc tgg ggg agc gca gag gcc gtg gat att Leu Leu Gly Val Gln Pro Ala Trp Gly Ser Ala Glu Ala Val Asp Ile 271 276 281 286	925
gac aga tct gtg gcc cag tac act ggg ggg att gcc aag cta gaa aga Asp Arg Ser Val Ala Gln Tyr Thr Gly Gly Ile Ala Lys Leu Glu Arg 287 292 297 302	973
gac atg tcc aat gtc agc ctg ggc ccg acc ccc atc ccc gag ctc acg Asp Met Ser Asn Val Ser Leu Gly Pro Thr Pro Ile Pro Glu Leu Thr 303 308 313 318	1021
cac atc atg gtt gga ctg gag agc tgc tcc ttc ctg gag gag gac ttc His Ile Met Val Gly Leu Glu Ser Cys Ser Phe Leu Glu Glu Asp Phe 319 324 329 334	1069
atc ccc ttt gca gtg ttg aac atg atg atg ggc gga ggt ggc tcc ttc Ile Pro Phe Ala Val Leu Asn Met Met Met Gly Gly Gly Gly Ser Phe 335 340 345 350	1117
tcg gct ggt ggg ccc ggc aag ggc atg ttc tcc agg ctc tac ctc aac Ser Ala Gly Gly Pro Gly Lys Gly Met Phe Ser Arg Leu Tyr Leu Asn 351 356 361 366	1165
gtg ctc aac agg cac cac tgg atg tat aac gcg acc tcc tac cac cac Val Leu Asn Arg His His Trp Met Tyr Asn Ala Thr Ser Tyr His His 367 372 377 382	1213
agc tac gag gac act ggc ctc ctt tgc atc cat gcc agc gcc gac cca	1261

Ser Tyr Glu Asp Thr Gly Leu Leu Cys Ile His Ala Ser Ala Asp Pro	
383 388 393 398	
aga cag gtt cga gaa atg gta gaa atc atc aca aag gag ttt att tta	1309
Arg Gln Val Arg Glu Met Val Glu Ile Ile Thr Lys Glu Phe Ile Leu	
399 404 409 414	
atg ggc gga acc gtg gac acg gtg gag ctg gaa cga gcc aag acg cag	1357
Met Gly Gly Thr Val Asp Thr Val Glu Leu Glu Arg Ala Lys Thr Gln	
415 420 425 430	
ctg aca tca atg ctc atg atg aac ctg gaa tcc agg cct gtg atc ttc	1405
Leu Thr Ser Met Leu Met Met Asn Leu Glu Ser Arg Pro Val Ile Phe	
431 436 441 446	
gag gat gtg ggg agg cag gtg ctg gcc act cgc tcc aga aag ctg ccg	1453
Glu Asp Val Gly Arg Gln Val Leu Ala Thr Arg Ser Arg Lys Leu Pro	
447 452 457 462	
cac gag ctg tgc acg ctc atc cgc aac gtg aag ccg gaa gat gtg aag	1501
His Glu Leu Cys Thr Leu Ile Arg Asn Val Lys Pro Glu Asp Val Lys	
463 468 473 478	
aga gtc gct tct aag atg ctc cga ggg aag ccg gca gtg gcc gcc ctg	1549
Arg Val Ala Ser Lys Met Leu Arg Gly Lys Pro Ala Val Ala Ala Leu	
479 484 489 494	
ggt gac ctg act gac ctg ccc acg tat gag cac atc cag acc gcc ctg	1597
Gly Asp Leu Thr Asp Leu Pro Thr Tyr Glu His Ile Gln Thr Ala Leu	
495 500 505 510	
tcg agt aag gac ggg cgc ctg ccc agg acg tac cgg ctc ttc cgg tag	1645
Ser Ser Lys Asp Gly Arg Leu Pro Arg Thr Tyr Arg Leu Phe Arg *	
511 516 521 526	
aaccgctccc cggcctgaca gacccagggga gctgcagctg gagcccgttc ccgtgctgtg	1705
tagtttggac acgaatttag tctaaaaagc tgtctggttg tataaacggt gcaaacaatg	1765
tcgccacagc acccacgcgg tttgcattct tttggaactc aatgtgccga tcagtggagt	1825
cagtatcgag cctgaccacc gcaagccagg aagcaggtga agtgcccagc gctggagtgc	1885
agcgtgccac gaggagggcg gtcggtgctt ccctcctcgg gctgtgggca catggggccc	1945
cgcaggttcc ttggaggagc cctgagctgg gaggcagcaa aggctgacct atcaaagcct	2005
cccggaggcc accgtgctgg gtaccaggac tcacctctga caagcaggag aaggtaaggg	2065
cccggtcagc tccaaggagc gcgctccacg cgcgtgcaca cagcttcctt ggtaataaag	2125
agctggcatc tttcttaaaa aaaaaaaaa	2153

<211> 4455
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(4080)

<400> 80

atg gcg gag gcc ggc ctg agg ggc tgg ctg ctg tgg gcc ctg ctc ctg	48
Met Ala Glu Ala Gly Leu Arg Gly Trp Leu Leu Trp Ala Leu Leu Leu	
1 5 10	
cgc ttg gcc cag agt gag cct tac aca acc atc cac cag cct ggc tac	96
Arg Leu Ala Gln Ser Glu Pro Tyr Thr Thr Ile His Gln Pro Gly Tyr	
17 22 27 32	
tgc gcc ttc tat gac gaa tgt ggg aag aac cca gag ctg tct gga agc	144
Cys Ala Phe Tyr Asp Glu Cys Gly Lys Asn Pro Glu Leu Ser Gly Ser	
33 38 43 48	
ctc atg aca ctc tcc aac gtg tcc tgc ctg tcc aac acg ccg gcc cgc	192
Leu Met Thr Leu Ser Asn Val Ser Cys Leu Ser Asn Thr Pro Ala Arg	
49 54 59 64	
aag atc aca ggt gat cac ctg atc cta tta cag aag atc tgc ccc cgc	240
Lys Ile Thr Gly Asp His Leu Ile Leu Leu Gln Lys Ile Cys Pro Arg	
65 70 75 80	
ctc tac acc ggc ccc aac acc caa gcc tgc tgc tcc gcc aag cag ctg	288
Leu Tyr Thr Gly Pro Asn Thr Gln Ala Cys Cys Ser Ala Lys Gln Leu	
81 86 91 96	
gta tca ctg gaa gcg agt ctg tcg atc acc aag gcc ctc ctc acc cgc	336
Val Ser Leu Glu Ala Ser Leu Ser Ile Thr Lys Ala Leu Leu Thr Arg	
97 102 107 112	
tgc cca gcc tgc tct gac aat ttt gtg aac ctg cac tgc cac aac acg	384
Cys Pro Ala Cys Ser Asp Asn Phe Val Asn Leu His Cys His Asn Thr	
113 118 123 128	
tgc agc ccc aat cag agc ctc ttc atc aat gtg acc cgc gtg gcc cag	432
Cys Ser Pro Asn Gln Ser Leu Phe Ile Asn Val Thr Arg Val Ala Gln	
129 134 139 144	
cta ggg gct gga caa ctc cca gct gtg gtg gcc tat gag gcc ttc tac	480
Leu Gly Ala Gly Gln Leu Pro Ala Val Val Ala Tyr Glu Ala Phe Tyr	
145 150 155 160	
cag cat agc ttt gcc gag cag agc tat gac tcc tgc agc cgt gtg cgc	528
Gln His Ser Phe Ala Glu Gln Ser Tyr Asp Ser Cys Ser Arg Val Arg	
161 166 171 176	
gtc cct gca gct gcc acg ctg gct gtg ggc acc atg tgt ggc gtg tat	576
Val Pro Ala Ala Ala Thr Leu Ala Val Gly Thr Met Cys Gly Val Tyr	
177 182 187 192	

ggc Gly 193	tct Ser	gcc Ala	ctt Leu	tgc Cys	aat Asn 198	gcc Ala	cag Gln	cgc Arg	tgg Trp	ctc Leu 203	aac Asn	ttc Phe	cag Gln	gga Gly	gac Asp 208	624
aca Thr 209	ggc Gly	aat Asn	ggt Gly	ctg Leu	gcc Ala 214	cca Pro	ctg Leu	gac Asp	atc Ile	acc Thr 219	ttc Phe	cac His	ctc Leu	ttg Leu	gag Glu 224	672
cct Pro 225	ggc Gly	cag Gln	gcc Ala	gtg Val	ggg Gly 230	agt Ser	ggg Gly	att Ile	cag Gln	cct Pro 235	ctg Leu	aat Asn	gag Glu	ggg Gly	gtt Val 240	720
gca Ala 241	cgt Arg	tgc Cys	aat Asn	gag Glu	tcc Ser 246	caa Gln	ggt Gly	gac Asp	gac Asp	gtg Val 251	gcg Ala	acc Thr	tgc Cys	tcc Ser	tgc Cys 256	768
caa Gln 257	gac Asp	tgt Cys	gct Ala	gca Ala	tcc Ser 262	tgt Cys	cct Pro	gcc Ala	ata Ile	gcc Ala 267	cgc Arg	ccc Pro	cag Gln	gcc Ala	ctc Leu 272	816
gac Asp 273	tcc Ser	acc Thr	ttc Phe	tac Tyr	ctg Leu 278	ggc Gly	cag Gln	atg Met	cgc Pro	ggc Gly 283	agt Ser	ctg Leu	gtc Val	ctc Leu	atc Ile 288	864
atc Ile 289	atc Ile	ctc Leu	tgc Cys	tct Ser	gtc Val 294	ttc Phe	gct Ala	gtg Val	gtc Val	acc Thr 299	atc Ile	ctg Leu	ctt Leu	gtg Val	gga Gly 304	912
ttc Phe 305	cgt Arg	gtg Val	gcc Ala	ccc Pro	gcc Ala 310	agg Arg	gac Asp	aaa Lys	agc Ser	aag Lys 315	atg Met	gtg Val	gac Asp	ccc Pro	aag Lys 320	960
aag Lys 321	ggc Gly	acc Thr	agc Ser	ctc Leu	tct Ser 326	gac Asp	aag Lys	ctc Leu	agc Ser	ttc Phe 331	tcc Ser	acc Thr	cac His	acc Thr	ctc Leu 336	1008
ctt Leu 337	ggc Gly	cag Gln	ttc Phe	ttc Phe	cag Gln 342	ggc Gly	tgg Trp	ggc Gly	acg Thr	tgg Trp 347	gtg Val	gct Ala	tgc Ser	tgg Trp	cct Pro 352	1056
ctg Leu 353	acc Thr	atc Ile	ttg Leu	gtg Val	cta Leu 358	tct Ser	gtc Val	atc Ile	ccg Pro	gtg Val 363	gtg Val	gcc Ala	ttg Leu	gca Ala	gcg Ala 368	1104
ggc Gly 369	ctg Leu	gtc Val	ttt Phe	aca Thr	gaa Glu 374	ctc Leu	act Thr	acg Thr	gac Asp	ccc Pro 379	gtg Val	gag Glu	ctg Leu	tgg Trp	tgc Ser 384	1152
gcc Ala 385	ccc Pro	aac Asn	agc Ser	caa Gln	gcc Ala 390	cgg Arg	agt Ser	gag Glu	aaa Lys	gct Ala 395	ttc Phe	cat His	gac Asp	cag Gln	cat His 400	1200
ttc Phe 401	ggc Gly	ccc Pro	ttc Phe	ttc Phe	cga Arg 406	acc Thr	aac Asn	cag Gln	gtg Val	atc Ile 411	ctg Leu	acg Thr	gct Ala	cct Pro	aac Asn 416	1248
cgg	tcc	agc	tac	agg	tat	gac	tct	ctg	ctg	ctg	ggg	ccc	aag	aac	ttc	1296

Arg 417	Ser	Ser	Tyr	Arg	Tyr 422	Asp	Ser	Leu	Leu	Leu 427	Gly	Pro	Lys	Asn	Phe 432	
agc 433	gga	atc	ctg	gac	ctg	gac	ttg	ctg	ctg	gag	ctg	cta	gag	ctg	cag	1344
Ser	Gly	Ile	Leu	Asp	Leu	Asp	Leu	Leu	Leu	Glu	Leu	Leu	Glu	Leu	Gln	
					438					443					448	
gag 449	agg	ctg	cgg	cac	ctc	cag	gta	tgg	tcg	ccc	gaa	gca	cag	cgc	aac	1392
Glu	Arg	Leu	Arg	His	Leu	Gln	Val	Trp	Ser	Pro	Glu	Ala	Gln	Arg	Asn	
					454					459					464	
atc 465	tcc	ctg	cag	gac	atc	tgc	tac	gcc	ccc	ctc	aat	ccg	gac	aat	acc	1440
Ile	Ser	Leu	Gln	Asp	Ile	Cys	Tyr	Ala	Pro	Leu	Asn	Pro	Asp	Asn	Thr	
					470					475					480	
agt 481	ctc	tac	gac	tgc	tgc	atc	aac	agc	ctc	ctg	cag	tat	ttc	cag	aac	1488
Ser	Leu	Tyr	Asp	Cys	Cys	Ile	Asn	Ser	Leu	Leu	Gln	Tyr	Phe	Gln	Asn	
					486					491					496	
aac 497	cgc	acg	ctc	ctg	ctg	ctc	aca	gcc	aac	cag	aca	ctg	atg	ggg	cag	1536
Asn	Arg	Thr	Leu	Leu	Leu	Leu	Thr	Ala	Asn	Gln	Thr	Leu	Met	Gly	Gln	
					502					507					512	
acc 513	tcc	caa	gtc	gac	tgg	aag	gac	cat	ttt	ctg	tac	tgt	gcc	aat	gcc	1584
Thr	Ser	Gln	Val	Asp	Trp	Lys	Asp	His	Phe	Leu	Tyr	Cys	Ala	Asn	Ala	
					518					523					528	
ccg 529	ctc	acc	ttc	aag	gat	ggc	aca	gcc	ctg	gcc	ctg	agc	tgc	atg	gct	1632
Pro	Leu	Thr	Phe	Lys	Asp	Gly	Thr	Ala	Leu	Ala	Leu	Ser	Cys	Met	Ala	
					534					539					544	
gac 545	tac	ggg	gcc	cct	gtc	ttc	ccc	ttc	ctt	gcc	att	ggg	ggg	tac	aaa	1680
Asp	Tyr	Gly	Ala	Pro	Val	Phe	Pro	Phe	Leu	Ala	Ile	Gly	Gly	Tyr	Lys	
					550					555					560	
gga 561	aag	gac	tat	tct	gag	gca	gag	gcc	ctg	atc	atg	acg	ttc	tcc	ctc	1728
Gly	Lys	Asp	Tyr	Ser	Glu	Ala	Glu	Ala	Leu	Ile	Met	Thr	Phe	Ser	Leu	
					566					571					576	
aac 577	aat	tac	cct	gcc	ggg	gac	ccc	cgt	ctg	gcc	cag	gcc	aag	ctg	tgg	1776
Asn	Asn	Tyr	Pro	Ala	Gly	Asp	Pro	Arg	Leu	Ala	Gln	Ala	Lys	Leu	Trp	
					582					587					592	
gag 593	gag	gcc	ttc	tta	gag	gaa	atg	cga	gcc	ttc	cag	cgt	cgg	atg	gct	1824
Glu	Glu	Ala	Phe	Leu	Glu	Glu	Met	Arg	Ala	Phe	Gln	Arg	Arg	Met	Ala	
					598					603					608	
ggc 609	atg	ttc	cag	gtc	acg	ttc	atg	gct	gag	cgc	tct	ctg	gaa	gac	gag	1872
Gly	Met	Phe	Gln	Val	Thr	Phe	Met	Ala	Glu	Arg	Ser	Leu	Glu	Asp	Glu	
					614					619					624	
atc 625	aat	cgc	acc	aca	gct	gaa	gac	ctg	ccc	atc	ttt	gcc	acc	agc	tac	1920
Ile	Asn	Arg	Thr	Thr	Ala	Glu	Asp	Leu	Pro	Ile	Phe	Ala	Thr	Ser	Tyr	
					630					635					640	
att 640	gtc	ata	ttc	ctg	tac	atc	tct	ctg	gcc	ctg	ggc	agc	tat	tcc	agc	1968
Ile	Val	Ile	Phe	Leu	Tyr	Ile	Ser	Leu	Ala	Leu	Gly	Ser	Tyr	Ser	Ser	

641	646	651	656	
tgg agc cga gtg atg	gtg gac tcc aag gcc	acg ctg ggc ctc ggc ggg	2016	
Trp Ser Arg Val Met	Val Asp Ser Lys Ala	Thr Leu Gly Leu Gly Gly		
657	662	667	672	
gtg gcc gtg gtc ctg	gga gca gtc atg gct	gcc atg ggc ttc ttc tcc	2064	
Val Ala Val Val Leu	Gly Ala Val Met Ala	Ala Met Gly Phe Phe Ser		
673	678	683	688	
tac ttg ggt atc cgc	tcc tcc ctg gtc atc	ctg caa gtg gtt cct ttc	2112	
Tyr Leu Gly Ile Arg	Ser Ser Leu Val Ile	Leu Gln Val Val Pro Phe		
689	694	699	704	
ctg gtg ctg tcc gtg	ggg gct gat aac atc	ttc atc ttt gtt ctc gag	2160	
Leu Val Leu Ser Val	Gly Ala Asp Asn Ile	Phe Ile Phe Val Leu Glu		
705	710	715	720	
tac cag agg ctg ccc	cgg agg cct ggg gag	cca cga gag gtc cac att	2208	
Tyr Gln Arg Leu Pro	Arg Arg Pro Gly Glu	Pro Arg Glu Val His Ile		
721	726	731	736	
ggg cga gcc cta ggc	agg gtg gct ccc agc	atg ctg ttg tgc agc ctc	2256	
Gly Arg Ala Leu Gly	Arg Val Ala Pro Ser	Met Leu Leu Cys Ser Leu		
737	742	747	752	
tct gag gcc atc tgc	ttc ttc cta ggg gcc	ctg acc ccc atg cca gct	2304	
Ser Glu Ala Ile Cys	Phe Phe Leu Gly Ala	Leu Thr Pro Met Pro Ala		
753	758	763	768	
gtg cgg acc ttt gcc	ctg acc tct ggc ctt	gca gtg atc ctt gac ttc	2352	
Val Arg Thr Phe Ala	Leu Thr Ser Gly Leu	Ala Val Ile Leu Asp Phe		
769	774	779	784	
ctc ctg cag atg tca	gcc ttt gtg gcc ctg	ctc tcc ctg gac agc aag	2400	
Leu Leu Gln Met Ser	Ala Phe Val Ala Leu	Leu Ser Leu Asp Ser Lys		
785	790	795	800	
agg cag gag gcc tcc	cgg ttg gac gtc tgc	tgc tgt gtc aag ccc cag	2448	
Arg Gln Glu Ala Ser	Arg Leu Asp Val Cys	Cys Cys Val Lys Pro Gln		
801	806	811	816	
gag ctg ccc ccg cct	ggc cag gga gag ggg	ctc ctg ctt ggc ttc ttc	2496	
Glu Leu Pro Pro Pro	Gly Gln Gly Glu Gly	Leu Leu Leu Gly Phe Phe		
817	822	827	832	
caa aag gct tat gcc	ccc ttc ctg ctg cac	tgg atc act cga ggt gtt	2544	
Gln Lys Ala Tyr Ala	Pro Phe Leu Leu His	Trp Ile Thr Arg Gly Val		
833	838	843	848	
gtg ctg ctg ctg ttt	ctc gcc ctg ttc gga	gtg agc ctc tac tcc atg	2592	
Val Leu Leu Leu Phe	Leu Ala Leu Phe Gly	Val Ser Leu Tyr Ser Met		
849	854	859	864	
tgc cac atc agc gtg	gga ctg gac cag gag	ctg gcc ctg ccc aag gac	2640	
Cys His Ile Ser Val	Gly Leu Asp Gln Glu	Leu Ala Leu Pro Lys Asp		
865	870	875	880	

tcg tac ctg ctt gac tat ttc ctc ttt ctg aac cgc tac ttc gag gtg Ser Tyr Leu Leu Asp Tyr Phe Leu Phe Leu Asn Arg Tyr Phe Glu Val 881 886 891 896	2688
ggg gcc ccg gtg tac ttt gtt acc acc ttg ggc tac aac ttc tcc agc Gly Ala Pro Val Tyr Phe Val Thr Thr Leu Gly Tyr Asn Phe Ser Ser 897 902 907 912	2736
gag gct ggg atg aat gcc atc tgc tcc agt gca ggc tgc aac aac ttc Glu Ala Gly Met Asn Ala Ile Cys Ser Ser Ala Gly Cys Asn Asn Phe 913 918 923 928	2784
tcc ttc acc cag aag atc cag tat gcc aca gag ttc cct gag cag tct Ser Phe Thr Gln Lys Ile Gln Tyr Ala Thr Glu Phe Pro Glu Gln Ser 929 934 939 944	2832
tac ctg gcc atc cct gcc tcc tcc tgg gtg gat gac ttc att gac tgg Tyr Leu Ala Ile Pro Ala Ser Ser Trp Val Asp Asp Phe Ile Asp Trp 945 950 955 960	2880
ctg acc ccg tcc tcc tgc tgc cgc ctt tat ata tct ggc ccc aat aag Leu Thr Pro Ser Ser Cys Cys Arg Leu Tyr Ile Ser Gly Pro Asn Lys 961 966 971 976	2928
gac aag ttc tgc ccc tcg acc gtc aac tct ctg aac tgc cta aag aac Asp Lys Phe Cys Pro Ser Thr Val Asn Ser Leu Asn Cys Leu Lys Asn 977 982 987 992	2976
tgc atg agc atc acg atg ggc tct gtg agg ccc tcg gtg gag cag ttc Cys Met Ser Ile Thr Met Gly Ser Val Arg Pro Ser Val Glu Gln Phe 993 998 1003 1008	3024
cat aag tat ctt ccc tgg ttc ctg aac gac cgg ccc aac atc aaa tgt His Lys Tyr Leu Pro Trp Phe Leu Asn Asp Arg Pro Asn Ile Lys Cys 1009 1014 1019 1024	3072
ccc aaa ggc ggc ctg gca gca tac agc acc tct gtg aac ttg act tca Pro Lys Gly Gly Leu Ala Ala Tyr Ser Thr Ser Val Asn Leu Thr Ser 1025 1030 1035 1040	3120
gat ggc cag gtt tta gac aca gtt gcc att ctg tca ccc agg ctg gag Asp Gly Gln Val Leu Asp Thr Val Ala Ile Leu Ser Pro Arg Leu Glu 1041 1046 1051 1056	3168
tac agt ggc aca atc tcg gct cac tgc aac ctc tac ctc ctg gat tca Tyr Ser Gly Thr Ile Ser Ala His Cys Asn Leu Tyr Leu Leu Asp Ser 1057 1062 1067 1072	3216
gcc tcc agg ttc atg gcc tat cac aag ccc ctg aaa aac tca cag gat Ala Ser Arg Phe Met Ala Tyr His Lys Pro Leu Lys Asn Ser Gln Asp 1073 1078 1083 1088	3264
tac aca gaa gct ctg cgg gca gct cga gag ctg gca gcc aac atc act Tyr Thr Glu Ala Leu Arg Ala Ala Arg Glu Leu Ala Ala Asn Ile Thr 1089 1094 1099 1104	3312

gct gac ctg cgg aaa gtg cct gga aca gac ccg gct ttt gag gtc ttc	3360
Ala Asp Leu Arg Lys Val Pro Gly Thr Asp Pro Ala Phe Glu Val Phe	
1105 1110 1115 1120	
ccc tac acg atc acc aat gtg ttt tat gag cag tac ctg acc atc ctc	3408
Pro Tyr Thr Ile Thr Asn Val Phe Tyr Glu Gln Tyr Leu Thr Ile Leu	
1121 1126 1131 1136	
cct gag ggg ctc ttc atg ctc agc ctc tgc ctt gtg ccc acc ttc gct	3456
Pro Glu Gly Leu Phe Met Leu Ser Leu Cys Leu Val Pro Thr Phe Ala	
1137 1142 1147 1152	
gtc tcc tgc ctc ctg ctg ggc ctg gac ctg cgc tcc ggc ctc ctc aac	3504
Val Ser Cys Leu Leu Leu Gly Leu Asp Leu Arg Ser Gly Leu Leu Asn	
1153 1158 1163 1168	
ctg ctc tcc att gtc atg atc ctc gtg gac act gtc ggc ttc atg gcc	3552
Leu Leu Ser Ile Val Met Ile Leu Val Asp Thr Val Gly Phe Met Ala	
1169 1174 1179 1184	
ctg tgg ggc atc agt tac aat gct gtg tcc ctc atc aac ctg gtc tcg	3600
Leu Trp Gly Ile Ser Tyr Asn Ala Val Ser Leu Ile Asn Leu Val Ser	
1185 1190 1195 1200	
gcg gtg ggc atg tct gtg gag ttt gtg tcc cac att acc cgc tcc ttt	3648
Ala Val Gly Met Ser Val Glu Phe Val Ser His Ile Thr Arg Ser Phe	
1201 1206 1211 1216	
gcc atc agc acc aag ccc acc tgg ctg gag agg gcc aaa gag gcc acc	3696
Ala Ile Ser Thr Lys Pro Thr Trp Leu Glu Arg Ala Lys Glu Ala Thr	
1217 1222 1227 1232	
atc tct atg gga agt gcg gtg ttt gca ggt gtg gcc atg acc aac ctg	3744
Ile Ser Met Gly Ser Ala Val Phe Ala Gly Val Ala Met Thr Asn Leu	
1233 1238 1243 1248	
cct ggc atc ctt gtc ctg ggc ctc gcc aag gcc cag ctc att cag atc	3792
Pro Gly Ile Leu Val Leu Gly Leu Ala Lys Ala Gln Leu Ile Gln Ile	
1249 1254 1259 1264	
ttc ttc ttc cgc ctc aac ctc ctg atc act ctg ctg ggc ctg ctg cat	3840
Phe Phe Phe Arg Leu Asn Leu Leu Ile Thr Leu Leu Gly Leu Leu His	
1265 1270 1275 1280	
ggc ttg gtc ttc ctg ccc gtc atc ctc agc tac gtg ggg cct gac gtt	3888
Gly Leu Val Phe Leu Pro Val Ile Leu Ser Tyr Val Gly Pro Asp Val	
1281 1286 1291 1296	
aac ccg gct ctg gca ctg gag cag aag cgg gct gag gag gcg gtg gca	3936
Asn Pro Ala Leu Ala Leu Glu Gln Lys Arg Ala Glu Glu Ala Val Ala	
1297 1302 1307 1312	
gca gtc atg gtg gcc tct tgc cca aat cac ccc tcc cga gtc tcc aca	3984
Ala Val Met Val Ala Ser Cys Pro Asn His Pro Ser Arg Val Ser Thr	
1313 1318 1323 1328	
gct gac aac atc tat gtc aac cac agc ttt gaa ggt tct atc aaa ggt	4032

Ala Asp Asn Ile Tyr Val Asn His Ser Phe Glu Gly Ser Ile Lys Gly
 1329 1334 1339 1344

gct ggt gcc atc agc aac ttc ttg ccc aac aat ggg cgg cag ttc tga 4080
 Ala Gly Ala Ile Ser Asn Phe Leu Pro Asn Asn Gly Arg Gln Phe *
 1345 1350 1355 1360

tacagccaga ggccctgtct aggctctatg gccctgaacc aaagggttat ggggatcttc 4140
 cttgtgactg ccccttgaca cagccctcc tcaaactcta ggggaggcca ttcccatgag 4200
 actgcctgtc actggaggat ggcctgctct tgaggatatcc aggcagcacc actgatggct 4260
 cttggggctg ggctggctct cccatcttca cctcgggcct ggatcccagg cctcaaacca 4320
 gccaacccg aacctttgga acagttttcc aaaaccttga cctgcagggg aatgaaaaat 4380
 cctggctctg tgctgtgcac ataggtgttt aataaacatt tgttggccga gggcaaaaaa 4440
 tccaatcaaa aattc 4455

<210> 81
 <211> 4374
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(3999)

<400> 81
 atg gcg gag gcc ggc ctg agg ggc tgg ctg ctg tgg gcc ctg ctc ctg 48
 Met Ala Glu Ala Gly Leu Arg Gly Trp Leu Leu Trp Ala Leu Leu Leu
 1 5 10

cgc ttg gcc cag agt gag cct tac aca acc atc cac cag cct ggc tac 96
 Arg Leu Ala Gln Ser Glu Pro Tyr Thr Thr Ile His Gln Pro Gly Tyr
 17 22 27 32

tgc gcc ttc tat gac gaa tgt ggg aag aac cca gag ctg tct gga agc 144
 Cys Ala Phe Tyr Asp Glu Cys Gly Lys Asn Pro Glu Leu Ser Gly Ser
 33 38 43 48

ctc atg aca ctc tcc aac gtg tcc tgc ctg tcc aac acg ccg gcc cgc 192
 Leu Met Thr Leu Ser Asn Val Ser Cys Leu Ser Asn Thr Pro Ala Arg
 49 54 59 64

aag atc aca ggt gat cac ctg atc cta tta cag aag atc tgc ccc cgc 240
 Lys Ile Thr Gly Asp His Leu Ile Leu Leu Gln Lys Ile Cys Pro Arg
 65 70 75 80

ctc tac acc ggc ccc aac acc caa gcc tgc tgc tcc gcc aag cag ctg 288
 Leu Tyr Thr Gly Pro Asn Thr Gln Ala Cys Cys Ser Ala Lys Gln Leu
 81 86 91 96

gta tca ctg gaa gcg agt ctg tcg atc acc aag gcc ctc ctc acc cgc	336
Val Ser Leu Glu Ala Ser Leu Ser Ile Thr Lys Ala Leu Leu Thr Arg	
97 102 107 112	
tgc cca gcc tgc tct gac aat ttt gtg aac ctg cac tgc cac aac acg	384
Cys Pro Ala Cys Ser Asp Asn Phe Val Asn Leu His Cys His Asn Thr	
113 118 123 128	
tgc agc ccc aat cag agc ctc ttc atc aat gtg acc cgc gtg gcc cag	432
Cys Ser Pro Asn Gln Ser Leu Phe Ile Asn Val Thr Arg Val Ala Gln	
129 134 139 144	
cta ggg gct gga caa ctc cca gct gtg gtg gcc tat gag gcc ttc tac	480
Leu Gly Ala Gly Gln Leu Pro Ala Val Val Ala Tyr Glu Ala Phe Tyr	
145 150 155 160	
cag cat agc ttt gcc gag cag agc tat gac tcc tgc agc cgt gtg cgc	528
Gln His Ser Phe Ala Glu Gln Ser Tyr Asp Ser Cys Ser Arg Val Arg	
161 166 171 176	
gtc cct gca gct gcc acg ctg gct gtg ggc acc atg tgt ggc gtg tat	576
Val Pro Ala Ala Ala Thr Leu Ala Val Gly Thr Met Cys Gly Val Tyr	
177 182 187 192	
ggc tct gcc ctt tgc aat gcc cag cgc tgg ctc aac ttc cag gga gac	624
Gly Ser Ala Leu Cys Asn Ala Gln Arg Trp Leu Asn Phe Gln Gly Asp	
193 198 203 208	
aca ggc aat ggt ctg gcc cca ctg gac atc acc ttc cac ctc ttg gag	672
Thr Gly Asn Gly Leu Ala Pro Leu Asp Ile Thr Phe His Leu Leu Glu	
209 214 219 224	
cct ggc cag gcc gtg ggg agt ggg att cag cct ctg aat gag ggg gtt	720
Pro Gly Gln Ala Val Gly Ser Gly Ile Gln Pro Leu Asn Glu Gly Val	
225 230 235 240	
gca cgt tgc aat gag tcc caa ggt gac gac gtg gcg acc tgc tcc tgc	768
Ala Arg Cys Asn Glu Ser Gln Gly Asp Asp Val Ala Thr Cys Ser Cys	
241 246 251 256	
caa gac tgt gct gca tcc tgt cct gcc ata gcc cgc ccc cag gcc ctc	816
Gln Asp Cys Ala Ala Ser Cys Pro Ala Ile Ala Arg Pro Gln Ala Leu	
257 262 267 272	
gac tcc acc ttc tac ctg ggc cag atg ccg ggc agt ctg gtc ctc atc	864
Asp Ser Thr Phe Tyr Leu Gly Gln Met Pro Gly Ser Leu Val Leu Ile	
273 278 283 288	
atc atc ctc tgc tct gtc ttc gct gtg gtc acc atc ctg ctt gtg gga	912
Ile Ile Leu Cys Ser Val Phe Ala Val Val Thr Ile Leu Leu Val Gly	
289 294 299 304	
ttc cgt gtg gcc ccc gcc agg gac aaa agc aag atg gtg gac ccc aag	960
Phe Arg Val Ala Pro Ala Arg Asp Lys Ser Lys Met Val Asp Pro Lys	
305 310 315 320	

aag ggc acc agc ctc tct gac aag ctc agc ttc tcc acc cac acc ctc	1008
Lys Gly Thr Ser Leu Ser Asp Lys Leu Ser Phe Ser Thr His Thr Leu	
321 326 331 336	
ctt ggc cag ttc ttc cag ggc tgg ggc acg tgg gtg gct tcg tgg cct	1056
Leu Gly Gln Phe Phe Gln Gly Trp Gly Thr Trp Val Ala Ser Trp Pro	
337 342 347 352	
ctg acc atc ttg gtg cta tct gtc atc ccg gtg gtg gcc ttg gca gcg	1104
Leu Thr Ile Leu Val Leu Ser Val Ile Pro Val Val Ala Leu Ala Ala	
353 358 363 368	
ggc ctg gtc ttt aca gaa ctc act acg gac ccc gtg gag ctg tgg tcg	1152
Gly Leu Val Phe Thr Glu Leu Thr Thr Asp Pro Val Glu Leu Trp Ser	
369 374 379 384	
gcc ccc aac agc caa gcc cgg agt gag aaa gct ttc cat gac cag cat	1200
Ala Pro Asn Ser Gln Ala Arg Ser Glu Lys Ala Phe His Asp Gln His	
385 390 395 400	
ttc ggc ccc ttc ttc cga acc aac cag gtg atc ctg acg gct cct aac	1248
Phe Gly Pro Phe Phe Arg Thr Asn Gln Val Ile Leu Thr Ala Pro Asn	
401 406 411 416	
cgg tcc agc tac agg tat gac tct ctg ctg ctg ggg ccc aag aac ttc	1296
Arg Ser Ser Tyr Arg Tyr Asp Ser Leu Leu Leu Gly Pro Lys Asn Phe	
417 422 427 432	
agc gga atc ctg gac ctg gac ttg ctg ctg gag ctg cta gag ctg cag	1344
Ser Gly Ile Leu Asp Leu Asp Leu Leu Leu Glu Leu Leu Glu Leu Gln	
433 438 443 448	
gag agg ctg cgg cac ctc cag gta tgg tcg ccc gaa gca cag cgc aac	1392
Glu Arg Leu Arg His Leu Gln Val Trp Ser Pro Glu Ala Gln Arg Asn	
449 454 459 464	
atc tcc ctg cag gac atc tgc tac gcc ccc ctc aat ccg gac aat acc	1440
Ile Ser Leu Gln Asp Ile Cys Tyr Ala Pro Leu Asn Pro Asp Asn Thr	
465 470 475 480	
agt ctc tac gac tgc tgc atc aac agc ctc ctg cag tat ttc cag aac	1488
Ser Leu Tyr Asp Cys Cys Ile Asn Ser Leu Leu Gln Tyr Phe Gln Asn	
481 486 491 496	
aac cgc acg ctc ctg ctg ctc aca gcc aac cag aca ctg atg ggg cag	1536
Asn Arg Thr Leu Leu Leu Leu Thr Ala Asn Gln Thr Leu Met Gly Gln	
497 502 507 512	
acc tcc caa gtc gac tgg aag gac cat ttt ctg tac tgt gcc aat gcc	1584
Thr Ser Gln Val Asp Trp Lys Asp His Phe Leu Tyr Cys Ala Asn Ala	
513 518 523 528	
ccg ctc acc ttc aag gat ggc aca gcc ctg gcc ctg agc tgc atg gct	1632
Pro Leu Thr Phe Lys Asp Gly Thr Ala Leu Ala Leu Ser Cys Met Ala	
529 534 539 544	
gac tac ggg gcc cct gtc ttc ccc ttc ctt gcc att ggg ggg tac aaa	1680

Asp Tyr Gly Ala Pro Val Phe Pro Phe Leu Ala Ile Gly Gly Tyr Lys	
545 550 555 560	
gga aag gac tat tct gag gca gag gcc ctg atc atg acg ttc tcc ctc	1728
Gly Lys Asp Tyr Ser Glu Ala Glu Ala Leu Ile Met Thr Phe Ser Leu	
561 566 571 576	
aac aat tac cct gcc ggg gac ccc cgt ctg gcc cag gcc aag ctg tgg	1776
Asn Asn Tyr Pro Ala Gly Asp Pro Arg Leu Ala Gln Ala Lys Leu Trp	
577 582 587 592	
gag gag gcc ttc tta gag gaa atg cga gcc ttc cag cgt cgg atg gct	1824
Glu Glu Ala Phe Leu Glu Glu Met Arg Ala Phe Gln Arg Arg Met Ala	
593 598 603 608	
ggc atg ttc cag gtc acg ttc atg gct gag cgc tct ctg gaa gac gag	1872
Gly Met Phe Gln Val Thr Phe Met Ala Glu Arg Ser Leu Glu Asp Glu	
609 614 619 624	
atc aat cgc acc aca gct gaa gac ctg ccc atc ttt gcc acc agc tac	1920
Ile Asn Arg Thr Thr Ala Glu Asp Leu Pro Ile Phe Ala Thr Ser Tyr	
625 630 635 640	
att gtc ata ttc ctg tac atc tct ctg gcc ctg ggc agc tat tcc agc	1968
Ile Val Ile Phe Leu Tyr Ile Ser Leu Ala Leu Gly Ser Tyr Ser Ser	
641 646 651 656	
tgg agc cga gtg atg gtg gac tcc aag gcc acg ctg ggc ctc ggc ggg	2016
Trp Ser Arg Val Met Val Asp Ser Lys Ala Thr Leu Gly Leu Gly Gly	
657 662 667 672	
gtg gcc gtg gtc ctg gga gca gtc atg gct gcc atg ggc ttc ttc tcc	2064
Val Ala Val Val Leu Gly Ala Val Met Ala Ala Met Gly Phe Phe Ser	
673 678 683 688	
tac ttg ggt atc cgc tcc tcc ctg gtc atc ctg caa gtg gtt cct ttc	2112
Tyr Leu Gly Ile Arg Ser Ser Leu Val Ile Leu Gln Val Val Pro Phe	
689 694 699 704	
ctg gtg ctg tcc gtg ggg gct gat aac atc ttc atc ttt gtt ctc gag	2160
Leu Val Leu Ser Val Gly Ala Asp Asn Ile Phe Ile Phe Val Leu Glu	
705 710 715 720	
tac cag agg ctg ccc cgg agg cct ggg gag cca cga gag gtc cac att	2208
Tyr Gln Arg Leu Pro Arg Arg Pro Gly Glu Pro Arg Glu Val His Ile	
721 726 731 736	
ggg cga gcc cta ggc agg gtg gct ccc agc atg ctg ttg tgc agc ctc	2256
Gly Arg Ala Leu Gly Arg Val Ala Pro Ser Met Leu Leu Cys Ser Leu	
737 742 747 752	
tct gag gcc atc tgc ttc ttc cta ggg gcc ctg acc ccc atg cca gct	2304
Ser Glu Ala Ile Cys Phe Phe Leu Gly Ala Leu Thr Pro Met Pro Ala	
753 758 763 768	
gtg cgg acc ttt gcc ctg acc tct ggc ctt gca gtg atc ctt gac ttc	2352
Val Arg Thr Phe Ala Leu Thr Ser Gly Leu Ala Val Ile Leu Asp Phe	

769	774	779	784	
ctc ctg cag atg tca gcc ttt gtg gcc ctg ctc tcc ctg gac agc aag				2400
Leu Leu Gln Met Ser Ala Phe Val Ala Leu Leu Ser Leu Asp Ser Lys				
785	790	795	800	
agg cag gag gcc tcc cgg ttg gac gtc tgc tgc tgt gtc aag ccc cag				2448
Arg Gln Glu Ala Ser Arg Leu Asp Val Cys Cys Cys Val Lys Pro Gln				
801	806	811	816	
gag ctg ccc ccg cct ggc cag gga gag ggg ctc ctg ctt ggc ttc ttc				2496
Glu Leu Pro Pro Pro Gly Gln Gly Glu Gly Leu Leu Leu Gly Phe Phe				
817	822	827	832	
caa aag gct tat gcc ccc ttc ctg ctg cac tgg atc act cga ggt gtt				2544
Gln Lys Ala Tyr Ala Pro Phe Leu Leu His Trp Ile Thr Arg Gly Val				
833	838	843	848	
gtg ctg ctg ctg ttt ctc gcc ctg ttc gga gtg agc ctc tac tcc atg				2592
Val Leu Leu Leu Phe Leu Ala Leu Phe Gly Val Ser Leu Tyr Ser Met				
849	854	859	864	
tgc cac atc agc gtg gga ctg gac cag gag ctg gcc ctg ccc aag gac				2640
Cys His Ile Ser Val Gly Leu Asp Gln Glu Leu Ala Leu Pro Lys Asp				
865	870	875	880	
tcg tac ctg ctt gac tat ttc ctc ttt ctg aac cgc tac ttc gag gtg				2688
Ser Tyr Leu Leu Asp Tyr Phe Leu Phe Leu Asn Arg Tyr Phe Glu Val				
881	886	891	896	
ggg gcc ccg gtg tac ttt gtt acc acc ttg ggc tac aac ttc tcc agc				2736
Gly Ala Pro Val Tyr Phe Val Thr Thr Leu Gly Tyr Asn Phe Ser Ser				
897	902	907	912	
gag gct ggg atg aat gcc atc tgc tcc agt gca ggc tgc aac aac ttc				2784
Glu Ala Gly Met Asn Ala Ile Cys Ser Ser Ala Gly Cys Asn Asn Phe				
913	918	923	928	
tcc ttc acc cag aag atc cag tat gcc aca gag ttc cct gag cag tct				2832
Ser Phe Thr Gln Lys Ile Gln Tyr Ala Thr Glu Phe Pro Glu Gln Ser				
929	934	939	944	
tac ctg gcc atc cct gcc tcc tcc tgg gtg gat gac ttc att gac tgg				2880
Tyr Leu Ala Ile Pro Ala Ser Ser Trp Val Asp Asp Phe Ile Asp Trp				
945	950	955	960	
ctg acc ccg tcc tcc tgc tgc cgc ctt tat ata tct ggc ccc aat aag				2928
Leu Thr Pro Ser Ser Cys Cys Arg Leu Tyr Ile Ser Gly Pro Asn Lys				
961	966	971	976	
gac aag ttc tgc ccc tcg acc gtc aac tct ctg aac tgc cta aag aac				2976
Asp Lys Phe Cys Pro Ser Thr Val Asn Ser Leu Asn Cys Leu Lys Asn				
977	982	987	992	
tgc atg agc atc acg atg ggc tct gtg agg ccc tcg gtg gag cag ttc				3024
Cys Met Ser Ile Thr Met Gly Ser Val Arg Pro Ser Val Glu Gln Phe				
993	998	1003	1008	

cat aag tat ctt ccc tgg ttc ctg aac gac cgg ccc aac atc aaa tgt	3072
His Lys Tyr Leu Pro Trp Phe Leu Asn Asp Arg Pro Asn Ile Lys Cys	
1009 1014 1019 1024	
ccc aaa ggc ggc ctg gca gca tac agc acc tct gtg aac ttg act tca	3120
Pro Lys Gly Gly Leu Ala Ala Tyr Ser Thr Ser Val Asn Leu Thr Ser	
1025 1030 1035 1040	
gat ggc cag gtt tta gcc tcc agg ttc atg gcc tat cac aag ccc ctg	3168
Asp Gly Gln Val Leu Ala Ser Arg Phe Met Ala Tyr His Lys Pro Leu	
1041 1046 1051 1056	
aaa aac tca cag gat tac aca gaa gct ctg cgg gca gct cga gag ctg	3216
Lys Asn Ser Gln Asp Tyr Thr Glu Ala Leu Arg Ala Ala Arg Glu Leu	
1057 1062 1067 1072	
gca gcc aac atc act gct gac ctg cgg aaa gtg cct gga aca gac ccg	3264
Ala Ala Asn Ile Thr Ala Asp Leu Arg Lys Val Pro Gly Thr Asp Pro	
1073 1078 1083 1088	
gct ttt gag gtc ttc ccc tac acg atc acc aat gtg ttt tat gag cag	3312
Ala Phe Glu Val Phe Pro Tyr Thr Ile Thr Asn Val Phe Tyr Glu Gln	
1089 1094 1099 1104	
tac ctg acc atc ctc cct gag ggg ctc ttc atg ctc agc ctc tgc ctt	3360
Tyr Leu Thr Ile Leu Pro Glu Gly Leu Phe Met Leu Ser Leu Cys Leu	
1105 1110 1115 1120	
gtg ccc acc ttc gct gtc tcc tgc ctc ctg ctg ggc ctg gac ctg cgc	3408
Val Pro Thr Phe Ala Val Ser Cys Leu Leu Leu Gly Leu Asp Leu Arg	
1121 1126 1131 1136	
tcc ggc ctc ctc aac ctg ctc tcc att gtc atg atc ctc gtg gac act	3456
Ser Gly Leu Leu Asn Leu Leu Ser Ile Val Met Ile Leu Val Asp Thr	
1137 1142 1147 1152	
gtc ggc ttc atg gcc ctg tgg ggc atc agt tac aat gct gtg tcc ctc	3504
Val Gly Phe Met Ala Leu Trp Gly Ile Ser Tyr Asn Ala Val Ser Leu	
1153 1158 1163 1168	
atc aac ctg gtc tgc ggc gtg ggc atg tct gtg gag ttt gtg tcc cac	3552
Ile Asn Leu Val Ser Ala Val Gly Met Ser Val Glu Phe Val Ser His	
1169 1174 1179 1184	
att acc cgc tcc ttt gcc atc agc acc aag ccc acc tgg ctg gag agg	3600
Ile Thr Arg Ser Phe Ala Ile Ser Thr Lys Pro Thr Trp Leu Glu Arg	
1185 1190 1195 1200	
gcc aaa gag gcc acc atc tct atg gga agt ggc gtg ttt gca ggt gtg	3648
Ala Lys Glu Ala Thr Ile Ser Met Gly Ser Ala Val Phe Ala Gly Val	
1201 1206 1211 1216	
gcc atg acc aac ctg cct ggc atc ctt gtc ctg ggc ctc gcc aag gcc	3696
Ala Met Thr Asn Leu Pro Gly Ile Leu Val Leu Gly Leu Ala Lys Ala	
1217 1222 1227 1232	


```

cag ctc att cag atc ttc ttc ttc cgc ctc aac ctc ctg atc act ctg      3744
Gln Leu Ile Gln Ile Phe Phe Phe Arg Leu Asn Leu Leu Ile Thr Leu
1233                1238                1243                1248

ctg ggc ctg ctg cat ggc ttg gtc ttc ctg ccc gtc atc ctc agc tac      3792
Leu Gly Leu Leu His Gly Leu Val Phe Leu Pro Val Ile Leu Ser Tyr
1249                1254                1259                1264

gtg ggg cct gac gtt aac ccg gct ctg gca ctg gag cag aag cgg gct      3840
Val Gly Pro Asp Val Asn Pro Ala Leu Ala Leu Glu Gln Lys Arg Ala
1265                1270                1275                1280

gag gag gcg gtg gca gca gtc atg gtg gcc tct tgc cca aat cac ccc      3888
Glu Glu Ala Val Ala Ala Val Met Val Ala Ser Cys Pro Asn His Pro
1281                1286                1291                1296

tcc cga gtc tcc aca gct gac aac atc tat gtc aac cac agc ttt gaa      3936
Ser Arg Val Ser Thr Ala Asp Asn Ile Tyr Val Asn His Ser Phe Glu
1297                1302                1307                1312

ggg tct atc aaa ggt gct ggt gcc atc agc aac ttc ttg ccc aac aat      3984
Gly Ser Ile Lys Gly Ala Gly Ala Ile Ser Asn Phe Leu Pro Asn Asn
1313                1318                1323                1328

ggg cgg cag ttc tga tacagccaga ggccctgtct aggctctatg gccctgaacc      4039
Gly Arg Gln Phe *
1329

aaagggttat ggggatcttc cttgtgactg ccccttgaca cagccctcc tcaaactcta      4099

ggggaggcca ttcccatgag actgcctgtc actggaggat ggctgtctct tgaggatatcc      4159

aggcagcacc actgatggct cttggggctg ggctggctct cccatcttca cctcgggcct      4219

ggatcccagg cctcaaacca gcccaaccgg aacctttgga acagttttcc aaaaccttga      4279

cctgcagggg aaatgaaaat cctggctctg tgctgtgcac ataggtgttt aataaacatt      4339

tgttggccga gggcaaaaaa tccaatcaaa aattc                                4374

```

```

<210> 82
<211> 1126
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (393) .. (1070)

<220>
<221> misc_feature
<222> (1) ... (1126)
<223> n = a,t,c or g

```

<400> 82
 tgtgggaaaa aantttagan ccnctgatcg ccttcggtac cgcnccgaa ttcccgggtc 60
 gacccacgcg tccgcccacg cgtccggagc cgtggaggta cgaacttaag acatgcctat 120
 tttattaatt tacttccaaa cgcaacgaaa ggtccatgga caatttgtgg gccatttaat 180
 tcagggcccc caattcgtac gtggagaagt gggaaatgcaa aagtactttg acctttaacc 240
 ttcggtccgg cgcggtggag ggaaacgcct ccgtctctat ataaggaatt ttccggtctc 300
 ttcggtcct ttttcctctc ttcagcgtgg ggcgcccaca atttgcgcgc tctctttctg 360
 ctgctcccca gctctcggat acagccgaca cc atg ggt ttc gga gac ctg aaa 413
 Met Gly Phe Gly Asp Leu Lys
 1 5
 agc cct gcc ggc ctc cag gtg ctc aac gat tac ctg gcg gac aag agc 461
 Ser Pro Ala Gly Leu Gln Val Leu Asn Asp Tyr Leu Ala Asp Lys Ser
 8 13 18 23
 tac atc gag ggg tat gtg cca tca caa gca gat gtg gca gta ttt gaa 509
 Tyr Ile Glu Gly Tyr Val Pro Ser Gln Ala Asp Val Ala Val Phe Glu
 24 29 34 39
 gcc gtg tcc agc cca ccg cct gcc gac ttg tgt cat gcc cta cgt tgg 557
 Ala Val Ser Ser Pro Pro Pro Ala Asp Leu Cys His Ala Leu Arg Trp
 40 45 50 55
 tat aat cac atc aag tct tac gaa aag gaa aag gcc agc ctg cca gga 605
 Tyr Asn His Ile Lys Ser Tyr Glu Lys Glu Lys Ala Ser Leu Pro Gly
 56 61 66 71
 gtg aag aaa gct ttg ggc aaa tat ggt cct gcc gat gtg gaa gac act 653
 Val Lys Lys Ala Leu Gly Lys Tyr Gly Pro Ala Asp Val Glu Asp Thr
 72 77 82 87
 aca gga agt gga gct aca gat agt aaa gat gat gat gac att gac ctc 701
 Thr Gly Ser Gly Ala Thr Asp Ser Lys Asp Asp Asp Asp Ile Asp Leu
 88 93 98 103
 ttt gga tct gat gat gag gag gaa agt gaa gaa gca aag agg cta agg 749
 Phe Gly Ser Asp Asp Glu Glu Glu Ser Glu Glu Ala Lys Arg Leu Arg
 104 109 114 119
 gaa gaa cgt ctt gca caa tat gaa tca aag aaa gcc aaa aaa cct gca 797
 Glu Glu Arg Leu Ala Gln Tyr Glu Ser Lys Lys Ala Lys Lys Pro Ala
 120 125 130 135
 ctt gtt gcc aag tct tcc atc tta cta gat gtg aaa cct tgg gat gat 845
 Leu Val Ala Lys Ser Ser Ile Leu Leu Asp Val Lys Pro Trp Asp Asp
 136 141 146 151
 gag aca gat atg gcg aaa tta gag gag tgc gtc aga agc att caa gca 893
 Glu Thr Asp Met Ala Lys Leu Glu Glu Cys Val Arg Ser Ile Gln Ala
 152 157 162 167

```

gac ggc tta gtc tgg ggc tca tct aaa cta gtt cca gtg gga tac gga      941
Asp Gly Leu Val Trp Gly Ser Ser Lys Leu Val Pro Val Gly Tyr Gly
168                      173                      178                      183

att aag aaa ctt caa ata cag tgt gta gtt gaa gat gat aaa gtt gga      989
Ile Lys Lys Leu Gln Ile Gln Cys Val Val Glu Asp Asp Lys Val Gly
184                      189                      194                      199

aca gat atg ctg gag gag cag atc act gct ttt gag gac tat gtg cag      1037
Thr Asp Met Leu Glu Glu Gln Ile Thr Ala Phe Glu Asp Tyr Val Gln
200                      205                      210                      215

tcc atg gat gtg gct gct ttc aac aag atc taa aatccatc ctggatcatg      1088
Ser Met Asp Val Ala Ala Phe Asn Lys Ile *
216                      221                      226

gcattttaaataaaaagattga aagattaaaa aaaaaaaaaa                        1126

```

```

<210> 83
<211> 2044
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (86)..(2044)

```

```

<400> 83

```

```

agcaccgggtc cggaattccc gggctcgaccc acgcgtccga ctagttctct gatttcactt      60

atagtcaaataaagaactct gtcac  atg ata aat atg tgt ttt cag gaa ctc      112
                        Met Ile Asn Met Cys Phe Gln Glu Leu
                        1                      5

gta aca ttc agg gat gtg gcc ata gaa ttc tcc cct gaa gag tgg aaa      160
Val Thr Phe Arg Asp Val Ala Ile Glu Phe Ser Pro Glu Glu Trp Lys
10                      15                      20                      25

tgt ctg gac cct gcc cag cag aat ttg tat aga gat gtg atg ttg gag      208
Cys Leu Asp Pro Ala Gln Gln Asn Leu Tyr Arg Asp Val Met Leu Glu
26                      31                      36                      41

aac tac agg aac ctg gtc tcc ctg ggt ttt gtg atc tct aac cca gac      256
Asn Tyr Arg Asn Leu Val Ser Leu Gly Phe Val Ile Ser Asn Pro Asp
42                      47                      52                      57

ctg gtc acc tgt ctg gag caa ata aaa gag ccc tgc aat ttg aag ata      304
Leu Val Thr Cys Leu Glu Gln Ile Lys Glu Pro Cys Asn Leu Lys Ile
58                      63                      68                      73

cat gag aca gca gcc aaa ccc cca gct ata tgt tct cct ttc agc caa      352
His Glu Thr Ala Ala Lys Pro Pro Ala Ile Cys Ser Pro Phe Ser Gln
74                      79                      84                      89

```

gac ctt tca cca gtg cag ggg ata gaa gat tca ttc cac aaa ctt ata	400
Asp Leu Ser Pro Val Gln Gly Ile Glu Asp Ser Phe His Lys Leu Ile	
90 95 100 105	
ctg aaa aga tac gag aaa tgt gga cat gag aat tta caa tta aga aaa	448
Leu Lys Arg Tyr Glu Lys Cys Gly His Glu Asn Leu Gln Leu Arg Lys	
106 111 116 121	
ggc tgt aaa cgt gtg aat gag tgt aag gtg cag aaa gga gtt aat aat	496
Gly Cys Lys Arg Val Asn Glu Cys Lys Val Gln Lys Gly Val Asn Asn	
122 127 132 137	
gga gtt tac cag tgc ttg tca act acc cag agc aaa ata ttt caa tgt	544
Gly Val Tyr Gln Cys Leu Ser Thr Thr Gln Ser Lys Ile Phe Gln Cys	
138 143 148 153	
aat aca tgt gtt aaa gtt ttt agt aaa ttt tca aat tca aac aaa cat	592
Asn Thr Cys Val Lys Val Phe Ser Lys Phe Ser Asn Ser Asn Lys His	
154 159 164 169	
aag ata aga cat act gga gag aaa ccc ttt aaa tgt aca gaa tgt ggc	640
Lys Ile Arg His Thr Gly Glu Lys Pro Phe Lys Cys Thr Glu Cys Gly	
170 175 180 185	
aga tcg ttt tac atg tca cac cta act caa cat aca gga att cat gct	688
Arg Ser Phe Tyr Met Ser His Leu Thr Gln His Thr Gly Ile His Ala	
186 191 196 201	
gga gag aaa ccc tac aat gtg aaa aat gtg gca aag ctt tac agg gtc	736
Gly Glu Lys Pro Tyr Asn Val Lys Asn Val Ala Lys Leu Tyr Arg Val	
202 207 212 217	
cac aat cca ctg aat gaa cat aag aga att cat act gga gag aaa ccc	784
His Asn Pro Leu Asn Glu His Lys Arg Ile His Thr Gly Glu Lys Pro	
218 223 228 233	
tac aca tgt gaa gaa tgt ggc aaa gct tta gac gtt ctg aac gaa cat	832
Tyr Thr Cys Glu Glu Cys Gly Lys Ala Leu Asp Val Leu Asn Glu His	
234 239 244 249	
aag aaa att cat act gga gag aaa ccc tac aaa tgt gaa gaa tgt ggc	880
Lys Lys Ile His Thr Gly Glu Lys Pro Tyr Lys Cys Glu Glu Cys Gly	
250 255 260 265	
aaa gcc ttt aca agg tcc aca aca ctg aat gaa cac aag aaa att cat	928
Lys Ala Phe Thr Arg Ser Thr Thr Leu Asn Glu His Lys Lys Ile His	
266 271 276 281	
act gga gag aaa ccc tac aaa tgt aaa gaa tgt ggc aaa gcc ttt aga	976
Thr Gly Glu Lys Pro Tyr Lys Cys Lys Glu Cys Gly Lys Ala Phe Arg	
282 287 292 297	
tgg tcc aca agc ctg aat gaa cat aag aat att cat act gga gag aaa	1024
Trp Ser Thr Ser Leu Asn Glu His Lys Asn Ile His Thr Gly Glu Lys	
298 303 308 313	
ccc tac aaa tgt aaa gaa tgt ggc aaa gcc ttt aga cag tcc agg agc	1072

Pro	Tyr	Lys	Cys	Lys	Glu	Cys	Gly	Lys	Ala	Phe	Arg	Gln	Ser	Arg	Ser		
314					319					324					329		
ctg	aat	gaa	cat	aaa	aat	att	cat	act	ggc	gaa	aaa	ccc	tac	aca	tgt	1120	
Leu	Asn	Glu	His	Lys	Asn	Ile	His	Thr	Gly	Glu	Lys	Pro	Tyr	Thr	Cys		
330					335					340					345		
gaa	aaa	tgt	ggc	aaa	gct	ttt	aac	caa	tcc	tca	agt	ctt	att	ata	cac	1168	
Glu	Lys	Cys	Gly	Lys	Ala	Phe	Asn	Gln	Ser	Ser	Ser	Leu	Ile	Ile	His		
346					351					356					361		
agg	agc	att	cat	tct	gaa	caa	aaa	ctt	tac	aaa	tgt	gaa	gaa	tgt	ggc	1216	
Arg	Ser	Ile	His	Ser	Glu	Gln	Lys	Leu	Tyr	Lys	Cys	Glu	Glu	Cys	Gly		
362					367					372					377		
aaa	gcc	ttt	act	tgg	tcc	tca	tcc	ctt	aat	aaa	cat	aag	aga	att	cat	1264	
Lys	Ala	Phe	Thr	Trp	Ser	Ser	Ser	Leu	Asn	Lys	His	Lys	Arg	Ile	His		
378					383					388					393		
act	gga	gag	aaa	ccc	tac	aca	tgt	gaa	gaa	tgt	ggc	aaa	gct	ttt	tat	1312	
Thr	Gly	Glu	Lys	Pro	Tyr	Thr	Cys	Glu	Glu	Cys	Gly	Lys	Ala	Phe	Tyr		
394					399					404					409		
agg	tcc	tca	cac	ctt	gct	aaa	cat	aag	aga	att	cat	act	gga	gag	aaa	1360	
Arg	Ser	Ser	His	Leu	Ala	Lys	His	Lys	Arg	Ile	His	Thr	Gly	Glu	Lys		
410					415					420					425		
ccc	tac	acg	tgc	gaa	gaa	tgt	ggc	aaa	gct	ttt	aac	caa	tcc	tca	act	1408	
Pro	Tyr	Thr	Cys	Glu	Glu	Cys	Gly	Lys	Ala	Phe	Asn	Gln	Ser	Ser	Thr		
426					431					436					441		
ctt	ata	tta	cac	aag	aga	atc	cat	tct	gga	caa	aaa	cct	tac	aaa	tgt	1456	
Leu	Ile	Leu	His	Lys	Arg	Ile	His	Ser	Gly	Gln	Lys	Pro	Tyr	Lys	Cys		
442					447					452					457		
gaa	gaa	tgt	ggc	aaa	gcc	ttt	aca	cgg	tcc	aca	aca	ctg	aac	gaa	cat	1504	
Glu	Glu	Cys	Gly	Lys	Ala	Phe	Thr	Arg	Ser	Thr	Thr	Leu	Asn	Glu	His		
458					463					468					473		
aag	aaa	att	cat	act	ggc	gag	aaa	ccc	tac	aaa	tgt	gaa	gaa	tgt	ggc	1552	
Lys	Lys	Ile	His	Thr	Gly	Glu	Lys	Pro	Tyr	Lys	Cys	Glu	Glu	Cys	Gly		
474					479					484					489		
aaa	gct	ttc	ata	tgg	tcc	gca	agc	ctg	aat	gaa	cat	aag	aat	att	cat	1600	
Lys	Ala	Phe	Ile	Trp	Ser	Ala	Ser	Leu	Asn	Glu	His	Lys	Asn	Ile	His		
490					495					500					505		
act	gga	gag	aaa	ccc	tac	aaa	tgt	aaa	gaa	tgt	ggc	aaa	gct	ttt	aac	1648	
Thr	Gly	Glu	Lys	Pro	Tyr	Lys	Cys	Lys	Glu	Cys	Gly	Lys	Ala	Phe	Asn		
506					511					516					521		
caa	tcc	tca	ggc	ctt	att	ata	cac	agg	agc	att	cat	tct	gaa	caa	aaa	1696	
Gln	Ser	Ser	Gly	Leu	Ile	Ile	His	Arg	Ser	Ile	His	Ser	Glu	Gln	Lys		
522					527					532					537		
ctt	tac	aaa	tgt	gaa	gaa	tgt	ggc	aaa	gcc	ttt	act	cgg	tcc	aca	gcc	1744	
Leu	Tyr	Lys	Cys	Glu	Glu	Cys	Gly	Lys	Ala	Phe	Thr	Arg	Ser	Thr	Ala		

538	543	548	553	
ctg aat gaa cat aag aaa att cat tct gga gag aaa ccc tac aaa tgc				1792
Leu Asn Glu His Lys Lys Ile His Ser Gly Glu Lys Pro Tyr Lys Cys				
554	559	564	569	
aaa gaa tgt ggc aaa gcc tat aac tta tcc tca acc ctt act aaa cat				1840
Lys Glu Cys Gly Lys Ala Tyr Asn Leu Ser Ser Thr Leu Thr Lys His				
570	575	580	585	
aag aga att cat act gga gag aaa ccc ttc aca tgt gaa gaa tgt ggc				1888
Lys Arg Ile His Thr Gly Glu Lys Pro Phe Thr Cys Glu Glu Cys Gly				
586	591	596	601	
aaa gcc ttc aat tgg tcc tca tcc ctt act aaa cat aag ata att cat				1936
Lys Ala Phe Asn Trp Ser Ser Ser Leu Thr Lys His Lys Ile Ile His				
602	607	612	617	
act gga gag aaa tcc tac aaa tgt gaa gaa tgt ggc aaa ggt ttt aat				1984
Thr Gly Glu Lys Ser Tyr Lys Cys Glu Glu Cys Gly Lys Gly Phe Asn				
618	623	628	633	
cgg ccc tca acc ctt act gta cac aag cga ttc ata ctg gca agg aac				2032
Arg Pro Ser Thr Leu Thr Val His Lys Arg Phe Ile Leu Ala Arg Asn				
634	639	644	649	
ata gtt gaa tga				2044
Ile Val Glu *				
650				
<210> 84				
<211> 1431				
<212> DNA				
<213> Homo sapiens				
<220>				
<221> CDS				
<222> (25) .. (1431)				
<400> 84				
gttactgtgt ctccagaaac acat	atg gac ctc aca aag ggc tgt gtg acc			51
	Met Asp Leu Thr Lys Gly Cys Val Thr			
	1 5			
ttt gag gac atc gcc att tac ttc tca cag gac gag tgg gga ctt ctt				99
Phe Glu Asp Ile Ala Ile Tyr Phe Ser Gln Asp Glu Trp Gly Leu Leu				
10 15 20 25				
gat gag gct cag aga ctc ctg tac ctt gaa gtg atg ctg gag aac ttt				147
Asp Glu Ala Gln Arg Leu Leu Tyr Leu Glu Val Met Leu Glu Asn Phe				
26 31 36 41				
gcc ctt gta gcc tca ctg ggt tgt ggc cat gga aca gag gat gaa gag				195

Ala	Leu	Val	Ala	Ser	Leu	Gly	Cys	Gly	His	Gly	Thr	Glu	Asp	Glu	Glu			
42						47				52					57			
aca	cct	tct	gac	cag	aat	gtt	tct	gta	gga	gtg	tca	cag	tca	aag	gca		243	
Thr	Pro	Ser	Asp	Gln	Asn	Val	Ser	Val	Gly	Val	Ser	Gln	Ser	Lys	Ala			
58					63					68					73			
ggt	tca	tcc	aca	cag	aag	act	caa	tcc	tgt	gag	atg	tgt	gtc	cca	gtc		291	
Gly	Ser	Ser	Thr	Gln	Lys	Thr	Gln	Ser	Cys	Glu	Met	Cys	Val	Pro	Val			
74					79					84					89			
ctg	aaa	gat	att	ttg	cat	cta	gct	gat	ctc	cct	ggg	cag	aaa	cca	tac		339	
Leu	Lys	Asp	Ile	Leu	His	Leu	Ala	Asp	Leu	Pro	Gly	Gln	Lys	Pro	Tyr			
90					95					100					105			
ttg	gtt	gga	gaa	tgt	aca	aac	cat	cac	cag	cac	cag	aag	cat	cac	agt		387	
Leu	Val	Gly	Glu	Cys	Thr	Asn	His	His	Gln	His	Gln	Lys	His	His	Ser			
106					111					116					121			
gca	aag	aaa	tcc	ttg	aag	agg	gac	atg	gac	aga	gcc	tca	tat	gtg	aag		435	
Ala	Lys	Lys	Ser	Leu	Lys	Arg	Asp	Met	Asp	Arg	Ala	Ser	Tyr	Val	Lys			
122					127					132					137			
tgc	tgc	cta	ttc	tgt	atg	tca	ttg	aag	ccc	ttt	cgc	aaa	tgg	gag	gtt		483	
Cys	Cys	Leu	Phe	Cys	Met	Ser	Leu	Lys	Pro	Phe	Arg	Lys	Trp	Glu	Val			
138					143					148					153			
gga	aag	gac	ctt	cca	gcc	atg	ttg	cgg	ctt	ctg	agg	tcc	ctg	gtc	ttt		531	
Gly	Lys	Asp	Leu	Pro	Ala	Met	Leu	Arg	Leu	Leu	Arg	Ser	Leu	Val	Phe			
154					159					164					169			
cct	gga	ggc	aag	aaa	ccc	ggc	aca	att	act	gaa	tgt	ggg	gag	gac	att		579	
Pro	Gly	Gly	Lys	Lys	Pro	Gly	Thr	Ile	Thr	Glu	Cys	Gly	Glu	Asp	Ile			
170					175					180					185			
cgc	agt	caa	aaa	agt	cat	tac	aag	tca	ggt	gaa	tgt	ggg	aag	gct	tcc		627	
Arg	Ser	Gln	Lys	Ser	His	Tyr	Lys	Ser	Gly	Glu	Cys	Gly	Lys	Ala	Ser			
186					191					196					201			
agg	cac	aaa	cac	act	cct	gtt	tac	cat	cca	aga	gtc	tac	act	gga	aaa		675	
Arg	His	Lys	His	Thr	Pro	Val	Tyr	His	Pro	Arg	Val	Tyr	Thr	Gly	Lys			
202					207					212					217			
aag	ctt	tat	gag	tgt	agc	aaa	tgt	ggg	aaa	gcc	ttc	cgt	ggc	aag	tac		723	
Lys	Leu	Tyr	Glu	Cys	Ser	Lys	Cys	Gly	Lys	Ala	Phe	Arg	Gly	Lys	Tyr			
218					223					228					233			
tca	ctt	gtt	cag	cac	cag	aga	gtc	cat	act	gga	gaa	agg	cct	tgg	gag		771	
Ser	Leu	Val	Gln	His	Gln	Arg	Val	His	Thr	Gly	Glu	Arg	Pro	Trp	Glu			
234					239					244					249			
tgc	aat	gaa	tgt	gga	aaa	ttc	ttt	agc	caa	acc	tcc	cac	ctg	aat	gat		819	
Cys	Asn	Glu	Cys	Gly	Lys	Phe	Phe	Ser	Gln	Thr	Ser	His	Leu	Asn	Asp			
250					255					260					265			
cat	cgg	aga	atc	cac	acc	gga	gaa	agg	cct	tat	gag	tgc	agc	gaa	tgt		867	
His	Arg	Arg	Ile	His	Thr	Gly	Glu	Arg	Pro	Tyr	Glu	Cys	Ser	Glu	Cys			

<213> Homo sapiens

<220>

<221> CDS

<222> (253)..(618)

<400> 85

```
ggaactctct gttcttgctt tttgttctgt ttgattgatt tattgggctt ctctttttat      60
atccagtagg ggaatcagat tgtggccaaa ggtagtgtat taactctaga aaaggagatt      120
atatctacag ttcctcaaac aatttttagat ttttcttttc aaggacagct agagaagata      180
atgacataat aactatttcc ttttttagga tctgaatcta aaaatgggga agcagacagt      240
tcagataaag aa      atg aaa cat ggg caa aaa tct ccc act gga aaa caa      288
                    Met Lys His Gly Gln Lys Ser Pro Thr Gly Lys Gln
                      1          5          10

aca agt cag cac tta aaa cga tta aaa aag tct ggt tta ggg cac ttg      336
Thr Ser Gln His Leu Lys Arg Leu Lys Lys Ser Gly Leu Gly His Leu
  13          18          23          28

aaa tgg acc aaa gct gag gac att gac ata gaa acc cca gga tct att      384
Lys Trp Thr Lys Ala Glu Asp Ile Asp Ile Glu Thr Pro Gly Ser Ile
  29          34          39          44

ctt gtc aac act aac ttg agg gca tta ata aat aaa cat acg ttt gct      432
Leu Val Asn Thr Asn Leu Arg Ala Leu Ile Asn Lys His Thr Phe Ala
  45          50          55          60

tcc tta cct cag cat ttt caa caa tac ctc ctg ctt ttg ctc cca gaa      480
Ser Leu Pro Gln His Phe Gln Gln Tyr Leu Leu Leu Leu Leu Pro Glu
  61          66          71          76

gtg gat agg cag atg gga agt gat gga att tta cgc ctc agt act tca      528
Val Asp Arg Gln Met Gly Ser Asp Gly Ile Leu Arg Leu Ser Thr Ser
  77          82          87          92

gct cta aat aat gaa ttc ttt gca tat gca gca caa ggg tgg aaa cag      576
Ala Leu Asn Asn Glu Phe Phe Ala Tyr Ala Ala Gln Gly Trp Lys Gln
  93          98          103          108

cga ctg gca gaa ggt aaa ttt gta ttt tct att att atg tga catattg      625
Arg Leu Ala Glu Gly Lys Phe Val Phe Ser Ile Ile Met  *
  109          114          119

gagtacacat accgtactga gcttgtagct ttctctgatt tttcagtcctt ttccccgaca      685
cagtacactt taatttagta aaaactcata tccctttcca aatgagttca ctgattcttt      745
tggtatactt gacattattg atgtcagata tttttgaaga aagcataatt ttatcttgga      805
catcataaaa tttttgatgc agcaacattt tcttgccgat ggtaatttta atgacattgt      865
```

<210> 86
 <211> 2229
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (99)..(1976)

<400> 86

```

ctacgtaccg gaccggaatc cgggtcgacc cacgcgtccg cagagggggtt tgtgtggctg      60

aagaggcagg aggaacagtg tatccacagc gtgggacc      atg cca ggc aca aaa      113
                                     Met Pro Gly Thr Lys
                                     1

cgg ttt caa cat gtc att gag acc ccg gag cct ggc aag tgg gag ttg      161
Arg Phe Gln His Val Ile Glu Thr Pro Glu Pro Gly Lys Trp Glu Leu
   6                      11                      16                      21

tct ggg tac gag gca gct gtg cca atc acg gag aag tca aac cca ctg      209
Ser Gly Tyr Glu Ala Ala Val Pro Ile Thr Glu Lys Ser Asn Pro Leu
  22                      27                      32                      37

acc cag gat cta gac aaa gca gat gct gag aac att gtt cga ctg cta      257
Thr Gln Asp Leu Asp Lys Ala Asp Ala Glu Asn Ile Val Arg Leu Leu
  38                      43                      48                      53

ggg caa tgt gat gct gag atc ttc cag gag gag ggg caa gcc ctg tcc      305
Gly Gln Cys Asp Ala Glu Ile Phe Gln Glu Glu Gly Gln Ala Leu Ser
  54                      59                      64                      69

aca tac cag aga ctc tac agc gaa tcc att ctg acc acc atg gta cag      353
Thr Tyr Gln Arg Leu Tyr Ser Glu Ser Ile Leu Thr Thr Met Val Gln
  70                      75                      80                      85

gtg gct ggg aaa gtt cag gaa gtg ctg aag gag cca gat ggg ggg ctg      401
Val Ala Gly Lys Val Gln Glu Val Leu Lys Glu Pro Asp Gly Gly Leu
  86                      91                      96                      101

gtt gtg ctg agt gga ggg ggc acc tct ggc cgg atg gca ttc ctc atg      449
Val Val Leu Ser Gly Gly Gly Thr Ser Gly Arg Met Ala Phe Leu Met
 102                      107                      112                      117

tcg gtg tcc ttt aat cag ctg atg aaa ggt ctg gga cag aaa cct ctt      497
Ser Val Ser Phe Asn Gln Leu Met Lys Gly Leu Gly Gln Lys Pro Leu
 118                      123                      128                      133

tac acc tac ctc att gca ggt ggt gac agg tct gtg gtg gcc tct agg      545
Tyr Thr Tyr Leu Ile Ala Gly Gly Asp Arg Ser Val Val Ala Ser Arg
 134                      139                      144                      149

gag ggg aca gaa gat agt gcc ttg cac ggg att gag gaa ctg aag aag      593
Glu Gly Thr Glu Asp Ser Ala Leu His Gly Ile Glu Glu Leu Lys Lys
 150                      155                      160                      165

```

gtg gct gcc ggg aag aag aga gtg att gtc att ggc att tct gtg gga Val Ala Ala Gly Lys Lys Arg Val Ile Val Ile Gly Ile Ser Val Gly 166 171 176 181	641
ctc tct gct ccc ttt gtg gca ggc cag atg gac tgc tgc atg aac aac Leu Ser Ala Pro Phe Val Ala Gly Gln Met Asp Cys Cys Met Asn Asn 182 187 192 197	689
aca gct gtc ttc ttg cca gtc ctg gtt ggc ttc aat cca gtg agc atg Thr Ala Val Phe Leu Pro Val Leu Val Gly Phe Asn Pro Val Ser Met 198 203 208 213	737
gcc aga aat gac ccc att gaa gac tgg agt tca aca ttc cga caa gta Ala Arg Asn Asp Pro Ile Glu Asp Trp Ser Ser Thr Phe Arg Gln Val 214 219 224 229	785
gca gag cgg atg cag aaa atg cag gag aaa cag aaa gct ttt gtg ctc Ala Glu Arg Met Gln Lys Met Gln Glu Lys Gln Lys Ala Phe Val Leu 230 235 240 245	833
aat cct gcc atc ggg ccc gag ggt ctc agc ggc tcc tcc cgg atg aaa Asn Pro Ala Ile Gly Pro Glu Gly Leu Ser Gly Ser Ser Arg Met Lys 246 251 256 261	881
ggg gga agt gcc acc aag att ctg ctg gaa acc ctg tta tta gca gcc Gly Gly Ser Ala Thr Lys Ile Leu Leu Glu Thr Leu Leu Leu Ala Ala 262 267 272 277	929
cat aag act gtg gac cag ggc att gca gca tct caa aga tgc ctc ctg His Lys Thr Val Asp Gln Gly Ile Ala Ala Ser Gln Arg Cys Leu Leu 278 283 288 293	977
gaa atc ttg cgg aca ttt gag cga gct cat cag gtg acc tac agc caa Glu Ile Leu Arg Thr Phe Glu Arg Ala His Gln Val Thr Tyr Ser Gln 294 299 304 309	1025
agc ccc aag att gcc acc ctg atg aag agt gtc agc acc agt ctg gag Ser Pro Lys Ile Ala Thr Leu Met Lys Ser Val Ser Thr Ser Leu Glu 310 315 320 325	1073
aag aaa ggc cac gtg tac ctg gtt ggc tgg cag acc ctg ggc atc att Lys Lys Gly His Val Tyr Leu Val Gly Trp Gln Thr Leu Gly Ile Ile 326 331 336 341	1121
gcc atc atg gat gga gta gag tgc atc cac acc ttt ggt gct gat ttc Ala Ile Met Asp Gly Val Glu Cys Ile His Thr Phe Gly Ala Asp Phe 342 347 352 357	1169
cga gat gtc cgt ggc ttt ctc att ggt gat cac agt gac atg ttt aac Arg Asp Val Arg Gly Phe Leu Ile Gly Asp His Ser Asp Met Phe Asn 358 363 368 373	1217
cag aag gct gag ctc acc aac cag ggt ccc cag ttc acc ttc tcc cag Gln Lys Ala Glu Leu Thr Asn Gln Gly Pro Gln Phe Thr Phe Ser Gln 374 379 384 389	1265
gag gac ttc ctg act tcc atc ctt ccc tct ctc acg gaa atc gat act	1313

Glu Asp Phe Leu Thr Ser Ile Leu Pro Ser Leu Thr Glu Ile Asp Thr	
390 395 400 405	
gtg gtc ttc att ttc acc ctg gat gac aac ctc acg gag gtg cag act	1361
Val Val Phe Ile Phe Thr Leu Asp Asp Asn Leu Thr Glu Val Gln Thr	
406 411 416 421	
ata gtg gag cag gtg aaa gag aag acc aac cac atc cag gcc ctg gca	1409
Ile Val Glu Gln Val Lys Glu Lys Thr Asn His Ile Gln Ala Leu Ala	
422 427 432 437	
cac agc acc gtg ggt cag acc ttg ctg atc cct ctg aag aag ctc ttt	1457
His Ser Thr Val Gly Gln Thr Leu Leu Ile Pro Leu Lys Lys Leu Phe	
438 443 448 453	
ccc tcc atc atc agc atc aca tgg cca ctg ctt ttc ttt gaa tat gaa	1505
Pro Ser Ile Ile Ser Ile Thr Trp Pro Leu Leu Phe Phe Glu Tyr Glu	
454 459 464 469	
ggg aac ttc atc cag aag ttc cag cgt gag cta agc acc aaa tgg gtg	1553
Gly Asn Phe Ile Gln Lys Phe Gln Arg Glu Leu Ser Thr Lys Trp Val	
470 475 480 485	
ctg aat aca gtg agt aca ggt gct cat gtg ctt ctt ggt aag atc cta	1601
Leu Asn Thr Val Ser Thr Gly Ala His Val Leu Leu Gly Lys Ile Leu	
486 491 496 501	
caa aac cac atg ttg gac ctt cgg att agc aac tcc aag ctc ttc tgg	1649
Gln Asn His Met Leu Asp Leu Arg Ile Ser Asn Ser Lys Leu Phe Trp	
502 507 512 517	
cgg gcg ctg gcc atg ctg cag cgg ttc tct gga cag tcc aag gct cga	1697
Arg Ala Leu Ala Met Leu Gln Arg Phe Ser Gly Gln Ser Lys Ala Arg	
518 523 528 533	
tgc atc gag agc ctc ctc cga gcg atc cac ttt ccc cag cca ctg tca	1745
Cys Ile Glu Ser Leu Leu Arg Ala Ile His Phe Pro Gln Pro Leu Ser	
534 539 544 549	
gat gat att cgg gct gct ccc atc tcc tgc cgt gtc cag gtt gca cat	1793
Asp Asp Ile Arg Ala Ala Pro Ile Ser Cys Arg Val Gln Val Ala His	
550 555 560 565	
gag aag gaa cag gtg ata ccc atc gcc ttg ctg agc ctc cta ttc cgg	1841
Glu Lys Glu Gln Val Ile Pro Ile Ala Leu Leu Ser Leu Leu Phe Arg	
566 571 576 581	
tgc tcg atc act gag gct cag gca cac ctg gct gca gct cct tct gtc	1889
Cys Ser Ile Thr Glu Ala Gln Ala His Leu Ala Ala Ala Pro Ser Val	
582 587 592 597	
tgt gag gct gtc agg agt gct ctt gct ggg cca ggt cag aag cgc act	1937
Cys Glu Ala Val Arg Ser Ala Leu Ala Gly Pro Gly Gln Lys Arg Thr	
598 603 608 613	
gcg gac ccc ctc gag atc cta gag cct gac gtt cag tga acccatgttt	1986
Ala Asp Pro Leu Glu Ile Leu Glu Pro Asp Val Gln *	

cca cct gag aaa gaa ggg gac cag gcc cag ctg gat gca gcc tcc gtg	505
Pro Pro Glu Lys Glu Gly Asp Gln Ala Gln Leu Asp Ala Ala Ser Val	
108 113 118 123	
tct tcc atc cag gtg gtg ggc gtc gtc gag gcg ctg atc cag agc gca	553
Ser Ser Ile Gln Val Val Gly Val Val Glu Ala Leu Ile Gln Ser Ala	
124 129 134 139	
gac acc ctc ttc cct gga gac atc aac ttc aac gtg tca ggc ctc ttc	601
Asp Thr Leu Phe Pro Gly Asp Ile Asn Phe Asn Val Ser Gly Leu Phe	
140 145 150 155	
tca gct gtt acc ctc cag gac aca gtc agt gac agg ctg gcc tct gag	649
Ser Ala Val Thr Leu Gln Asp Thr Val Ser Asp Arg Leu Ala Ser Glu	
156 161 166 171	
gaa ctt ccg tcc act gcc gtg ccc acc cca gcc acc acc ccg gct ccg	697
Glu Leu Pro Ser Thr Ala Val Pro Thr Pro Ala Thr Thr Pro Ala Pro	
172 177 182 187	
gct ccg gct cca gct cca gct ccg gcc cca gcc ttg gct tca gca gct	745
Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Leu Ala Ser Ala Ala	
188 193 198 203	
acc aag gaa agg aca gag tct gag gtg cct ccc aga cca gcc tcc ccc	793
Thr Lys Glu Arg Thr Glu Ser Glu Val Pro Pro Arg Pro Ala Ser Pro	
204 209 214 219	
aag gtc acc agg agt ccc ccg gag aca gct gcc cca gtg gag gac atg	841
Lys Val Thr Arg Ser Pro Pro Glu Thr Ala Ala Pro Val Glu Asp Met	
220 225 230 235	
gct cgg agg acc aag cgc ccg gcg cca gcc cgg ccc acc atg ccg ccc	889
Ala Arg Arg Thr Lys Arg Pro Ala Pro Ala Arg Pro Thr Met Pro Pro	
236 241 246 251	
ccc cag gtc tcc ggc tcc cgc tcc tcc cct cca gcc ccg ccc ttg ccc	937
Pro Gln Val Ser Gly Ser Arg Ser Ser Pro Pro Ala Pro Pro Leu Pro	
252 257 262 267	
cct ggc tct ggc agc cct ggg acc ccc caa gcc ctg ccc cga cgt ctg	985
Pro Gly Ser Gly Ser Pro Gly Thr Pro Gln Ala Leu Pro Arg Arg Leu	
268 273 278 283	
gtt ggc agc agc ctc cga gcc ccc aca gtg cca ccc ccg tta ccc ccc	1033
Val Gly Ser Ser Leu Arg Ala Pro Thr Val Pro Pro Pro Leu Pro Pro	
284 289 294 299	
aca ccc cct cag cct gcc cgg cgc caa agc cgg cgt tca cca gcc tcc	1081
Thr Pro Pro Gln Pro Ala Arg Arg Gln Ser Arg Arg Ser Pro Ala Ser	
300 305 310 315	
ccc agc ccg gcc tcc cca ggt cca gcc tcc ccc agc cca gtc tct ttg	1129
Pro Ser Pro Ala Ser Pro Gly Pro Ala Ser Pro Ser Pro Val Ser Leu	
316 321 326 331	
agt aac cct gca cag gtg gac ctg ggg gct gcc aca gca gag gga gga	1177

```

Ser Asn Pro Ala Gln Val Asp Leu Gly Ala Ala Thr Ala Glu Gly Gly
332                               337                               342                               347

gcc cct gag gct atc agt ggg gtc ccc act ccc cca gct atc ccc cct      1225
Ala Pro Glu Ala Ile Ser Gly Val Pro Thr Pro Pro Ala Ile Pro Pro
348                               353                               358                               363

cag ccc cgc ccc agg agc ctt gcc tca gag acc aac tga gtggctgggt      1274
Gln Pro Arg Pro Arg Ser Leu Ala Ser Glu Thr Asn  *
364                               369                               374

tctccctaag cagccctcag caccacctcc ctccccacct ggccctccca ggacagctct      1334

cgccccccac aaaggggcat gggcctccag cctttgccca caagtgcctc agtgcccact      1394

gggtcggccc ccatggccag gagggctcag gacaatcctc tatttcctga ccttttcctc      1454

gtccaccctg ggcttgggga cccccccacc ggactctcca ctctccggca ggtcctaggg      1514

gagccaccgg aaggaaggag aggtttgcct gctcctacgg gactgattct tctcttgccg      1574

acatgttttt tgtaaggctg gtaaataaat tattttggac                          1614

<210> 88
<211> 1188
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (179)..(1141)

<400> 88
gttggacgag gctggaagaa gggagtgaga ctgctcagag aggcaggatt cctgctgact      60

ccagggggac acctggcacc tcagcttcct ttccacttc tccaggctgc atggaggggt      120

gccgggcagg ggctccttg aagggaaacct cctgcagcct caagcaccag gtcatgac      178
atg aca tct atc cct ttc cca ggt gac cga ctc ctg cag gtg gat gga      226
Met Thr Ser Ile Pro Phe Pro Gly Asp Arg Leu Leu Gln Val Asp Gly
1 5 10 15

gtg att ctg tgc ggc ctc acc cac aag cag gct gtg cag tgc ctg aag      274
Val Ile Leu Cys Gly Leu Thr His Lys Gln Ala Val Gln Cys Leu Lys
17 22 27 32

ggc cct ggg cag gtt gca aga ctg gtc tta gag aga aga gtc ccc agg      322
Gly Pro Gly Gln Val Ala Arg Leu Val Leu Glu Arg Arg Val Pro Arg
33 38 43 48

agt aca cag cag tgt cct tct gct aat gac agc atg gga gat gaa cgc      370
Ser Thr Gln Gln Cys Pro Ser Ala Asn Asp Ser Met Gly Asp Glu Arg
49 54 59 64

```

acg gct gtt tcc ttg gta aca gcc ttg cct ggc agg cct tcg agc tgt	418
Thr Ala Val Ser Leu Val Thr Ala Leu Pro Gly Arg Pro Ser Ser Cys	
65 70 75 80	
gtc tcg gtg aca gat ggt cct aag ttt gaa gtc aaa cta aaa aag aat	466
Val Ser Val Thr Asp Gly Pro Lys Phe Glu Val Lys Leu Lys Lys Asn	
81 86 91 96	
gcc aat ggt ttg gga ttc agt ttc gtg cag atg gag aaa gag agc tgc	514
Ala Asn Gly Leu Gly Phe Ser Phe Val Gln Met Glu Lys Glu Ser Cys	
97 102 107 112	
agc cat ctc aaa agt gat ctt gtg agg att aag agg ctc ttt ccg ggg	562
Ser His Leu Lys Ser Asp Leu Val Arg Ile Lys Arg Leu Phe Pro Gly	
113 118 123 128	
cag cca gct gag gag aat ggg gcc att gca gct ggt gac att atc ctg	610
Gln Pro Ala Glu Glu Asn Gly Ala Ile Ala Ala Gly Asp Ile Ile Leu	
129 134 139 144	
gcc gtg aat gga agg tcc acg gaa ggc ctc atc ttc cag gag gtg ctg	658
Ala Val Asn Gly Arg Ser Thr Glu Gly Leu Ile Phe Gln Glu Val Leu	
145 150 155 160	
cat tta ctg aga ggg gcc cca cag gaa gtc acg ctc ctc ctt tgc cga	706
His Leu Leu Arg Gly Ala Pro Gln Glu Val Thr Leu Leu Leu Cys Arg	
161 166 171 176	
ccc cct cca ggt gcg ctg cct gag atg gag cag gaa tgg cag aca cct	754
Pro Pro Pro Gly Ala Leu Pro Glu Met Glu Gln Glu Trp Gln Thr Pro	
177 182 187 192	
gaa ctc tca gct gac aaa gaa ttc acc agg gca aca tgt act gac tca	802
Glu Leu Ser Ala Asp Lys Glu Phe Thr Arg Ala Thr Cys Thr Asp Ser	
193 198 203 208	
tgt acc agc ccc atc ctg gat caa gag gac agc tgg agg gac agt gcc	850
Cys Thr Ser Pro Ile Leu Asp Gln Glu Asp Ser Trp Arg Asp Ser Ala	
209 214 219 224	
tcc cca gat gca ggg gaa ggc ctg ggt ctc agg cca gag tct tcc caa	898
Ser Pro Asp Ala Gly Glu Gly Leu Gly Leu Arg Pro Glu Ser Ser Gln	
225 230 235 240	
aag gcc atc aga gag gca caa tgg ggc caa aac aga gag aga cct tgg	946
Lys Ala Ile Arg Glu Ala Gln Trp Gly Gln Asn Arg Glu Arg Pro Trp	
241 246 251 256	
gcc agt tcc ttg aca cat tct cct gag tcc cac cct cat tta tgc aaa	994
Ala Ser Ser Leu Thr His Ser Pro Glu Ser His Pro His Leu Cys Lys	
257 262 267 272	
ctt cac caa gaa agg gat gaa tca aca ttg gcg acc tct ttg gaa aag	1042
Leu His Gln Glu Arg Asp Glu Ser Thr Leu Ala Thr Ser Leu Glu Lys	
273 278 283 288	
gat gtg agg caa aac tgc tat tca gtt tgt gat atc atg aga ctt gga	1090

Asp Val Arg Gln Asn Cys Tyr Ser Val Cys Asp Ile Met Arg Leu Gly
 289 294 299 304
 aga tat tcc ttc tca tct cct cta acc aga ctt tcg aca gat att ttc 1138
 Arg Tyr Ser Phe Ser Ser Pro Leu Thr Arg Leu Ser Thr Asp Ile Phe
 305 310 315 320
 tga gcaccttctc tgcattgtctg cagtgtgtg taaaatgccc tcgtgcc 1188
 *
 321

<210> 89
 <211> 1402
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (893)..(1234)

<400> 89
 aaaaatacta tctatcctct caccgttgat ggcaactgtct tccccaaaag cccaaggaa 60
 ctctgaagg agaagccctt ccaactctgtg cccttcctca tgggtgtcaa caaccatgag 120
 ttcagctggc tcatccccag gggctggggg ctctggata caatggagca gatgagccgg 180
 gaggacatgc tggccatctc aacaccgctc ttgaccagtc tggatgtgcc ccctgagatg 240
 atgcccaccg tcatagatga atacctagga agcaactcgg acgcacaagc caaatgccag 300
 gcgttccagg aattcatggg tgacgtattc atcaatgttc ccaccgtcag tttttcaaga 360
 taccttcgag attctggaag ccctgtcttt ttctatgagt tccagcatcg acccagttct 420
 tttgcgaaga tcaaacctgc ctgggtgaag gctgatcatg gggccgaggg tgcttttgtg 480
 ttcggagggtc ccttcctcat ggaagagagc tccgcctgg cctttccaga ggccacagag 540
 gaggagaagc agctaagcct caccatgatg gccagtgga cccactttgc ccggacagga 600
 cctcccacac tttggggcat cgttgccact ggagcctctc ttcgggtgac gttgccctc 660
 cctgtgccc ccaagctggc cccttcccac tcttcagacc ttgaccagga cccagggaaa 720
 caaggcaatc gctggcggtg cgggcctctg ggccgtcctc tggggttccg agaggacccc 780
 accttacaga tgaggaaatt agaatcagag aggggcagta ccgtgcctga ggccacacag 840
 gctgaggccc caggataagt tccttgtgtg ggcctcagat ggcctgtggg ac atg 895
 Met
 1

ctg agc aat gag gac gtg gta agg ctg gtg gtg ggg cac ctg gct gag	943
Leu Ser Asn Glu Asp Val Val Arg Leu Val Val Gly His Leu Ala Glu	
2 7 12 17	
gca gat tgg cac aag aca gac ctg gcc cag aga ccc gcc aac ttg ggg	991
Ala Asp Trp His Lys Thr Asp Leu Ala Gln Arg Pro Ala Asn Leu Gly	
18 23 28 33	
ctc atg cag agc ctg ctg ctg cag agg aaa gcc agc ggg ctc cac gag	1039
Leu Met Gln Ser Leu Leu Leu Gln Arg Lys Ala Ser Gly Leu His Glu	
34 39 44 49	
gct gac caa aat gca gcc acg cgg ctg atc aga cat gcc atc ggg aac	1087
Ala Asp Gln Asn Ala Ala Thr Arg Leu Ile Arg His Ala Ile Gly Asn	
50 55 60 65	
aat gag tat ggg gag atg gag gca gag cgg ctg gcg gcg atg ctg aca	1135
Asn Glu Tyr Gly Glu Met Glu Ala Glu Arg Leu Ala Ala Met Leu Thr	
66 71 76 81	
ttg cca gag gac ttg gcg agg atg tac agg gat gat atc act gtc act	1183
Leu Pro Glu Asp Leu Ala Arg Met Tyr Arg Asp Asp Ile Thr Val Thr	
82 87 92 97	
gtg gtg tat ttt aac tca gaa tca atc ggt gca tat tac aag ggg ggt	1231
Val Val Tyr Phe Asn Ser Glu Ser Ile Gly Ala Tyr Tyr Lys Gly Gly	
98 103 108 113	
taa gaat ctcccatcct attgtcaagg ttaacataaaa tgctcttcta aaatgtttca	1288
* 114	
cttactccta aactagctat ccaaacctat gatgtgagtg cccagacatc tacatatcac	1348
ctttcctttt ggtttttgct ctgagctacc tcaatcattc taaagcttta agtt	1402

<210> 90
 <211> 2610
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (165)..(2267)

<400> 90	
ccccccatcg aacgcctgcg gtaccgggtcc ggaatccctg ggtcgaccca cgcgtccggc	60
caggccagag acagctgcgc tgtgcgggca gctagtccca gtactccgag tcggtcgcgg	120
gccgacaggc atccccctgag cgccctgctgg gctcttatca cgcg atg gca tcc act	176
Met Ala Ser Thr	

gtg gaa gga ggc gac aca gct ctg ctc cca gaa ttc ccc agg ggg ccc	224
Val Glu Gly Gly Asp Thr Ala Leu Leu Pro Glu Phe Pro Arg Gly Pro	
5 10 15 20	
ctc gat gcc tac cga gca aga gcg tcc ttc agc tgg aag gag ctg gcg	272
Leu Asp Ala Tyr Arg Ala Arg Ala Ser Phe Ser Trp Lys Glu Leu Ala	
21 26 31 36	
ctg ttc acg gaa ggg gag ggc atg ctc cgc ttt aag aaa acc atc ttc	320
Leu Phe Thr Glu Gly Glu Gly Met Leu Arg Phe Lys Lys Thr Ile Phe	
37 42 47 52	
tca gct ctt gag aat gac cct ctt ttc gct cgt tcc cct gga gcc gat	368
Ser Ala Leu Glu Asn Asp Pro Leu Phe Ala Arg Ser Pro Gly Ala Asp	
53 58 63 68	
ctg tcc ttg gag aag tat cgc gag ctg aac ttc ctt cga tgc aag cgg	416
Leu Ser Leu Glu Lys Tyr Arg Glu Leu Asn Phe Leu Arg Cys Lys Arg	
69 74 79 84	
atc ttc gag tat gac ttc ctc agt gtc gaa gac atg ttc aag agc cct	464
Ile Phe Glu Tyr Asp Phe Leu Ser Val Glu Asp Met Phe Lys Ser Pro	
85 90 95 100	
ctg aag gtc ccc gcc ttg att cag tgc ctg ggc atg tat gac tct tct	512
Leu Lys Val Pro Ala Leu Ile Gln Cys Leu Gly Met Tyr Asp Ser Ser	
101 106 111 116	
ctg gct gcc aag tac ctc ctc cat agc ttg gtt ttt gga tca gca gtt	560
Leu Ala Ala Lys Tyr Leu Leu His Ser Leu Val Phe Gly Ser Ala Val	
117 122 127 132	
tac agt tct ggt tct gaa aga cat ctc aca tat att caa aag atc ttc	608
Tyr Ser Ser Gly Ser Glu Arg His Leu Thr Tyr Ile Gln Lys Ile Phe	
133 138 143 148	
agg atg gag att ttt gga tgt ttt gct ctg acc gaa tta agc cac ggc	656
Arg Met Glu Ile Phe Gly Cys Phe Ala Leu Thr Glu Leu Ser His Gly	
149 154 159 164	
agt aat acc aag gcc att cgc aca act gcc cac tac gat cct gcc act	704
Ser Asn Thr Lys Ala Ile Arg Thr Thr Ala His Tyr Asp Pro Ala Thr	
165 170 175 180	
gag gaa ttc atc ata cat tcc cct gat ttc gaa gct gcc aag ttt tgg	752
Glu Glu Phe Ile Ile His Ser Pro Asp Phe Glu Ala Ala Lys Phe Trp	
181 186 191 196	
gtt ggc aac atg ggc aag aca gcc act cac gcg gtg gtg ttt gct aag	800
Val Gly Asn Met Gly Lys Thr Ala Thr His Ala Val Val Phe Ala Lys	
197 202 207 212	
ctg tgt gtg cca ggg gac cag tgc cat ggg ctg cat ccc ttt atc gtg	848
Leu Cys Val Pro Gly Asp Gln Cys His Gly Leu His Pro Phe Ile Val	
213 218 223 228	
cag atc cgg gac ccg aag acc ctt ctt ccc atg cct gga gtg atg gtt	896

Gln	Ile	Arg	Asp	Pro	Lys	Thr	Leu	Leu	Pro	Met	Pro	Gly	Val	Met	Val	
229					234					239					244	
ggc	gac	ata	gga	aaa	aaa	ctc	ggg	cag	aac	ggt	ctg	gat	aat	ggt	ttc	944
Gly	Asp	Ile	Gly	Lys	Lys	Leu	Gly	Gln	Asn	Gly	Leu	Asp	Asn	Gly	Phe	
245					250					255					260	
gcc	atg	ttc	cac	aag	gtc	aga	gtt	cct	cgc	cag	agc	ctt	ctg	aac	cgg	992
Ala	Met	Phe	His	Lys	Val	Arg	Val	Pro	Arg	Gln	Ser	Leu	Leu	Asn	Arg	
261					266					271					276	
atg	gga	gac	gtc	acc	ccc	gag	ggc	acc	tat	gtc	agc	ccc	ttt	aag	gac	1040
Met	Gly	Asp	Val	Thr	Pro	Glu	Gly	Thr	Tyr	Val	Ser	Pro	Phe	Lys	Asp	
277					282					287					292	
gtc	agg	cag	cgc	ttt	gga	gcg	tcc	ctg	ggg	agc	ctg	tcc	tcg	ggc	cgg	1088
Val	Arg	Gln	Arg	Phe	Gly	Ala	Ser	Leu	Gly	Ser	Leu	Ser	Ser	Gly	Arg	
293					298					303					308	
gtc	tcc	atc	gtg	agc	ctg	gcc	atc	ctt	aac	cta	aag	ctg	gcc	gtg	gcc	1136
Val	Ser	Ile	Val	Ser	Leu	Ala	Ile	Leu	Asn	Leu	Lys	Leu	Ala	Val	Ala	
309					314					319					324	
atc	gct	ctt	cgc	ttc	tca	gcc	act	cgg	cgt	cag	ttt	gga	ccc	aca	gag	1184
Ile	Ala	Leu	Arg	Phe	Ser	Ala	Thr	Arg	Arg	Gln	Phe	Gly	Pro	Thr	Glu	
325					330					335					340	
gag	gag	gaa	ata	cca	gtg	ctt	gag	tat	cca	atg	cag	caa	tgg	cgc	ttg	1232
Glu	Glu	Glu	Ile	Pro	Val	Leu	Glu	Tyr	Pro	Met	Gln	Gln	Trp	Arg	Leu	
341					346					351					356	
ctt	cca	tat	ctg	gca	gct	gtc	tac	gcc	tta	gac	cat	ttc	tcc	aag	tcg	1280
Leu	Pro	Tyr	Leu	Ala	Ala	Val	Tyr	Ala	Leu	Asp	His	Phe	Ser	Lys	Ser	
357					362					367					372	
ctc	ttc	ctg	gac	ctg	gtg	gag	ctc	cag	cga	gga	ctt	gca	tcg	gga	gac	1328
Leu	Phe	Leu	Asp	Leu	Val	Glu	Leu	Gln	Arg	Gly	Leu	Ala	Ser	Gly	Asp	
373					378					383					388	
cgc	agc	gcc	aga	cag	gca	gag	ctt	gga	cgt	gag	atc	cac	gcc	ctg	gca	1376
Arg	Ser	Ala	Arg	Gln	Ala	Glu	Leu	Gly	Arg	Glu	Ile	His	Ala	Leu	Ala	
389					394					399					404	
tcg	gcc	agc	aag	ccc	ctg	gcc	tcg	tgg	acc	acc	cag	caa	gga	att	cag	1424
Ser	Ala	Ser	Lys	Pro	Leu	Ala	Ser	Trp	Thr	Thr	Gln	Gln	Gly	Ile	Gln	
405					410					415					420	
gaa	tgc	cgg	gag	gcg	tgt	gga	gga	cac	ggc	tat	ctg	gcc	atg	aac	cgg	1472
Glu	Cys	Arg	Glu	Ala	Cys	Gly	Gly	His	Gly	Tyr	Leu	Ala	Met	Asn	Arg	
421					426					431					436	
ttg	ggt	gtc	ctt	aga	gat	gac	aac	gat	ccc	aac	tgc	aca	tac	gaa	ggt	1520
Leu	Gly	Val	Leu	Arg	Asp	Asp	Asn	Asp	Pro	Asn	Cys	Thr	Tyr	Glu	Gly	
437					442					447					452	
gac	aac	aac	atc	ctg	ctg	cag	cag	aca	agc	aac	tat	ttg	ctg	ggt	ctc	1568
Asp	Asn	Asn	Ile	Leu	Leu	Gln	Gln	Thr	Ser	Asn	Tyr	Leu	Leu	Gly	Leu	

453	458	463	468	
ctg gca cac cag gtc cac gat gga gct tgc ttc cgc agt ccg ctg aag				1616
Leu Ala His Gln Val His Asp Gly Ala Cys Phe Arg Ser Pro Leu Lys				
469	474	479	484	
tca gtg gac ttt ctg gac gcc tat ccc ggc atc ctt gac cag aag ttt				1664
Ser Val Asp Phe Leu Asp Ala Tyr Pro Gly Ile Leu Asp Gln Lys Phe				
485	490	495	500	
gag gtc tcc agt gtt gcc gac tgc ttg gac tct gca gtc gcc ctg gca				1712
Glu Val Ser Ser Val Ala Asp Cys Leu Asp Ser Ala Val Ala Leu Ala				
501	506	511	516	
gca tac aag tgg ctg gtt tgc tac ctg ctc cga gag act tat caa aaa				1760
Ala Tyr Lys Trp Leu Val Cys Tyr Leu Leu Arg Glu Thr Tyr Gln Lys				
517	522	527	532	
tta aac caa gag aaa aga tca gga agc agt gac ttt gaa gca agg aac				1808
Leu Asn Gln Glu Lys Arg Ser Gly Ser Ser Asp Phe Glu Ala Arg Asn				
533	538	543	548	
aaa tgc cag gtg tcc cac ggc cgt ccg ttg gcg ctg gcc ttc gtg gac				1856
Lys Cys Gln Val Ser His Gly Arg Pro Leu Ala Leu Ala Phe Val Asp				
549	554	559	564	
ctc acg gtg gtc cag agg ttc cac gag cac gtg cac cag cct tcc gtg				1904
Leu Thr Val Val Gln Arg Phe His Glu His Val His Gln Pro Ser Val				
565	570	575	580	
ccg ccc tcg ctg cgg gcc gtg ctg ggg cgg ctc agt gct ctg tac gcc				1952
Pro Pro Ser Leu Arg Ala Val Leu Gly Arg Leu Ser Ala Leu Tyr Ala				
581	586	591	596	
ctg tgg tcc ctg agc cgc cac gcg gcc ctg ctc tac cga gga gga tac				2000
Leu Trp Ser Leu Ser Arg His Ala Ala Leu Leu Tyr Arg Gly Gly Tyr				
597	602	607	612	
ttc tcc ggt gag cag gcg gga gaa gtg ttg gag agc gcc gtc ctg gct				2048
Phe Ser Gly Glu Gln Ala Gly Glu Val Leu Glu Ser Ala Val Leu Ala				
613	618	623	628	
ttg tgt tcc cag ctg aaa gac gat gca gtt gcc ctg gta gac gtg atc				2096
Leu Cys Ser Gln Leu Lys Asp Asp Ala Val Ala Leu Val Asp Val Ile				
629	634	639	644	
gct cct cct gac ttt gtt ctg gac tca ccg att ggc aga gcc gac ggc				2144
Ala Pro Pro Asp Phe Val Leu Asp Ser Pro Ile Gly Arg Ala Asp Gly				
645	650	655	660	
gag ctc tac aaa aac ctc tgg ggc gct gtc ctg cag gaa agc aag gtg				2192
Glu Leu Tyr Lys Asn Leu Trp Gly Ala Val Leu Gln Glu Ser Lys Val				
661	666	671	676	
ttg gag cgg gca tcc tgg tgg cca gag ttt tct gtg aac aaa cct gtc				2240
Leu Glu Arg Ala Ser Trp Trp Pro Glu Phe Ser Val Asn Lys Pro Val				
677	682	687	692	

ata gga agt ctg aaa tcg aag ctc tag tggga ctggcacatt cagccaagtc 2292
 Ile Gly Ser Leu Lys Ser Lys Leu *
 693 698

taatgaaacg aagggaacta atcagacgtg gacctcaact tctgattcca gaacacgccg 2352

gagattgctg ctgctttctg agcccgccacc tgtgcgccta aactgctgat tggcctcaac 2412

tgcccaggcg gacgggaggg aggcacccgg cgggctggac taatctggga tcgcggtgat 2472

ttgcagcgtg gaaaagaaat gcagatgac atgtctacct gatgcgccgt gggttttttg 2532

ataattagaa tttcgcacat tcagttttca gggttcagct cctttctcta aagtaaacag 2592

cccattgtca gggaaaaa 2610

<210> 91
 <211> 1071
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (177)..(878)

<400> 91

atgaccacta tagggaattht ggccctcgag caagaattcg gcacgagggt ggtaggctgc 60

gacccttcc tcccacagcc ccttcccgcc cctcgccggg catccgccga caggtacata 120

ccaagaaatt gaattgctga gtcacaggag agatttacia atagtgtttt ggcac 176
 atg gaa cgt gta ggt tgt act tta acg aca act tac gcc cac cct aga 224
 Met Glu Arg Val Gly Cys Thr Leu Thr Thr Thr Tyr Ala His Pro Arg
 1 5 10 15

cca aca cca acc aac ttt cta cca gcc atc agt acc atg gcc tca agc 272
 Pro Thr Pro Thr Asn Phe Leu Pro Ala Ile Ser Thr Met Ala Ser Ser
 17 22 27 32

tac agg gac cgc ttt ccc cac tcc aat ttg acc cat agc ctg agc ctt 320
 Tyr Arg Asp Arg Phe Pro His Ser Asn Leu Thr His Ser Leu Ser Leu
 33 38 43 48

cct tgg aga ccc agc aca tac tac aaa gtc gcc tcc aat tcc cca agc 368
 Pro Trp Arg Pro Ser Thr Tyr Tyr Lys Val Ala Ser Asn Ser Pro Ser
 49 54 59 64

gtg gcc ccg tac tgc acc aga tca cag agg gtg tcc gag aat acc atg 416
 Val Ala Pro Tyr Cys Thr Arg Ser Gln Arg Val Ser Glu Asn Thr Met
 65 70 75 80

ctt ccc ttt gtt tcc aac aga acc act ttc ttc aca aga tac aca ccg 464
 Leu Pro Phe Val Ser Asn Arg Thr Thr Phe Phe Thr Arg Tyr Thr Pro

gaattcccca gacttgtaag ccgggggctg agcctcaggg caggggtgca gatgggggtg	60
cagcctcccc gcttcccggc gactccggga aggtcagcgc gggcagtcgg ggcgcgctcc	120
tgcgcccggg cctcgccggc aacccgggtcc ccacctgaaa ccccgctgc cactccgttc	180
cagagggcca atagccgtgc aacctgcccc ggatggggcg ggacttatgc aaatagtgtc	240
gccttcggga ggcacatagt gatacaagag ctggaaggcg gctccggcgc agaccttgga	300
gagcacagct gccggccccgc gagccagcct cggttcccgc ggcccgccga ggctcggagc	360
catccagcga cccggcgacc ggccctcaggc cccgcc atg ggg aag acc aac agc	414
Met Gly Lys Thr Asn Ser	
1	
aag ctg gcc ccc gag gtg ctg gag gac ctt gtt cag aac act gag ttc	462
Lys Leu Ala Pro Glu Val Leu Glu Asp Leu Val Gln Asn Thr Glu Phe	
7 12 17 22	
agc gag cag gag ctg aag cag tgg tac aag ggc ttc ctg aag gac tgc	510
Ser Glu Gln Glu Leu Lys Gln Trp Tyr Lys Gly Phe Leu Lys Asp Cys	
23 28 33 38	
ccc agc ggc atc ctc aac ctg gag gag ttt cag cag ctc tac atc aag	558
Pro Ser Gly Ile Leu Asn Leu Glu Glu Phe Gln Gln Leu Tyr Ile Lys	
39 44 49 54	
ttc ttc ccc tac ggc gac gcc tcc aag ttc gcg cag cac gct ttc cgc	606
Phe Phe Pro Tyr Gly Asp Ala Ser Lys Phe Ala Gln His Ala Phe Arg	
55 60 65 70	
acc ttc gac aag aac ggc gac ggc acc atc gac ttc cgg gag ttc atc	654
Thr Phe Asp Lys Asn Gly Asp Gly Thr Ile Asp Phe Arg Glu Phe Ile	
71 76 81 86	
tgc gcc ctg tcg gtc acc tcc cgc ggc agc ttc gag cag aag ctc aac	702
Cys Ala Leu Ser Val Thr Ser Arg Gly Ser Phe Glu Gln Lys Leu Asn	
87 92 97 102	
tgg gcc ttt gag atg tac gac ctg gac ggc gac ggg cgc atc acg cgc	750
Trp Ala Phe Glu Met Tyr Asp Leu Asp Gly Asp Gly Arg Ile Thr Arg	
103 108 113 118	
ctg gag atg ctg gag atc atc gag gca atc tac aag atg gtg ggc acc	798
Leu Glu Met Leu Glu Ile Ile Glu Ala Ile Tyr Lys Met Val Gly Thr	
119 124 129 134	
gtg atc atg atg cgc atg aac cag gac ggg ctc acg ccc cag cag cgt	846
Val Ile Met Met Arg Met Asn Gln Asp Gly Leu Thr Pro Gln Gln Arg	
135 140 145 150	
gtg gac aag atc ttc aag aag atg gac cag gat aag gac gac cag att	894
Val Asp Lys Ile Phe Lys Lys Met Asp Gln Asp Lys Asp Asp Gln Ile	
151 156 161 166	
aca ttg gag gag ttc aag gag gca gcc aag agt gac cca tcc att gtg	942


```

Thr Leu Glu Glu Phe Lys Glu Ala Ala Lys Ser Asp Pro Ser Ile Val
167                      172                      177                      182

ttg ctg ctg cag tgt gac atg cag aag tag a agctgggtgag gggcagggtc      993
Leu Leu Leu Gln Cys Asp Met Gln Lys  *
183                      188

cctggccaga aggggcatgg ccacctccca acctgatgac ctctctggct ggcctcccag    1053
gaggagggac actccagccc ccctctcttg cccacccagt cctctgcccc agcccttcct    1113
cccctccatc aagatctttg agggaccacc tcacctgca aaagagacag gtcctccagt    1173
accctgtctt ctagccccac ctcccacttg gccagaacca atgtccattg ggcatagggg    1233
agttggcttt tgccccagga ggtgaggtta aggagttggg ggccctgggg ttctggttag    1293
gaattctctt gatcctggga ttatgcttta tgggatgtgg tcccacaggc ctgtcacagg    1353
gccaaattgg gtctgtccat tcctgaggct ccagatccca taaagggggg ctcttcccca    1413
tcccttctac tctacctggc ccttcacagc ccagcctttg gagcgttcat tcagtccttt    1473
cttcagctaa tgattactga cacctgtttg gtgctaagga tatggtcatt tacaagacac    1533
atcttgtgcc ctctggaagc tcatagggtt gtgaggcaaa cttccagccg tcagggtctc    1593
agctaagcag aaggtgctgg aaggcggaat tcat                                  1627

<210> 93
<211> 1371
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (117)..(1133)

<400> 93
taagcttgcg gccgcttcta gtagtttcca ggcgctgccg ggcggctggc actaagcgg      60

cctgaggctg tggctacggc tgctccggag ctggtggcgc cgcgatagga gagccg      116
atg gcc aag tgg ggt gag gga gac cca cgc tgg atc gtg gag gag cgg      164
Met Ala Lys Trp Gly Glu Gly Asp Pro Arg Trp Ile Val Glu Glu Arg
  1              5              10              15

gcg gac gcc acc aac gtc aac aac tgg cac tgg acg gag aga gat gct      212
Ala Asp Ala Thr Asn Val Asn Asn Trp His Trp Thr Glu Arg Asp Ala
  17              22              27              32

tca aat tgg tcc acg gat aag ctg aaa aca ctg ttc ttg gca gtg cag      260
Ser Asn Trp Ser Thr Asp Lys Leu Lys Thr Leu Phe Leu Ala Val Gln
  33              38              43              48

```

gtt	caa	aat	gaa	gaa	ggc	aag	tgt	gag	gtg	acg	gaa	gtg	agt	aag	ctt	308
Val	Gln	Asn	Glu	Glu	Gly	Lys	Cys	Glu	Val	Thr	Glu	Val	Ser	Lys	Leu	
49					54					59					64	
gat	gga	gag	gca	tcc	att	aac	aat	cgc	aaa	ggg	aaa	ctt	atc	ttc	ttt	356
Asp	Gly	Glu	Ala	Ser	Ile	Asn	Asn	Arg	Lys	Gly	Lys	Leu	Ile	Phe	Phe	
65					70					75					80	
tat	gaa	tgg	agc	gtc	aaa	cta	aac	tgg	aca	ggg	act	tct	aag	tca	gga	404
Tyr	Glu	Trp	Ser	Val	Lys	Leu	Asn	Trp	Thr	Gly	Thr	Ser	Lys	Ser	Gly	
81					86					91					96	
gta	cag	tac	aaa	gga	cat	gtg	gag	atc	ccc	aat	ttg	tct	gat	gaa	aac	452
Val	Gln	Tyr	Lys	Gly	His	Val	Glu	Ile	Pro	Asn	Leu	Ser	Asp	Glu	Asn	
97					102					107					112	
agc	gtg	gat	gaa	gtg	gag	att	agt	gtg	agc	ctt	gcc	aaa	gat	gag	cct	500
Ser	Val	Asp	Glu	Val	Glu	Ile	Ser	Val	Ser	Leu	Ala	Lys	Asp	Glu	Pro	
113					118					123					128	
gac	aca	aat	ctc	gtg	gcc	tta	atg	aag	gaa	gaa	ggg	gtg	aaa	ctt	cta	548
Asp	Thr	Asn	Leu	Val	Ala	Leu	Met	Lys	Glu	Glu	Gly	Val	Lys	Leu	Leu	
129					134					139					144	
aga	gaa	gca	atg	gga	att	tac	atc	agc	acc	ctc	aaa	aca	gag	ttc	acc	596
Arg	Glu	Ala	Met	Gly	Ile	Tyr	Ile	Ser	Thr	Leu	Lys	Thr	Glu	Phe	Thr	
145					150					155					160	
cag	ggc	atg	atc	tta	cct	aca	atg	aat	gga	gag	tca	gta	gac	cca	gtg	644
Gln	Gly	Met	Ile	Leu	Pro	Thr	Met	Asn	Gly	Glu	Ser	Val	Asp	Pro	Val	
161					166					171					176	
ggg	cag	cca	gca	ctg	aaa	act	gag	gag	cgc	aag	gct	aag	cct	gct	cct	692
Gly	Gln	Pro	Ala	Leu	Lys	Thr	Glu	Glu	Arg	Lys	Ala	Lys	Pro	Ala	Pro	
177					182					187					192	
tca	aaa	acc	cag	gcc	aga	cct	gtt	gga	gtc	aaa	atc	ccc	act	tgt	aag	740
Ser	Lys	Thr	Gln	Ala	Arg	Pro	Val	Gly	Val	Lys	Ile	Pro	Thr	Cys	Lys	
193					198					203					208	
atc	act	ctt	aag	gaa	acc	ttc	ctg	acg	tca	cca	gag	gag	ctc	tat	aga	788
Ile	Thr	Leu	Lys	Glu	Thr	Phe	Leu	Thr	Ser	Pro	Glu	Glu	Leu	Tyr	Arg	
209					214					219					224	
gtg	ttt	acc	acc	caa	gag	ctg	gtg	cag	gcc	ttt	acc	cat	gct	cct	gca	836
Val	Phe	Thr	Thr	Gln	Glu	Leu	Val	Gln	Ala	Phe	Thr	His	Ala	Pro	Ala	
225					230					235					240	
aca	tta	gaa	gca	gac	aga	ggg	gga	aag	ttc	cac	atg	gta	gat	ggc	aac	884
Thr	Leu	Glu	Ala	Asp	Arg	Gly	Gly	Lys	Phe	His	Met	Val	Asp	Gly	Asn	
241					246					251					256	
gtc	tct	ggg	gaa	ttt	act	gat	ctg	gtc	cct	gag	aaa	cat	att	gtg	atg	932
Val	Ser	Gly	Glu	Phe	Thr	Asp	Leu	Val	Pro	Glu	Lys	His	Ile	Val	Met	
257					262					267					272	
aag	tgg	agg	ttt	aaa	tct	tgg	cca	gag	gga	cac	ttt	gcc	acc	atc	acc	980

Lys Trp Arg Phe Lys Ser Trp Pro Glu Gly His Phe Ala Thr Ile Thr	
273 278 283 288	
ttg acc ttc atc gac aag aac gga gag act gag ctg tgc atg gaa ggt	1028
Leu Thr Phe Ile Asp Lys Asn Gly Glu Thr Glu Leu Cys Met Glu Gly	
289 294 299 304	
cga ggc atc cct gct cct gag gaa gag cgg aca cga cag ggc tgg cag	1076
Arg Gly Ile Pro Ala Pro Glu Glu Glu Arg Thr Arg Gln Gly Trp Gln	
305 310 315 320	
cgg tac tac ttt gag ggc att aaa cag acc ttt ggc tat ggc gca cgc	1124
Arg Tyr Tyr Phe Glu Gly Ile Lys Gln Thr Phe Gly Tyr Gly Ala Arg	
321 326 331 336	
tta ttt tag ggccagc ggcaggggac tccagcctgc tggacacttc agtccagctc	1180
Leu Phe *	
337	
tctcctgact ggggcttgcg actcacagga ttgcatcgtc ccagctgcta acttggggcc	1240
ggggcccctc ccttccacat ataccttggg tttgtgcatg ttttctgctg ggtgggttca	1300
gagggcaatt tctcttttat gtgtacatat gctaaataaa cataatttaa aaaacaaaaa	1360
aaaaaaaaa a	1371
<210> 94	
<211> 1036	
<212> DNA	
<213> Homo sapiens	
<220>	
<221> CDS	
<222> (1)..(933)	
<400> 94	
atg tct tat ctt aag caa ccg cct tac gca gtc aat ggg ctg agt ctg	48
Met Ser Tyr Leu Lys Gln Pro Pro Tyr Ala Val Asn Gly Leu Ser Leu	
1 5 10	
acc act tcg ggt atg gac ttg ctg cac ccc tcc gtg ggc tac ccg ggt	96
Thr Thr Ser Gly Met Asp Leu Leu His Pro Ser Val Gly Tyr Pro Gly	
17 22 27 32	
ttg cct tct gag gaa gca gtc cca ggg cat tta ctg acc aag cag aga	144
Leu Pro Ser Glu Glu Ala Val Pro Gly His Leu Leu Thr Lys Gln Arg	
33 38 43 48	
aca ggg gtt ggg aaa acc acc ccc cgg aaa cag cgc cgg gag agg acg	192
Thr Gly Val Gly Lys Thr Thr Pro Arg Lys Gln Arg Arg Glu Arg Thr	
49 54 59 64	
acg ttc act cgg gcg cag cta gat gtg ctg gaa gca ctg ttt gcc aag	240

Thr	Phe	Thr	Arg	Ala	Gln	Leu	Asp	Val	Leu	Glu	Ala	Leu	Phe	Ala	Lys	
65					70					75					80	
acc	cgg	tac	cca	gac	atc	ttc	atg	cga	gag	gag	gtg	gca	ctg	aaa	atc	288
Thr	Arg	Tyr	Pro	Asp	Ile	Phe	Met	Arg	Glu	Glu	Val	Ala	Leu	Lys	Ile	
81					86					91					96	
aac	ttg	ccc	gag	tcg	agg	gtg	cag	gta	tgg	ttt	aag	aat	cga	aga	gct	336
Asn	Leu	Pro	Glu	Ser	Arg	Val	Gln	Val	Trp	Phe	Lys	Asn	Arg	Arg	Ala	
97					102					107					112	
aag	tgc	cgc	caa	caa	cag	caa	caa	cag	cag	aat	gga	ggg	caa	aac	aaa	384
Lys	Cys	Arg	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Asn	Gly	Gly	Gln	Asn	Lys	
113					118					123					128	
gtg	aga	cct	gcc	aaa	aag	aag	aca	tct	cca	gct	cgg	gaa	gtg	agt	tca	432
Val	Arg	Pro	Ala	Lys	Lys	Lys	Thr	Ser	Pro	Ala	Arg	Glu	Val	Ser	Ser	
129					134					139					144	
gag	agt	gga	aca	agt	ggc	caa	ttc	act	ccc	ccc	tct	agc	acc	tca	gtc	480
Glu	Ser	Gly	Thr	Ser	Gly	Gln	Phe	Thr	Pro	Pro	Ser	Ser	Thr	Ser	Val	
145					150					155					160	
ccg	acc	att	gcc	agc	agc	agt	gct	cct	gtg	tct	atc	tgg	agc	cca	gct	528
Pro	Thr	Ile	Ala	Ser	Ser	Ser	Ala	Pro	Val	Ser	Ile	Trp	Ser	Pro	Ala	
161					166					171					176	
tcc	atc	tcc	cca	ctg	tca	gat	ccc	ttg	tcc	acc	tcc	tct	tcc	tgc	atg	576
Ser	Ile	Ser	Pro	Leu	Ser	Asp	Pro	Leu	Ser	Thr	Ser	Ser	Ser	Cys	Met	
177					182					187					192	
cag	agg	tcc	tat	ccc	atg	acc	tat	act	cag	gct	tca	ggg	tat	agt	caa	624
Gln	Arg	Ser	Tyr	Pro	Met	Thr	Tyr	Thr	Gln	Ala	Ser	Gly	Tyr	Ser	Gln	
193					198					203					208	
gga	tat	gct	ggc	tca	act	tcc	tac	ttt	ggg	ggc	atg	gac	tgt	gga	tca	672
Gly	Tyr	Ala	Gly	Ser	Thr	Ser	Tyr	Phe	Gly	Gly	Met	Asp	Cys	Gly	Ser	
209					214					219					224	
tat	ttg	acc	cct	atg	cat	cac	cag	ctt	ccc	gga	cca	ggg	gcc	aca	ctc	720
Tyr	Leu	Thr	Pro	Met	His	His	Gln	Leu	Pro	Gly	Pro	Gly	Ala	Thr	Leu	
225					230					235					240	
agt	ccc	atg	ggg	acc	aat	gca	gtc	acc	agc	cat	ctc	aat	cag	tcc	cca	768
Ser	Pro	Met	Gly	Thr	Asn	Ala	Val	Thr	Ser	His	Leu	Asn	Gln	Ser	Pro	
241					246					251					256	
gct	tct	ctt	tcc	acc	cag	gga	tat	gga	gct	tca	agc	ttg	ggg	ttt	aac	816
Ala	Ser	Leu	Ser	Thr	Gln	Gly	Tyr	Gly	Ala	Ser	Ser	Leu	Gly	Phe	Asn	
257					262					267					272	
tca	acc	act	gat	tgc	ttg	gat	tat	aag	gac	caa	act	gcc	tcc	tgg	aag	864
Ser	Thr	Thr	Asp	Cys	Leu	Asp	Tyr	Lys	Asp	Gln	Thr	Ala	Ser	Trp	Lys	
273					278					283					288	
ctt	aac	ttc	aat	gct	gac	tgc	ttg	gat	tat	aaa	gat	cag	aca	tcc	tcg	912
Leu	Asn	Phe	Asn	Ala	Asp	Cys	Leu	Asp	Tyr	Lys	Asp	Gln	Thr	Ser	Ser	

289	294	299	304	
tgg aaa ttc cag gtt ttg tga ag acctgtagaa cctctttttg tgggtgattt				965
Trp Lys Phe Gln Val Leu *				
305	310			
ttaaataatac tgggctggac attccagttt tagccaggca ttggttaaaa gagttagatg				1025
ggatgatgcc g				1036
<210>	95			
<211>	2623			
<212>	DNA			
<213>	Homo sapiens			
<220>				
<221>	CDS			
<222>	(93)..(1460)			
<400>	95			
ggagtgaccg ccgtcgatta cgcctattta ggtgacacta tagaacaagt ttgtacaaaa				60
aagcaggctg gtaccggtcc ggaattcccg gg atg gcg cag cgg gac tgg acc				113
	Met Ala Gln Arg Asp Trp Thr			
	1 5			
tgg gtg ccg agc gga gcc gct gcc atg ggc ctg ggc gtc agc gct gag				161
Trp Val Pro Ser Gly Ala Ala Ala Met Gly Leu Gly Val Ser Ala Glu				
8 13 18 23				
cag ccc gca ggc ggc gcc gag ggc ttc cac ctg cac ggg gtg cag gag				209
Gln Pro Ala Gly Gly Ala Glu Gly Phe His Leu His Gly Val Gln Glu				
24 29 34 39				
aac tcc cca gcc cag cag gcg ggc ctg gag ccc tac ttt gac ttc atc				257
Asn Ser Pro Ala Gln Gln Ala Gly Leu Glu Pro Tyr Phe Asp Phe Ile				
40 45 50 55				
atc acc att ggg cac tcg agg ctg aac aag gag aat gac acc ctg aag				305
Ile Thr Ile Gly His Ser Arg Leu Asn Lys Glu Asn Asp Thr Leu Lys				
56 61 66 71				
gca cta ctg aaa gcc aat gtg gag aag ccc gtg aag ctg gag gtg ttc				353
Ala Leu Leu Lys Ala Asn Val Glu Lys Pro Val Lys Leu Glu Val Phe				
72 77 82 87				
aat atg aag acc atg agg gtg cgc gag gtg gag gtg gtg ccc agc aac				401
Asn Met Lys Thr Met Arg Val Arg Glu Val Glu Val Val Pro Ser Asn				
88 93 98 103				
atg tgg ggc ggc cag ggc cta ctg ggt gcc agt gtg cgc ttc tgc agc				449
Met Trp Gly Gly Gln Gly Leu Leu Gly Ala Ser Val Arg Phe Cys Ser				
104 109 114 119				

ttc cgc agg gcc agt gag cag gtg tgg cat gtg ctg gat gtg gaa cca	497
Phe Arg Arg Ala Ser Glu Gln Val Trp His Val Leu Asp Val Glu Pro	
120 125 130 135	
tct tca cct gct gcc ctt gcc ggc ctg cgc ccc tac aca gac tat gtg	545
Ser Ser Pro Ala Ala Leu Ala Gly Leu Arg Pro Tyr Thr Asp Tyr Val	
136 141 146 151	
gtt ggt tcg gac cag att ctc cag gag tcc gag gac ttc ttt acg ctc	593
Val Gly Ser Asp Gln Ile Leu Gln Glu Ser Glu Asp Phe Phe Thr Leu	
152 157 162 167	
atc gag tct cat gag ggg aag ccc ttg aag ctg atg gtg tat aac tcc	641
Ile Glu Ser His Glu Gly Lys Pro Leu Lys Leu Met Val Tyr Asn Ser	
168 173 178 183	
aag tca gac tcc tgc cgg gag gtg act gta act ccc aac gca gcc tgg	689
Lys Ser Asp Ser Cys Arg Glu Val Thr Val Thr Pro Asn Ala Ala Trp	
184 189 194 199	
ggg gga gag ggc agt ctg gga tgt ggc att ggc tat ggg tat cta cac	737
Gly Gly Glu Gly Ser Leu Gly Cys Gly Ile Gly Tyr Gly Tyr Leu His	
200 205 210 215	
cgg atc cca act cag ccc ccc agc tac cac aag aag cca cct ggc acc	785
Arg Ile Pro Thr Gln Pro Pro Ser Tyr His Lys Lys Pro Pro Gly Thr	
216 221 226 231	
cca cca cct tct gct cta cca ctt ggt gcc cca cca cct gat gct cta	833
Pro Pro Pro Ser Ala Leu Pro Leu Gly Ala Pro Pro Pro Asp Ala Leu	
232 237 242 247	
cca cct gga ccc acc ccc gag gac tct cct tcc ctg gag aca ggt tcc	881
Pro Pro Gly Pro Thr Pro Glu Asp Ser Pro Ser Leu Glu Thr Gly Ser	
248 253 258 263	
agg cag agt gac tac atg gag gcc ctg ctg cag gca cct ggc tcc tcc	929
Arg Gln Ser Asp Tyr Met Glu Ala Leu Leu Gln Ala Pro Gly Ser Ser	
264 269 274 279	
atg gag gat ccc ctt cct ggg cct ggg agt ccc agc cac agt gct cca	977
Met Glu Asp Pro Leu Pro Gly Pro Gly Ser Pro Ser His Ser Ala Pro	
280 285 290 295	
gac cct gat gga ctt ccc cat ttc atg gag act cct ctt cag ccc cca	1025
Asp Pro Asp Gly Leu Pro His Phe Met Glu Thr Pro Leu Gln Pro Pro	
296 301 306 311	
cct cca gtg cag cga gtt atg gac cca ggc ttc ctg gac gtg tcg gga	1073
Pro Pro Val Gln Arg Val Met Asp Pro Gly Phe Leu Asp Val Ser Gly	
312 317 322 327	
att tct ctc ttg gac aac agc aat gcc agt gtg tgg ccc agc ctg ccc	1121
Ile Ser Leu Leu Asp Asn Ser Asn Ala Ser Val Trp Pro Ser Leu Pro	
328 333 338 343	
tct tcc aca gaa ctg acc acc aca gct gtc tca acc tca ggg cca gag	1169

Ser Ser Thr Glu Leu Thr Thr Thr Ala Val Ser Thr Ser Gly Pro Glu	
344 349 354 359	
gac atc tgc tcc agc agc agt tct cat gag cgg ggt ggt gag gct aca	1217
Asp Ile Cys Ser Ser Ser Ser Ser Ser His Glu Arg Gly Gly Glu Ala Thr	
360 365 370 375	
tgg tct ggg tca gag ttt gag gtc tcc ttc ctg gac agc cca ggt gcc	1265
Trp Ser Gly Ser Glu Phe Glu Val Ser Phe Leu Asp Ser Pro Gly Ala	
376 381 386 391	
caa gcc cag gcg gac cac ctg cct cag ctg act ctt cct gac agt ctc	1313
Gln Ala Gln Ala Asp His Leu Pro Gln Leu Thr Leu Pro Asp Ser Leu	
392 397 402 407	
acc tct gca gcc tca cca gaa gat ggg ctg tcc gcc gag ctg ctt gaa	1361
Thr Ser Ala Ala Ser Pro Glu Asp Gly Leu Ser Ala Glu Leu Leu Glu	
408 413 418 423	
gct cag gct gag gag gaa cca gca agc aca gag ggc cta gat act ggg	1409
Ala Gln Ala Glu Glu Glu Pro Ala Ser Thr Glu Gly Leu Asp Thr Gly	
424 429 434 439	
acg gag gct gag ggg ctg gac agc caa gcc cag atc tct acc aca gaa	1457
Thr Glu Ala Glu Gly Leu Asp Ser Gln Ala Gln Ile Ser Thr Thr Glu	
440 445 450 455	
taa cacc ctgggctgtg acaaggccca tgatgacatt tcatgaggcc cagatgtggg	1514
* 456	
caggcagccc gggctgcact atgcgggtcag gattccttgc tgctttggtg ggacatgagg	1574
cctcagtggg tgggtgagagg gggccatggc tttgtgggag gatattctttt ggccgtgtac	1634
cctcaggtcc agtgcttggg cctgctctgg tccactggggc ttcccaggag gcagcagggt	1694
ctggtcataa tccagtgtga agatgagggtg aggaaggaag ggggttgctgt ccagtgttgg	1754
cctggtcgct ttgattcttc ctgcacagct cagcccaccc catctgtact ggaagggacc	1814
ctggagccct gggaccaccc cctttcaagt cccaaacact gaggcctctg tcatgtgtcc	1874
ttgtccctag gctacaatgc tacacttggc tcaggctgat caccatgcta gtcacaggag	1934
ggagagagag gcagtgtact tgcccccatc tcctggaggg aggtgcgttg gaaattctag	1994
gcccttcagc agagacccat ttgtgcccag accacaatat ttcttcttcc tcagggacta	2054
catgccacag acctgtatcc ccagtggcaa ctctgttag ctcccaaact taaacagtga	2114
tctcttctaa atatacaagg catctaccca gcccgaatag tgaataaaag tcacaaatth	2174
aagttcaaca ccctaagcaa tttctcaaag ccagtctacc tgactagggtc tatccacgca	2234
cggttcccaa ccccaagggg gaattagggg attagattaa gagtaggtaa agaccctttt	2294

gttctttcct gttgtagggg aggaagctgt tctccccacc ccaggtgcct ttggagggtta 2354
aggctagggtt aggccctgca ctccacctgg ggacggcccc tcatcacctg aagtcctctg 2414
ctgtgttgac tggaccctca gttccccacac tgctaattac tatgaaagct gctctggcct 2474
cgtcttctag cttgtgccta gttgaaagtc tcacctttac aggatcattt gtaatgctgg 2534
tgtacatgca gggaaactcac aagctgtgtc aggtatgcag gacaaggaat gtctgctctg 2594
gggggcacag gccaaactata tggagggag 2623

<210> 96
<211> 1499
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (195)..(944)

<400> 96
catcgcatgc ggtcccctgc ggtaccgggc cggaattccc gggtcgaccc acgcgtccgc 60
ccacgcgtcc ggtaaggaac gccggctctt cgcctctcag cgcggcttgt cctttgttcc 120
ggacgcccgc tcctcagccc tgcggctcct ggggtcgctg ctgcatcccg cacgcctcca 180
cgggctgcag accc atg gcc gag cgc ggg gaa ctg gac ttg acc ggc gcc 230
Met Ala Glu Arg Gly Glu Leu Asp Leu Thr Gly Ala
1 5 10
aaa cag aac aca gga gtg tgg cta gtc aag gtt cct aaa tat ttg tca 278
Lys Gln Asn Thr Gly Val Trp Leu Val Lys Val Pro Lys Tyr Leu Ser
13 18 23 28
cag caa tgg gct aaa gcc tct gga aga ggt gaa gtt ggg aaa ctg cgg 326
Gln Gln Trp Ala Lys Ala Ser Gly Arg Gly Glu Val Gly Lys Leu Arg
29 34 39 44
att gcc aag act caa gga agg act gag gtg tca ttt act ttg aat gag 374
Ile Ala Lys Thr Gln Gly Arg Thr Glu Val Ser Phe Thr Leu Asn Glu
45 50 55 60
gat ctt gca aat att cat gat att ggt gga aaa cca gct tca gtc agt 422
Asp Leu Ala Asn Ile His Asp Ile Gly Gly Lys Pro Ala Ser Val Ser
61 66 71 76
gct cct aga gaa cat cca ttt gtc ttg caa agt gtt gga gga cag aca 470
Ala Pro Arg Glu His Pro Phe Val Leu Gln Ser Val Gly Gly Gln Thr
77 82 87 92
tta aca gta ttt act gag agc tca tca gat aag ctg tca ttg gaa gga 518
Leu Thr Val Phe Thr Glu Ser Ser Ser Asp Lys Leu Ser Leu Glu Gly

93	98	103	108	
ata gtg gta caa aga gct gaa tgc cga cca gct gcc agt gaa aac tac				566
Ile Val Val Gln Arg Ala Glu Cys Arg Pro Ala Ala Ser Glu Asn Tyr				
109	114	119	124	
atg cga tta aaa aga ttg caa ata gaa gag tct tcc aaa cca gtg agg				614
Met Arg Leu Lys Arg Leu Gln Ile Glu Glu Ser Ser Lys Pro Val Arg				
125	130	135	140	
cta tca caa cag ctg gac aaa gtt gta aca acc aat tac aaa cct gtt				662
Leu Ser Gln Gln Leu Asp Lys Val Val Thr Thr Asn Tyr Lys Pro Val				
141	146	151	156	
gct aat cat caa tac aat atc gaa tat gaa agg aaa aag aaa gaa gac				710
Ala Asn His Gln Tyr Asn Ile Glu Tyr Glu Arg Lys Lys Lys Glu Asp				
157	162	167	172	
gga aag cga gct cga gct gat aaa caa cat gtt tta gac atg cta ttt				758
Gly Lys Arg Ala Arg Ala Asp Lys Gln His Val Leu Asp Met Leu Phe				
173	178	183	188	
tca gcc ttt gag aaa cat caa tac tat aat ctt aag gac ttg gtg gac				806
Ser Ala Phe Glu Lys His Gln Tyr Tyr Asn Leu Lys Asp Leu Val Asp				
189	194	199	204	
atc aca aaa caa cct gtg gtg tac ctg aag gaa atc tta aaa gaa att				854
Ile Thr Lys Gln Pro Val Val Tyr Leu Lys Glu Ile Leu Lys Glu Ile				
205	210	215	220	
ggg gtt cag aat gta aaa ggg atc cac aaa aac aca tgg gag ctg aag				902
Gly Val Gln Asn Val Lys Gly Ile His Lys Asn Thr Trp Glu Leu Lys				
221	226	231	236	
cca gag tac aga cac tat caa gga gaa gaa aag agt gac taa gaagact				951
Pro Glu Tyr Arg His Tyr Gln Gly Glu Glu Lys Ser Asp *				
237	242	247		
cctagccagc atgctagtga aacgactagc agcgatgcta tgcaaaaggc gctgatactg				1011
gaaggcttga acaccgtatg ttaatagggg ttaagtgaca gtactttgat ttctctcggt				1071
aaatttttta aacctgtaat tcttgtaaag tttcttaact gtttttttga ggagaaagaa				1131
cagatttatt tatagactta acttgattta aaccagatta ttcacagtag gaataggggt				1191
tggaggatta agagggtttt tcttaaatat tagcttttaa tgtgtacaat taggaaattt				1251
ttttaagtga ggactctcta cccttgccgt atctaaggag ctgaggtaat acagatccaa				1311
ggagaattgt atagcaagaa aaaaacagtc aactacagaa actcttaaaa ggaataaaaa				1371
cccaaagttc cttattttga aattgtcaaa gaacaaagcg gtgtttttct tttaaacagg				1431
tgatcacggt tcgtgttcat actcaacggt aataaaagga gagagtttgt agtgaaaaaa				1491
aaaaaaaa				1499

[illegible]

<400> 97

```
<210> 98
<211> 4304
<212> DNA
<213> Homo sapiens
```

<400> 98

364

gag Glu 3	cgc Arg	ggc Gly	agg Arg	aag Lys	cgg Arg 8	ccg Pro	tgc Cys	ggc Gly	ccg Pro	ggt Gly 13	gaa Glu	cac His	ggc Gly	caa Gln	agg Arg 18	103
att Ile 19	gag Glu	tgg Trp	cga Arg	aaa Lys	tgg Trp 24	aag Lys	caa Gln	cag Gln	aag Lys	aaa Lys 29	gag Glu	gag Glu	aaa Lys	aaa Lys	aaa Lys 34	151
tgg Trp 35	aag Lys	gat Asp	ctc Leu	aag Lys	ctg Leu 40	atg Met	aaa Lys	aaa Lys	ctg Leu	gag Glu 45	cgg Arg	cag Gln	cgg Arg	gca Ala	cag Gln 50	199
gag Glu 51	gaa Glu	cag Gln	gca Ala	aag Lys	cgc Arg 56	ctg Leu	gaa Glu	gag Glu	gag Glu	gag Glu 61	gca Ala	gcg Ala	gca Ala	gag Glu	aag Lys 66	247
gag Glu 67	gac Asp	cgc Arg	ggg Gly	cgg Arg	ccc Pro 72	tac Tyr	aca Thr	ctg Leu	agc Ser	gta Val 77	gcc Ala	ctg Leu	ccg Pro	ggc Gly	tcc Ser 82	295
atc Ile 83	ctg Leu	gac Asp	aat Asn	gct Ala	cag Gln 88	tcg Ser	ccg Pro	gag Glu	ctt Leu	cgc Arg 93	acc Thr	tac Tyr	ttg Leu	gcc Ala	ggt Gly 98	343
cag Gln 99	att Ile	gcc Ala	aga Arg	gcc Ala	tgt Cys 104	gcc Ala	atc Ile	ttc Phe	tgt Cys	gtg Val 109	gat Asp	gag Glu	atc Ile	gtg Val	gtg Val 114	391
ttt Phe 115	gat Asp	gag Glu	gag Glu	ggc Gly	cag Gln 120	gat Asp	gcc Ala	aag Lys	act Thr	gtg Val 125	gag Glu	ggg Gly	gaa Glu	ttc Phe	aca Thr 130	439
gga Gly 131	gtt Val	ggg Gly	aag Lys	aag Lys	ggg Gly 136	cag Gln	gcg Ala	tgc Cys	gta Val	cag Gln 141	ctg Leu	gcc Ala	cgg Arg	atc Ile	ctg Leu 146	487
cag Gln 147	tac Tyr	ctg Leu	gag Glu	tgt Cys	cca Pro 152	cag Gln	tac Tyr	ctg Leu	agg Arg	aag Lys 157	gcg Ala	ttc Phe	ttc Phe	ccc Pro	aag Lys 162	535
cac His 163	cag Gln	gat Asp	cta Leu	cag Gln	ttt Phe 168	gca Ala	ggg Gly	ctc Leu	ctg Leu	aac Asn 173	ccc Pro	ctg Leu	gac Asp	agc Ser	ccc Pro 178	583
cac His 179	cac His	atg Met	cgt Arg	cag Gln	gat Asp 184	gag Glu	gaa Glu	tcc Ser	gag Glu	ttc Phe 189	cga Arg	gag Glu	ggc Gly	atc Ile	gtg Val 194	631
gtg Val 195	gat Asp	cgg Arg	ccc Pro	acc Thr	cgg Arg 200	cca Pro	ggc Gly	cac His	ggc Gly	tcc Ser 205	ttt Phe	gtc Val	aac Asn	tgt Cys	ggc Gly 210	679
atg Met 211	aaa Lys	aag Lys	gag Glu	gtg Val	aag Lys 216	att Ile	gac Asp	aag Lys	aac Asn	ctg Leu 221	gag Glu	ccc Pro	ggg Gly	ctt Leu	cgg Arg 226	727
gtg	act	gtg	cga	ctg	aac	cag	cag	cag	cac	cca	gac	tgc	aag	acc	tac	775

	Val	Thr	Val	Arg	Leu	Asn	Gln	Gln	Gln	His	Pro	Asp	Cys	Lys	Thr	Tyr	
227						232					237					242	
cat	ggc	aaa	gtg	gta	tca	tcg	cag	gac	cct	cgc	acc	aaa	gct	ggg	ctc		823
His	Gly	Lys	Val	Val	Ser	Ser	Gln	Asp	Pro	Arg	Thr	Lys	Ala	Gly	Leu		
243					248					253					258		
tac	tgg	ggc	tac	acc	gtc	cga	ctg	gct	tcc	tgc	ctc	agt	gct	gtg	ttt		871
Tyr	Trp	Gly	Tyr	Thr	Val	Arg	Leu	Ala	Ser	Cys	Leu	Ser	Ala	Val	Phe		
259					264					269					274		
gct	gag	gcc	ccc	ttc	caa	gat	ggg	tat	gac	ctg	acc	atc	ggg	acg	tca		919
Ala	Glu	Ala	Pro	Phe	Gln	Asp	Gly	Tyr	Asp	Leu	Thr	Ile	Gly	Thr	Ser		
275					280					285					290		
gag	cgc	ggc	tca	gat	gtg	gct	tct	gcc	cag	ctt	ccc	aac	ttc	agg	cat		967
Glu	Arg	Gly	Ser	Asp	Val	Ala	Ser	Ala	Gln	Leu	Pro	Asn	Phe	Arg	His		
291					296					301					306		
gct	ctt	gtg	gtg	ttc	ggg	ggc	ctc	cag	ggg	ctg	gaa	gct	gga	gcg	gat		1015
Ala	Leu	Val	Val	Phe	Gly	Gly	Leu	Gln	Gly	Leu	Glu	Ala	Gly	Ala	Asp		
307					312					317					322		
gct	gac	ccc	aac	ctg	gag	gtg	gct	gaa	ccc	agt	gtc	ctc	ttt	gac	ctg		1063
Ala	Asp	Pro	Asn	Leu	Glu	Val	Ala	Glu	Pro	Ser	Val	Leu	Phe	Asp	Leu		
323					328					333					338		
tac	gtc	aat	acc	tgt	cct	ggc	cag	ggg	agc	cgt	acc	atc	cgc	acg	gag		1111
Tyr	Val	Asn	Thr	Cys	Pro	Gly	Gln	Gly	Ser	Arg	Thr	Ile	Arg	Thr	Glu		
339					344					349					354		
gaa	gcc	atc	ctc	atc	tcc	ctg	gcc	gcc	ctg	cag	cct	ggc	ctc	acc	cag		1159
Glu	Ala	Ile	Leu	Ile	Ser	Leu	Ala	Ala	Leu	Gln	Pro	Gly	Leu	Thr	Gln		
355					360					365					370		
gcg	ggg	gcc	cgg	cac	acc	tga	aa	gttctaagg	g	ccgaggaca	t	cagtgaagc					1212
Ala	Gly	Ala	Arg	His	Thr	*											
371					376												
agcagtgaaa	ccaggggctc	tgcaggtcac	ttgggacgga	cgccaccaga	cttgtctcca												1272
aaaatcacca	cctttaatac	tccccggcct	gcacacacct	acagtctcac	tgggctccac												1332
cctcacttac	tgccccgcgt	gatggccttg	aggetgectg	cccgcgccag	gatgtttggc												1392
aaaaagagca	gccccgaagc	cgctcaatg	ctctcgatgg	gcaccaggaa	gcgctccagt												1452
gggatggcct	catccacagg	tgcgttgggc	atcacgtagg	tgcggagctc	aatttgccca												1512
cctgctgcct	ccaggatcag	caccttgaag	aagtgtgtgg	gcactgccac	gtggttcttg												1572
ccgatgacct	ggtactttac	gtaggatttc	ccatcagcct	ctgtcctgtg	ggcagacca												1632
ggcacacgtg	ggcagggggc	ctggatgaac	ccaaagccac	ctcttcagg	cagccttccc												1692
tgatctgtcc	tctaaacttct	gtcaacctgc															

agcctgcctg gctcctcctt gaggctggaa ctctctccag ggtgggtaac tctttccctc	1812
tgttttcctt atgccccaaac ctgggtcagg cagagtgggc gacaataaac gctgctagga	1872
gaatcgagcc ttctgaatat tcacattcgt ctgaggggag acttaacgac tgtccatctc	1932
tccccacaga ggtgagcaac aagtgggcaa ggaccatgac aggtgacatc ccagcaccag	1992
cacaggtgcc aggacaccgg acgggggctc cccctcagca gagtctcctc ccttcacca	2052
ggccctagga ggcacctgct aatgaaattt gatcagtgcc ccaaccaccg ccttggccag	2112
cctatgccga gcccttacca tggaccaggc cctggggaag catgtgacat caaccaagag	2172
gtcacaggtt ttgcagaggg ggacacaggt catttgccca cagcaccaag gaactaggtg	2232
atgaggcctg gactccatcc cgagcctgtg gattccagag tgagctgctc agcctggacc	2292
tgttgctct cagccccagc cctctgcagg ccagaaaaac cacggagcac acccagaggt	2352
gctcagttgc ttccacctga gaggcagggc tgcacaggag caagagtgga ggccctgggt	2412
caggcagatc tagattcaaa ctcccagaa ggggtggagg aagtgctcca agcagagcag	2472
agactgaagg cgggagagcc tgggtgcaccg cggacctgca gggggaaggc gtgagagctc	2532
ggtgcactgg ggacctgcat ggggaaggcg ggagagctcg gtgcactggg gacctgcatg	2592
gggaaggcgt gagagctcgg tgcactgggg acctgcatgg ggaaggcggg agagctcgg	2652
gcacctcgga cctgcagagg gaaggtggga gagcttggtg caccgcagac ctgcaggggg	2712
aaggcgggag agcttggtgc actgcagacc tgcgggggga aggtgggaga gcttggtgca	2772
ctgcagacct gcgggggggt ccatattggc agaacaagat tgggtgggca tgccaagagg	2832
tgacagcagg gagaagcggg ggcagattca gggcctgctg ctgcccattg gcagaggaga	2892
gatggtcagg ggtacccgac aggtcttttg ctgtggaggt ggaatgagg gactcgaggc	2952
agggaaagctg acaggcttgc caagaaacca gatgagtagg gaactggtat tgaccagag	3012
cctggggcaa gcctggccct gtgagtggca gtaggggcct cgggtgagtg ggaggttctg	3072
ccgccccct ggtttccacc ttacctgggc aggaagagtg gccctgtgca gacatagacg	3132
ttttggtagc tgcgggtcaa gctgcggcta tatttctcca ggttggtcca ggcattctgg	3192
ttgaggtggg gcacctggta ggagagatag ggcttagcag gactgtggct gggacccttc	3252
ctcctctatc agagggccgc cccaggtcct gaggggatgg acaggctcag agatatccag	3312
tgagacaagc ggggggaaac tgaggctcaa ggaatgaaag tactccctg aaaccaggg	3372
ctgatagagt gctagccacc accctctgtc cctcccacag cccaggtgtc aaagtctttt	3432
ctcagctccc aagagtcgaa tgaaggaaga gcctgtctcc acctttcaga gaggactgag	3492

```
gcctgtcccc agccccaccc aggggtctcct gggaagacca gcccttccaa ctaccaaccc 3552
gttccttttcc ccagtctgag ccacaggaag agcctagcgg ggaatgccat gaatcgacct 3612
ccatcctgag ctctccaggc ctgggacaat ggaaagtgga tagggggctg tcttcccaga 3672
aggaagctgg gtcagagggtt ggtgccccat gggctccacc cagagcccca tggcagtctc 3732
catocattgg tgccaggacc tgctgggaac aggctgagag ggtggttggc ccagtgcaca 3792
gtgcctggca ctaacaacct gatcgtgggc cagggtgtctg cctcgaaaact gcctgaaggc 3852
aggcagggta ggacaatgtc tggaggctca cggttttata gactaggggt ccccaacccc 3912
tgggctacag accggtacca gaaccgggcc acacagcagg aggtgagcag caggcgagca 3972
aggggaagctt catctgtatt tacagccacc cccccattga tcccacagca gcctgagctc 4032
cgctcctgt cagatcagtg gcggctggag attgtcatag gagctggaac cctatggtga 4092
actgcgcattg tgaggagggtt gcgcgcttct tttgaaaacc taatgcctga tctgtcgttg 4152
ttgcccattca cctccagata ggactgtcta gttgcaggaa aacaagctca gggctccac 4212
ggatcctaca ttactgtgag ttgtatattt cactatatgt tacaatgtaa taataataga 4272
aataaaatgt acataaatgt aaaaaaaaaa aa 4304
```

```
<210> 99
<211> 1323
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (294) .. (1229)
```

```
<400> 99
atttggccct cgaggccaag aattcggcac gagccatgca cagggtgcagc taccatataa 60
caatccacac agttcctgac acatcatagg cttcaatac atactttcca gttgaattgg 120
aaagaaatgt gttaagtctc agttatgtcg tgatgcaaact gctcacaaaa tatctgttta 180
gggccatctt ttcacaaaa gaattgtatc tccgaatact taacatcagc aatctgagta 240
aataaacttg ctcatcaagg acaacttctt tcttataatt cttgtctgca ggc atg 296
Met
1
```

```
tct aat ttt act cat tat gcc tat ctg ctt atg ata gag tca ctg atg 344
Ser Asn Phe Thr His Tyr Ala Tyr Leu Leu Met Ile Glu Ser Leu Met
2 7 12 17
```

ttg ggg aaa gtt ccc ccg cat gtc ccc agt cat cat ttc ata ttt cat	392
Leu Gly Lys Val Pro Pro His Val Pro Ser His His Phe Ile Phe His	
18 23 28 33	
gat gat ggg agt gcc aga cag aag gga gag agt gat tac aag gtc atc	440
Asp Asp Gly Ser Ala Arg Gln Lys Gly Glu Ser Asp Tyr Lys Val Ile	
34 39 44 49	
ata cag cag tgg ttc tca aag agt ggt ccc tgg acc acc agc agc aat	488
Ile Gln Gln Trp Phe Ser Lys Ser Gly Pro Trp Thr Thr Ser Ser Asn	
50 55 60 65	
gtt acc tgg ggc ttg tta gaa ctg caa caa agc att tct gaa tca gct	536
Val Thr Trp Gly Leu Leu Glu Leu Gln Gln Ser Ile Ser Glu Ser Ala	
66 71 76 81	
gtt tta acc att cct cca gga gat tct ggt gca ggc tca aat ttg ata	584
Val Leu Thr Ile Pro Pro Gly Asp Ser Gly Ala Gly Ser Asn Leu Ile	
82 87 92 97	
acc atg ttt cta cgt aac aga aaa gaa aca gat ctg tgc agt ggg aga	632
Thr Met Phe Leu Arg Asn Arg Lys Glu Thr Asp Leu Cys Ser Gly Arg	
98 103 108 113	
agt aaa gtg aac aga gga tgg aat tct ggc aga tgc aaa caa agg ggc	680
Ser Lys Val Asn Arg Gly Trp Asn Ser Gly Arg Cys Lys Gln Arg Gly	
114 119 124 129	
aag act gag cag cct gga gag ccc ttg gaa cat gtg tat gtg act ata	728
Lys Thr Glu Gln Pro Gly Glu Pro Leu Glu His Val Tyr Val Thr Ile	
130 135 140 145	
aaa cat gct gta gcc ctg gaa tcc cga cat caa aag gga gag ctt cag	776
Lys His Ala Val Ala Leu Glu Ser Arg His Gln Lys Gly Glu Leu Gln	
146 151 156 161	
tgc ctg ata aaa atg tgc att cct ctt agc aaa cca ctc caa atg ttc	824
Cys Leu Ile Lys Met Cys Ile Pro Leu Ser Lys Pro Leu Gln Met Phe	
162 167 172 177	
ttt tct cca ccc cac tgg gaa gct tgg ctg cag aga gta cag caa ctt	872
Phe Ser Pro Pro His Trp Glu Ala Trp Leu Gln Arg Val Gln Gln Leu	
178 183 188 193	
gcg aaa aac aca aga tac ttc aga caa aga ctg cag gaa atg gga ttc	920
Ala Lys Asn Thr Arg Tyr Phe Arg Gln Arg Leu Gln Glu Met Gly Phe	
194 199 204 209	
att atc tat ggc aat gag aat gct tct gtt gtt cct ctg ctt ctt tat	968
Ile Ile Tyr Gly Asn Glu Asn Ala Ser Val Val Pro Leu Leu Leu Tyr	
210 215 220 225	
atg cct ggt aaa gta gcg gct ttt gca agg cat atg cta gag aaa aaa	1016
Met Pro Gly Lys Val Ala Ala Phe Ala Arg His Met Leu Glu Lys Lys	
226 231 236 241	

```

att gga gtg gtg gtc gtg gga ttt cca gcc act ccc ctc gca gaa gct      1064
Ile Gly Val Val Val Val Gly Phe Pro Ala Thr Pro Leu Ala Glu Ala
242                      247                      252                      257

cgg gct cgg ttt tgt gtt tca gcg gca cat acc cgg gag atg tta gac      1112
Arg Ala Arg Phe Cys Val Ser Ala Ala His Thr Arg Glu Met Leu Asp
258                      263                      268                      273

acg gtt tta gaa gct ctt gat gaa atg ggt gat ctc ttg caa ctg aaa      1160
Thr Val Leu Glu Ala Leu Asp Glu Met Gly Asp Leu Leu Gln Leu Lys
274                      279                      284                      289

tat tcc cgg cac aag aag tca gca cgt cct gag ctc tat gat gag acg      1208
Tyr Ser Arg His Lys Lys Ser Ala Arg Pro Glu Leu Tyr Asp Glu Thr
290                      295                      300                      305

agc ttt gaa ctc gaa gat taa gt ttactgggtcc tgaatgacac ataaagactt      1261
Ser Phe Glu Leu Glu Asp *
306                      311

tgcgagaaaag acctccctcc ttgcctcaca aggaatataa atggattttct ccccttctct      1321

ca                                                                    1323

```

```

<210> 100
<211> 1035
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (571) .. (858)

```

```

<400> 100
aggagctcgc ggcttggaat tcgcacgagg ctctaagaa ttctctaacc tgccttctgc      60

ccttaggctc cggtagattg caaacgacct gctttctttc tgatcccggg ctgcgttcgg      120

accctgtcgc tatagaaaat cccaagtaag gtacctgccg tcggcagatc tgagctttct      180

tcttggaacac ctaataccca cagtcctcca gaccctgtc ggatagtaaa tccaagtaa      240

ggtagcttct gctggaagat ctgagctttc ttcttggaac cctaaaacct acagtcctcc      300

agtgaaggat ccagtgaatg tttccagggt aacgggtcata atgcctact ggtccaacgt      360

tcagaagtaa cacaggcacc tggacaatac acagtagatg tggaaggaca cggttgtaca      420

tttatccagg ccacccttaa gtacaatgtt ctctaccta agaaggcatc tggattttct      480

ctttccttgg aaatagtaaa gaactactct tcgactgctt ttgacctcac agtgacctc      540

aaatacactg gaattcgcaa taaatccagt      atg gtg gtt ata gat gta aaa      591
Met Val Val Ile Asp Val Lys

```


1

5

atg cta tca gga ttt act cca acc atg tca tcc att gaa gag ctt gaa 639
 Met Leu Ser Gly Phe Thr Pro Thr Met Ser Ser Ile Glu Glu Leu Glu
 8 13 18 23

aac aag ggc caa gtg atg aag act gaa gtc aag aat gac cat gtt ctt 687
 Asn Lys Gly Gln Val Met Lys Thr Glu Val Lys Asn Asp His Val Leu
 24 29 34 39

ttc tac ttg gaa aat ggt ttt ggt cga gca gac agt ttc cct ttt tct 735
 Phe Tyr Leu Glu Asn Gly Phe Gly Arg Ala Asp Ser Phe Pro Phe Ser
 40 45 50 55

gtt gag cag agc aac ctt gtg ttc aac att cag cca gcc cca gcc atg 783
 Val Glu Gln Ser Asn Leu Val Phe Asn Ile Gln Pro Ala Pro Ala Met
 56 61 66 71

gtc tac gat tac tat gaa aaa gaa gaa tat gcc cta gct ttt tac aac 831
 Val Tyr Asp Tyr Tyr Glu Lys Glu Glu Tyr Ala Leu Ala Phe Tyr Asn
 72 77 82 87

atc gac agt agt tca gtt tcc gag tga gacaa agcaattact agaagagttg 883
 Ile Asp Ser Ser Ser Val Ser Glu *
 88 93

gagaagcatt tcttgtaaca aactgattct tctgtatcaa acctggaaaa aaatcatgaa 943

ccatctgaca tcgtgaacag tctgcagtgg gctatggttt cttgtcaagt cttatttcct 1003

tatcatccca ttaaagtgtg tcatttttgca aa 1035

<210> 101

<211> 3182

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (97)..(2307)

<400> 101

ctgtcgcgct ctctcggcg agcgcgctcc cggcccgcgc gctccgggct ccggtttctc 60

ccggctcctg tcagtgcggt gactgcgctg ggaaac atg gcg acc gag gga atg 114
 Met Ala Thr Glu Gly Met
 1

atc ctt act aac cac gac cat caa atc cgt gtc gga gtc ctt aca gtg 162
 Ile Leu Thr Asn His Asp His Gln Ile Arg Val Gly Val Leu Thr Val
 7 12 17 22

agt gat agt tgc ttc agg aat ctt gca gaa gac cgc agt ggg ata aat 210
 Ser Asp Ser Cys Phe Arg Asn Leu Ala Glu Asp Arg Ser Gly Ile Asn

23	28	33	38	
ctc aaa gat ctc gta caa gat cct tct ttg ttg ggt ggg act ata tca				258
Leu Lys Asp Leu Val Gln Asp Pro Ser Leu Leu Gly Gly Thr Ile Ser				
39	44	49	54	
gca tac aag ata gta cca gat gaa ata gaa gaa atc aag gaa acc ctg				306
Ala Tyr Lys Ile Val Pro Asp Glu Ile Glu Glu Ile Lys Glu Thr Leu				
55	60	65	70	
ata gat tgg tgt gat gaa aag gaa ctt aat ttg ata tta aca act gga				354
Ile Asp Trp Cys Asp Glu Lys Glu Leu Asn Leu Ile Leu Thr Thr Gly				
71	76	81	86	
gga aca gga ttt gca cca cga gat gtc act cca gag gcc aca aaa gaa				402
Gly Thr Gly Phe Ala Pro Arg Asp Val Thr Pro Glu Ala Thr Lys Glu				
87	92	97	102	
gta ata gaa cgg gaa gca cca ggg atg gcc ctg gca atg ctg atg gga				450
Val Ile Glu Arg Glu Ala Pro Gly Met Ala Leu Ala Met Leu Met Gly				
103	108	113	118	
tca ctt aat gtt aca cct ctg ggc atg ctc tct agg cct gta tgt gga				498
Ser Leu Asn Val Thr Pro Leu Gly Met Leu Ser Arg Pro Val Cys Gly				
119	124	129	134	
atc aga ggg aaa acg ctc ata att aac ctg cca ggt agc aag aaa gga				546
Ile Arg Gly Lys Thr Leu Ile Ile Asn Leu Pro Gly Ser Lys Lys Gly				
135	140	145	150	
tct cag gaa tgc ttt caa ttc ata ctg cca gct cta cct cat gcc att				594
Ser Gln Glu Cys Phe Gln Phe Ile Leu Pro Ala Leu Pro His Ala Ile				
151	156	161	166	
gac ctt tta cgt gat gcc att gta aaa gta aag gag gtg cat gat gaa				642
Asp Leu Leu Arg Asp Ala Ile Val Lys Val Lys Glu Val His Asp Glu				
167	172	177	182	
ctt gaa gat ttg cct tcc cca cct ccc cct ctt tcc cct cct cct act				690
Leu Glu Asp Leu Pro Ser Pro Pro Pro Pro Leu Ser Pro Pro Pro Thr				
183	188	193	198	
acc agc ccc cat aaa cag aca gaa gac aaa gga gtt caa tgt gag gaa				738
Thr Ser Pro His Lys Gln Thr Glu Asp Lys Gly Val Gln Cys Glu Glu				
199	204	209	214	
gag gaa gaa gag aag aaa gac agt ggt gtt gct tca aca gaa gat agt				786
Glu Glu Glu Glu Lys Lys Asp Ser Gly Val Ala Ser Thr Glu Asp Ser				
215	220	225	230	
tcc tca tca cat ata act gca gca gcc att gct gcc aag att cca gac				834
Ser Ser Ser His Ile Thr Ala Ala Ala Ile Ala Ala Lys Ile Pro Asp				
231	236	241	246	
tcc atc att tct cgt ggt gtt cag gtg ctc cca cga gac aca gcc tcc				882
Ser Ile Ile Ser Arg Gly Val Gln Val Leu Pro Arg Asp Thr Ala Ser				
247	252	257	262	

ctc agc act act cct tca gaa tcg cct cgt gct cag gct aca tct cgc	930
Leu Ser Thr Thr Pro Ser Glu Ser Pro Arg Ala Gln Ala Thr Ser Arg	
263 268 273 278	
ctc tct aca gct tcc tgc cca aca cca aaa gtc cag tcc agg tgc agc	978
Leu Ser Thr Ala Ser Cys Pro Thr Pro Lys Val Gln Ser Arg Cys Ser	
279 284 289 294	
agc aag gag aac att ctc aga gcc agt cac agt gct gtc gat atc acc	1026
Ser Lys Glu Asn Ile Leu Arg Ala Ser His Ser Ala Val Asp Ile Thr	
295 300 305 310	
aag gtg gct aga aga cat cgc atg tct cct ttt cct ctg aca tct atg	1074
Lys Val Ala Arg Arg His Arg Met Ser Pro Phe Pro Leu Thr Ser Met	
311 316 321 326	
gac aaa gcc ttt atc aca gtc ctg gag atg act ccg gtg ctt ggg aca	1122
Asp Lys Ala Phe Ile Thr Val Leu Glu Met Thr Pro Val Leu Gly Thr	
327 332 337 342	
gaa atc atc aat tac cga gat gga atg ggg cga gtc ctt gct caa gat	1170
Glu Ile Ile Asn Tyr Arg Asp Gly Met Gly Arg Val Leu Ala Gln Asp	
343 348 353 358	
gta tat gca aaa gac aat tta ccc ccc ttc cca gca tca gta aaa gat	1218
Val Tyr Ala Lys Asp Asn Leu Pro Pro Phe Pro Ala Ser Val Lys Asp	
359 364 369 374	
ggc tat gct gtc cga gct gct gat ggc cca gga gat cgt ttc atc att	1266
Gly Tyr Ala Val Arg Ala Ala Asp Gly Pro Gly Asp Arg Phe Ile Ile	
375 380 385 390	
ggg gaa tcc caa gct ggt gaa cag cca act cag aca gta atg cca gga	1314
Gly Glu Ser Gln Ala Gly Glu Gln Pro Thr Gln Thr Val Met Pro Gly	
391 396 401 406	
caa gtc atg cgg gtt aca aca ggt gct cca ata ccc tgc ggt gct gat	1362
Gln Val Met Arg Val Thr Thr Gly Ala Pro Ile Pro Cys Gly Ala Asp	
407 412 417 422	
gca gta gta caa gtg gaa gat acc gaa ctt atc agg gaa tca gat gat	1410
Ala Val Val Gln Val Glu Asp Thr Glu Leu Ile Arg Glu Ser Asp Asp	
423 428 433 438	
ggc act gaa gaa ctt gaa gtg cga att ctg gtg caa gct cgg cca ggc	1458
Gly Thr Glu Glu Leu Glu Val Arg Ile Leu Val Gln Ala Arg Pro Gly	
439 444 449 454	
caa gat atc aga ccc atc ggc cat gac att aaa aga ggg gaa tgt gtt	1506
Gln Asp Ile Arg Pro Ile Gly His Asp Ile Lys Arg Gly Glu Cys Val	
455 460 465 470	
ttg gcc aaa gga acc cac atg ggc ccc tca gag att ggt ctt ctg gca	1554
Leu Ala Lys Gly Thr His Met Gly Pro Ser Glu Ile Gly Leu Leu Ala	
471 476 481 486	

act gta ggt gtc aca gag gtt gaa gtt aat aag ttt cca gtg gtt gca	1602
Thr Val Gly Val Thr Glu Val Glu Val Asn Lys Phe Pro Val Val Ala	
487 492 497 502	
gtc atg tca aca ggg aat gag ctg cta aat cct gaa gat gac ctc tta	1650
Val Met Ser Thr Gly Asn Glu Leu Leu Asn Pro Glu Asp Asp Leu Leu	
503 508 513 518	
cca ggg aag att cga gac agc aat cgt tca act ctt cta gca aca att	1698
Pro Gly Lys Ile Arg Asp Ser Asn Arg Ser Thr Leu Leu Ala Thr Ile	
519 524 529 534	
cag gaa cat ggt tac ccc acg atc aac ttg ggt att gta gga gac aac	1746
Gln Glu His Gly Tyr Pro Thr Ile Asn Leu Gly Ile Val Gly Asp Asn	
535 540 545 550	
cca gat gac tta ctc aat gcc ttg aat gag ggt atc agt cgt gct gat	1794
Pro Asp Asp Leu Leu Asn Ala Leu Asn Glu Gly Ile Ser Arg Ala Asp	
551 556 561 566	
gtc atc atc aca tca ggg ggt gta tcc atg ggg gaa aag gac tat ctc	1842
Val Ile Ile Thr Ser Gly Gly Val Ser Met Gly Glu Lys Asp Tyr Leu	
567 572 577 582	
aag cag gtg ctg gac att gat ctt cat gct cag atc cat ttt ggc agg	1890
Lys Gln Val Leu Asp Ile Asp Leu His Ala Gln Ile His Phe Gly Arg	
583 588 593 598	
gtt ttt atg aaa cca ggc ttg cca aca aca ttt gca act ttg gat att	1938
Val Phe Met Lys Pro Gly Leu Pro Thr Thr Phe Ala Thr Leu Asp Ile	
599 604 609 614	
gat ggt gta aga aaa ata atc ttt gca cta cct ggg aat cct gta tcg	1986
Asp Gly Val Arg Lys Ile Ile Phe Ala Leu Pro Gly Asn Pro Val Ser	
615 620 625 630	
gct gtg gtc acc tgc aat ctc ttt gtt gtg cct gca ctg agg aaa atg	2034
Ala Val Val Thr Cys Asn Leu Phe Val Val Pro Ala Leu Arg Lys Met	
631 636 641 646	
cag ggc atc ttg gat cct cgg cca acc atc atc aaa gca agg tta tca	2082
Gln Gly Ile Leu Asp Pro Arg Pro Thr Ile Ile Lys Ala Arg Leu Ser	
647 652 657 662	
tgt gat gta aaa ctt gat cct cgt cca gaa tac cat cgg tgt ata cta	2130
Cys Asp Val Lys Leu Asp Pro Arg Pro Glu Tyr His Arg Cys Ile Leu	
663 668 673 678	
act tgg cat cac caa gaa cca cta cct tgg gca cag agt aca ggt aat	2178
Thr Trp His His Gln Glu Pro Leu Pro Trp Ala Gln Ser Thr Gly Asn	
679 684 689 694	
caa atg agc agc cgt ctg atg agc atg cgc agt gcc aat gga ttg ttg	2226
Gln Met Ser Ser Arg Leu Met Ser Met Arg Ser Ala Asn Gly Leu Leu	
695 700 705 710	
atg cta cct cca aag aca gaa cag tac gtg gag ctc cac aaa ggc gag	2274

Met	Leu	Pro	Pro	Lys	Thr	Glu	Gln	Tyr	Val	Glu	Leu	His	Lys	Gly	Glu	
711					716					721					726	
gtg	gtg	gat	gtc	atg	gtc	att	gga	cgg	cta	tga	tggtcacc	agcaggagaa				2325
Val	Val	Asp	Val	Met	Val	Ile	Gly	Arg	Leu	*						
727					732					737						
agctttgatg	catgtccaca	tatcattgac	tgtatcctgt	aatatgcaac	ggcacagcta											2385
gttttcccga	tttggataaa	agttgatctg	tatagtcaac	atcttgaact	atatttcaaa											2445
tgaatttaaa	tatcttttaa	agaaaaaac	acataaaaat	aaatcttaac	agaaaattct											2505
gttctgatta	tatcaaggca	aatttttccct	ttcttgcaaa	ttgctttgtg	tgttcaatgc											2565
taggtctgat	agcgatagct	tttagtagac	agcggtaggt	gcctgcagaa	cttgtgtttt											2625
tctcatcttt	aaaatacaac	tacttatgct	cttaaataca	ggctgtctgc	ttatttatac											2685
tagcgtaggc	aacacttgga	tttcccttct	tagtatgctt	cataactgct	ttacagagag											2745
cttttgcttg	ttcttttctca	tgtatctcgt	gtttatgtgc	acagtgccaa	aagaagactg											2805
actgggtgga	ggctctgcct	tgcctcaaga	accatccctt	gcagagcatc	cagggagggt											2865
tctcgcccca	atagcctcac	ggcacagtac	tcttgggcag	taactggaca	ccttttattt											2925
gaagaaacaa	actgaagaaa	aatgcttcc	ttaagtgtg	acagcctttt	taaccaatac											2985
atttaaaatt	gtacagaaca	aaaaaataaa	atcaaagact	gatcttgtac	agatattagt											3045
gttaccagca	ttcatgtgga	aatcaagagc	aaagacaaaa	taatgttaaa	caattctgta											3105
ccataacatt	ttctgtaatg	atactgaaac	ttaatgaata	aaaaaattcc	ttgatcatta											3165
tttaaaaaaa	aaaaaaa															3182

<210> 102
 <211> 2582
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (130)..(2082)

<400>	102															
cctaagctgg	gctatccctg	caatcatgtc	atgctctcct	gctgcgattt	tgattagcct											60
ctcatagtac	ctgaggatcg	ccgacctgca	gagcccgag	ctgcaccacg	gagagtttca											120
gaggcagag	atg	gcg	ggc	cga	gag	gcc	ctg	tca	ctg	ggc	aca	gag	gcc			168
	Met	Ala	Gly	Arg	Glu	Ala	Leu	Ser	Leu	Gly	Thr	Glu	Ala			
	1				5					10						

gag ctg ccg aac agc ctg ccg ggc gat gac cag gat gag tgc ctt ctc	216
Glu Leu Pro Asn Ser Leu Pro Gly Asp Asp Gln Asp Glu Cys Leu Leu	
14 19 24 29	
ctc ccg gga gag ctg tgc cag cac ctt tgc atc aat act gtg ggt tct	264
Leu Pro Gly Glu Leu Cys Gln His Leu Cys Ile Asn Thr Val Gly Ser	
30 35 40 45	
tac cac tgt gcc tgc ttt cct ggc ttc tca ctg cag gac gat ggc cgc	312
Tyr His Cys Ala Cys Phe Pro Gly Phe Ser Leu Gln Asp Asp Gly Arg	
46 51 56 61	
act tgc cgc cca gag ggt cac cct cca cag ccg gaa gcc cca cag gag	360
Thr Cys Arg Pro Glu Gly His Pro Pro Gln Pro Glu Ala Pro Gln Glu	
62 67 72 77	
cct gca ctg aag tca gaa ttt tcc cag gtg gcc tct aac acc atc ccg	408
Pro Ala Leu Lys Ser Glu Phe Ser Gln Val Ala Ser Asn Thr Ile Pro	
78 83 88 93	
ctg cca ctg ccg cag ccc aat acc tgc aaa gac aat gga ccc tgc aag	456
Leu Pro Leu Pro Gln Pro Asn Thr Cys Lys Asp Asn Gly Pro Cys Lys	
94 99 104 109	
cag gtg tgc agc act gtt ggg ggc tca gcc ata tgc tcc tgt ttt ccc	504
Gln Val Cys Ser Thr Val Gly Gly Ser Ala Ile Cys Ser Cys Phe Pro	
110 115 120 125	
ggc tat gcc atc atg gcg gat ggc gtg tcc tgt gaa gac caa gac gag	552
Gly Tyr Ala Ile Met Ala Asp Gly Val Ser Cys Glu Asp Gln Asp Glu	
126 131 136 141	
tgc ctg atg ggt gct cac gat tgt agc cgg cga cag ttc tgt gtg aac	600
Cys Leu Met Gly Ala His Asp Cys Ser Arg Arg Gln Phe Cys Val Asn	
142 147 152 157	
acc ctg gga tcc ttc tac tgt gtc aac cac aca gtg ctc tgt gcc gat	648
Thr Leu Gly Ser Phe Tyr Cys Val Asn His Thr Val Leu Cys Ala Asp	
158 163 168 173	
ggc tat atc ctc aat gcg cac agg aag tgc gtg gac atc aac gag tgt	696
Gly Tyr Ile Leu Asn Ala His Arg Lys Cys Val Asp Ile Asn Glu Cys	
174 179 184 189	
gtg acg gac ctg cac acg tgc agc cgg ggc gag cac tgt gtg aac aca	744
Val Thr Asp Leu His Thr Cys Ser Arg Gly Glu His Cys Val Asn Thr	
190 195 200 205	
ctg ggc tcc ttc cac tgc tac aag gca ctc acc tgt gag cca ggc tat	792
Leu Gly Ser Phe His Cys Tyr Lys Ala Leu Thr Cys Glu Pro Gly Tyr	
206 211 216 221	
gcc ctc aag gat ggc gag tgc gaa gac gtg gat gag tgt gcg atg ggc	840
Ala Leu Lys Asp Gly Glu Cys Glu Asp Val Asp Glu Cys Ala Met Gly	
222 227 232 237	

acg Thr 238	cac His	acc Thr	tgc Cys	cag Gln	ccg Pro 243	ggc Gly	ttc Phe	ttg Leu	tgc Cys	cag Gln 248	aac Asn	acc Thr	aag Lys	ggc Gly	tcc Ser 253	888
ttc Phe 254	tac Tyr	tgc Cys	cag Gln	gcc Ala	agg Arg 259	cag Gln	cgc Arg	tgc Cys	atg Met	gat Asp 264	ggc Gly	ttc Phe	ctg Leu	cag Gln	gat Asp 269	936
cct Pro 270	gaa Glu	ggc Gly	aac Asn	tgt Cys	gtg Val 275	gac Asp	atc Ile	aac Asn	gag Glu	tgc Cys 280	acg Thr	tca Ser	ctg Leu	tcc Ser	gag Glu 285	984
cca Pro 286	tgt Cys	cgg Arg	cca Pro	ggc Gly	ttc Phe 291	agc Ser	tgc Cys	atc Ile	aac Asn	acg Thr 296	gtg Val	ggc Gly	tcc Ser	tac Tyr	acg Thr 301	1032
tgc Cys 302	cag Gln	agg Arg	aac Asn	ccg Pro	ctg Leu 307	atc Ile	tgc Cys	gcg Ala	cgc Arg	ggc Gly 312	tac Tyr	cac His	gcc Ala	agc Ser	gat Asp 317	1080
gat Asp 318	ggg Gly	acc Thr	aag Lys	tgt Cys	gtg Val 323	gac Asp	gtg Val	aat Asn	gag Glu	tgt Cys 328	gag Glu	aca Thr	ggt Gly	gtg Val	cac His 333	1128
cgc Arg 334	tgc Cys	ggt Gly	gag Glu	ggc Gly	caa Gln 339	gtg Val	tgc Cys	cac His	aac Asn	ctc Leu 344	cct Pro	ggc Gly	tcc Ser	tac Tyr	cgc Arg 349	1176
tgt Cys 350	gac Asp	tgc Cys	aaa Lys	gcc Ala	ggc Gly 355	ttt Phe	cag Gln	cgg Arg	gat Asp	gcc Ala 360	ttc Phe	ggc Gly	cgg Arg	ggc Gly	tgc Cys 365	1224
atc Ile 366	gac Asp	gtg Val	aat Asn	gag Glu	tgc Cys 371	tgg Trp	gcc Ala	tcg Ser	cca Pro	ggc Gly 376	cgc Arg	ctg Leu	tgc Cys	cag Gln	cac His 381	1272
acg Thr 382	tgt Cys	gag Glu	aac Asn	aca Thr	ctc Leu 387	ggc Gly	tcc Ser	tac Tyr	cgc Arg	tgt Cys 392	tcc Ser	tgc Cys	gcc Ala	tcc Ser	ggg Gly 397	1320
ttc Phe 398	ctg Leu	cta Leu	gca Ala	gcg Ala	gac Asp 403	ggc Gly	aag Lys	cgc Arg	tgt Cys	gaa Glu 408	gac Asp	gtg Val	aat Asn	gag Glu	tgt Cys 413	1368
gag Glu 414	gcc Ala	cag Gln	cgc Arg	tgc Cys	agc Ser 419	cag Gln	gag Glu	tgt Cys	gcc Ala	aac Asn 424	atc Ile	tat Tyr	ggc Gly	tcc Ser	tac Tyr 429	1416
cag Gln 430	tgc Cys	tac Tyr	tgc Cys	cgc Arg	cag Gln 435	ggc Gly	tac Tyr	cag Gln	ctg Leu	gct Ala 440	gag Glu	gat Asp	ggg Gly	cac His	acc Thr 445	1464
tgc Cys 446	aca Thr	gac Asp	atc Ile	gac Asp	gag Glu 451	tgt Cys	gct Ala	caa Gln	ggc Gly	gcc Ala 456	ggc Gly	atc Ile	ctc Leu	tgc Cys	acc Thr 461	1512
ttc	cgc	tgt	ctc	aac	gtg	cca	ggg	agc	tac	caq	tqt	qca	tqc	cct	qag	1560

Phe Arg Cys Leu Asn Val Pro Gly Ser Tyr Gln Cys Ala Cys Pro Glu	
462 467 472 477	
cag ggc tac acc atg acg gcc aac ggg agg tcc tgc aag gac gtg gat	1608
Gln Gly Tyr Thr Met Thr Ala Asn Gly Arg Ser Cys Lys Asp Val Asp	
478 483 488 493	
gag tgt gca ctg ggt acc cac aac tgt tcc gag gct gag acc tgc cac	1656
Glu Cys Ala Leu Gly Thr His Asn Cys Ser Glu Ala Glu Thr Cys His	
494 499 504 509	
aac atc cag ggt agc ttc cgc tgc ctg cgc ttc gag tgt cct ccc aac	1704
Asn Ile Gln Gly Ser Phe Arg Cys Leu Arg Phe Glu Cys Pro Pro Asn	
510 515 520 525	
tat gtc caa gtc tcc aaa acg aag tgc gag cgc acc acg tgc cat gac	1752
Tyr Val Gln Val Ser Lys Thr Lys Cys Glu Arg Thr Thr Cys His Asp	
526 531 536 541	
ttc ctg gag tgc cag aac tcg cca gcg cgc atc acg cac tac cag ctc	1800
Phe Leu Glu Cys Gln Asn Ser Pro Ala Arg Ile Thr His Tyr Gln Leu	
542 547 552 557	
aac ttc cag acg ggc ctc ctg gtg cct gcg cat atc ttc cgc att ggc	1848
Asn Phe Gln Thr Gly Leu Leu Val Pro Ala His Ile Phe Arg Ile Gly	
558 563 568 573	
ccc gcg cca gcc ttc aca ggg gac acc atc gcc ctg aac atc atc aag	1896
Pro Ala Pro Ala Phe Thr Gly Asp Thr Ile Ala Leu Asn Ile Ile Lys	
574 579 584 589	
ggc aat gag gag ggc tac ttt ggc acg cgc agg ctc aat gcc tac acg	1944
Gly Asn Glu Glu Gly Tyr Phe Gly Thr Arg Arg Leu Asn Ala Tyr Thr	
590 595 600 605	
ggt gtg gtc tac ctg cag cgg gcc gtg ctg gag ccc cgg gac ttt gcc	1992
Gly Val Val Tyr Leu Gln Arg Ala Val Leu Glu Pro Arg Asp Phe Ala	
606 611 616 621	
ctg gat gtg gag atg aag ctc tgg agg cag ggc tcc gtc acc acc ttc	2040
Leu Asp Val Glu Met Lys Leu Trp Arg Gln Gly Ser Val Thr Thr Phe	
622 627 632 637	
ctg gcc aag atg cac atc ttc ttc acc acc ttt gcc ctg tga ggtgcc	2089
Leu Ala Lys Met His Ile Phe Phe Thr Thr Phe Ala Leu *	
638 643 648	
gcacggggcca cctgcgggtg tggcgcagcc cagggctcac actgcgtggg agggactggg	2149
tcactattgt ggtttttact ataactttgt aaattaactt aattttgctg acttgactcc	2209
tgtggcttct ggacccctcc tctgccccgc aggaggaagt tccacggcag gtggtgcgtt	2269
cccacgcagg caccaagtgg aagcttgac ggtggggccac ggccgtggcg ggtgccctgt	2329
gggtgaggct gggtgatgac ctgaggacca gagacacgcg accatgttgg ggctcttgg	2389


```
ctcctctgga tgacccgtcc ccaaagttga cattccattt catgttccac tgtgattaat 2449
tcttttcttt tttaaaaaat catttttaaag ttttttgttt aattataaag tagtacatgt 2509
acattataaa aaaaaaagtt caactagtat gaaagggtta taaagtaaca gaggaaaaca 2569
aaaaaaaaaa aaa 2582
```

```
<210> 103
<211> 2441
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (130)..(1941)
```

```
<400> 103
cctaagctgg gctatccctg caatcatgtc atgctctcct gctgcgattt tgattagcct 60
ctcatagtac ctgaggatcg ccgacctgca gagcccgcag ctgcaccacg gagagtttca 120
gaggcagag atg gcg ggc cga gag gcc ctg tca ctg ggc aca gag gcc 168
Met Ala Gly Arg Glu Ala Leu Ser Leu Gly Thr Glu Ala
1 5 10

gag ctg ccg aac agc ctg ccg ggc gat gac cag gat gag tgc ctt ctc 216
Glu Leu Pro Asn Ser Leu Pro Gly Asp Asp Gln Asp Glu Cys Leu Leu
14 19 24 29

ctc ccg gga gag ctg tgc cag cac ctt tgc atc aat act gtg ggt tct 264
Leu Pro Gly Glu Leu Cys Gln His Leu Cys Ile Asn Thr Val Gly Ser
30 35 40 45

tac cac tgt gcc tgc ttt cct ggc ttc tca ctg cag gac gat ggc cgc 312
Tyr His Cys Ala Cys Phe Pro Gly Phe Ser Leu Gln Asp Asp Gly Arg
46 51 56 61

act tgc cgc cca gag ggt cac cct cca cag ccg gaa gcc cca cag gag 360
Thr Cys Arg Pro Glu Gly His Pro Pro Gln Pro Glu Ala Pro Gln Glu
62 67 72 77

cct gca ctg aag tca gaa ttt tcc cag gtg gcc tct aac acc atc ccg 408
Pro Ala Leu Lys Ser Glu Phe Ser Gln Val Ala Ser Asn Thr Ile Pro
78 83 88 93

ctg cca ctg ccg cag ccc aat acc tgc aaa gac aat gga ccc tgc aag 456
Leu Pro Leu Pro Gln Pro Asn Thr Cys Lys Asp Asn Gly Pro Cys Lys
94 99 104 109

cag gtg tgc agc act gtt ggg ggc tca gcc ata tgc tcc tgt ttt ccc 504
Gln Val Cys Ser Thr Val Gly Gly Ser Ala Ile Cys Ser Cys Phe Pro
110 115 120 125
```

ggc tat gcc atc atg gcg gat ggc gtg tcc tgt gaa gac atc aac gag Gly Tyr Ala Ile Met Ala Asp Gly Val Ser Cys Glu Asp Ile Asn Glu 126 131 136 141	552
tgt gtg acg gac ctg cac acg tgc agc cgg ggc gag cac tgt gtg aac Cys Val Thr Asp Leu His Thr Cys Ser Arg Gly Glu His Cys Val Asn 142 147 152 157	600
aca ctg ggc tcc ttc cac tgc tac aag gca ctc acc tgt gag cca ggc Thr Leu Gly Ser Phe His Cys Tyr Lys Ala Leu Thr Cys Glu Pro Gly 158 163 168 173	648
tat gcc ctc aag gat ggc gag tgc gaa gac gtg gat gag tgt gcg atg Tyr Ala Leu Lys Asp Gly Glu Cys Glu Asp Val Asp Glu Cys Ala Met 174 179 184 189	696
ggc acg cac acc tgc cag ccg ggc ttc ttg tgc cag aac acc aag ggc Gly Thr His Thr Cys Gln Pro Gly Phe Leu Cys Gln Asn Thr Lys Gly 190 195 200 205	744
tcc ttc tac tgc cag gcc agg cag cgc tgc atg gat ggc ttc ctg cag Ser Phe Tyr Cys Gln Ala Arg Gln Arg Cys Met Asp Gly Phe Leu Gln 206 211 216 221	792
gat cct gaa ggc aac tgt gtg gac atc aac gag tgc acg tca ctg tcc Asp Pro Glu Gly Asn Cys Val Asp Ile Asn Glu Cys Thr Ser Leu Ser 222 227 232 237	840
gag cca tgt cgg cca ggc ttc agc tgc atc aac acg gtg ggc tcc tac Glu Pro Cys Arg Pro Gly Phe Ser Cys Ile Asn Thr Val Gly Ser Tyr 238 243 248 253	888
acg tgc cag agg aac ccg ctg atc tgc gcg cgc ggc tac cac gcc agc Thr Cys Gln Arg Asn Pro Leu Ile Cys Ala Arg Gly Tyr His Ala Ser 254 259 264 269	936
gat gat ggg acc aag tgt gtg gac gtg aat gag tgt gag aca ggt gtg Asp Asp Gly Thr Lys Cys Val Asp Val Asn Glu Cys Glu Thr Gly Val 270 275 280 285	984
cac cgc tgc ggt gag ggc caa gtg tgc cac aac ctc cct ggc tcc tac His Arg Cys Gly Glu Gly Gln Val Cys His Asn Leu Pro Gly Ser Tyr 286 291 296 301	1032
cgc tgt gac tgc aaa gcc ggc ttt cag cgg gat gcc ttc ggc cgg ggc Arg Cys Asp Cys Lys Ala Gly Phe Gln Arg Asp Ala Phe Gly Arg Gly 302 307 312 317	1080
tgc atc gac gtg aat gag tgc tgg gcc tcg cca ggc cgc ctg tgc cag Cys Ile Asp Val Asn Glu Cys Trp Ala Ser Pro Gly Arg Leu Cys Gln 318 323 328 333	1128
cac acg tgt gag aac aca ctc ggc tcc tac cgc tgt tcc tgc gcc tcc His Thr Cys Glu Asn Thr Leu Gly Ser Tyr Arg Cys Ser Cys Ala Ser 334 339 344 349	1176
ggg ttc ctg cta gca gcg gac ggc aag cgc tgt gaa gac gtg aat gag	1224

Gly	Phe	Leu	Leu	Ala	Ala	Asp	Gly	Lys	Arg	Cys	Glu	Asp	Val	Asn	Glu		
350					355					360					365		
tgt	gag	gcc	cag	cgc	tgc	agc	cag	gag	tgt	gcc	aac	atc	tat	ggc	tcc	1272	
Cys	Glu	Ala	Gln	Arg	Cys	Ser	Gln	Glu	Cys	Ala	Asn	Ile	Tyr	Gly	Ser		
366					371					376					381		
tac	cag	tgc	tac	tgc	cgc	cag	ggc	tac	cag	ctg	gct	gag	gat	ggg	cac	1320	
Tyr	Gln	Cys	Tyr	Cys	Arg	Gln	Gly	Tyr	Gln	Leu	Ala	Glu	Asp	Gly	His		
382					387					392					397		
acc	tgc	aca	gac	atc	gac	gag	tgt	gct	caa	ggc	gcc	ggc	atc	ctc	tgc	1368	
Thr	Cys	Thr	Asp	Ile	Asp	Glu	Cys	Ala	Gln	Gly	Ala	Gly	Ile	Leu	Cys		
398					403					408					413		
acc	ttc	cgc	tgt	ctc	aac	gtg	cca	ggg	agc	tac	cag	tgt	gca	tgc	cct	1416	
Thr	Phe	Arg	Cys	Leu	Asn	Val	Pro	Gly	Ser	Tyr	Gln	Cys	Ala	Cys	Pro		
414					419					424					429		
gag	cag	ggc	tac	acc	atg	acg	gcc	aac	ggg	agg	tcc	tgc	aag	gac	gtg	1464	
Glu	Gln	Gly	Tyr	Thr	Met	Thr	Ala	Asn	Gly	Arg	Ser	Cys	Lys	Asp	Val		
430					435					440					445		
gat	gag	tgt	gca	ctg	ggc	acc	cac	aac	tgt	tcc	gag	gct	gag	acc	tgc	1512	
Asp	Glu	Cys	Ala	Leu	Gly	Thr	His	Asn	Cys	Ser	Glu	Ala	Glu	Thr	Cys		
446					451					456					461		
cac	aac	atc	cag	ggc	agc	ttc	cgc	tgc	ctg	cgc	ttc	gag	tgt	cct	ccc	1560	
His	Asn	Ile	Gln	Gly	Ser	Phe	Arg	Cys	Leu	Arg	Phe	Glu	Cys	Pro	Pro		
462					467					472					477		
aac	tat	gtc	caa	gtc	tcc	aaa	acg	aag	tgc	gag	cgc	acc	acg	tgc	cat	1608	
Asn	Tyr	Val	Gln	Val	Ser	Lys	Thr	Lys	Cys	Glu	Arg	Thr	Thr	Cys	His		
478					483					488					493		
gac	ttc	ctg	gag	tgc	cag	aac	tcg	cca	gcg	cgc	atc	acg	cac	tac	cag	1656	
Asp	Phe	Leu	Glu	Cys	Gln	Asn	Ser	Pro	Ala	Arg	Ile	Thr	His	Tyr	Gln		
494					499					504					509		
ctc	aac	ttc	cag	acg	ggc	ctc	ctg	gtg	cct	gcg	cat	atc	ttc	cgc	att	1704	
Leu	Asn	Phe	Gln	Thr	Gly	Leu	Leu	Val	Pro	Ala	His	Ile	Phe	Arg	Ile		
510					515					520					525		
ggc	ccc	gcg	cca	gcc	ttc	aca	ggg	gac	acc	atc	gcc	ctg	aac	atc	atc	1752	
Gly	Pro	Ala	Pro	Ala	Phe	Thr	Gly	Asp	Thr	Ile	Ala	Leu	Asn	Ile	Ile		
526					531					536					541		
aag	ggc	aat	gag	gag	ggc	tac	ttt	ggc	acg	cgc	agg	ctc	aat	gcc	tac	1800	
Lys	Gly	Asn	Glu	Glu	Gly	Tyr	Phe	Gly	Thr	Arg	Arg	Leu	Asn	Ala	Tyr		
542					547					552					557		
acg	ggc	gtg	gtc	tac	ctg	cag	cgg	gcc	gtg	ctg	gag	ccc	cgg	gac	ttt	1848	
Thr	Gly	Val	Val	Tyr	Leu	Gln	Arg	Ala	Val	Leu	Glu	Pro	Arg	Asp	Phe		
558					563					568					573		
gcc	ctg	gat	gtg	gag	atg	aag	ctc	tgg	agg	cag	ggc	tcc	gtc	acc	acc	1896	
Ala	Leu	Asp	Val	Glu	Met	Lys	Leu	Trp	Arg	Gln	Gly	Ser	Val	Thr	Thr		

574	579	584	589	
ttc ctg gcc aag atg cac atc ttc ttc acc acc ttt gcc ctg tga ggt				1944
Phe Leu Ala Lys Met His Ile Phe Phe Thr Thr Phe Ala Leu *				
590	595	600		
gccagcacgg gccacctgcg ggtgtggcgc agcccagggc tcacactgcg tgggagggac				2004
tgggtcacta ttgtggtttt tactataact ttgtaaatta acttaatttt gctgacttga				2064
ctcctgtggc ttctggaccc ctctctgccc ccgcaggagg aagttccacg gcaggtgggtg				2124
cgttcccacg caggcaccaa gtggaagctt gcacgggtggg ccacggcccg ggcgggtgcc				2184
ctgtgggtga ggctgggtga tgacctgagg accagagaca cgcgaccatg ttggggctct				2244
tggactcctc tggatgaccc gtccccaag ttgacattcc atttcatgtt ccaactgtgat				2304
taattctttt cttttttaaa aaatcatttt aaagtttttt gtttaattat aaagtagtac				2364
atgtacatta taaaaaaaa agttcaacta gtatgaaagg gttataaagt aacagaggaa				2424
aacaaaaaaaa aaaaaaa				2441

<210> 104
 <211> 970
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (231)..(452)

ttgcccactg acccggcagt tatgagcctg gctttggcac tcccagcttt gtgactttgg	60
gtgagcctta cagcccctga gtccctacacc cagaagggtgg ctgaggggaac tgaggccagc	120
atttttcctc ctgcccctgg ggggtttgggg ccggcttctc ccctcttctg aagcacaaaag	180
tcccctcccc acctaccctt cctgcagatg gcttctcaaa ctcgggcatc atg gaa	236
	Met Glu
	1
gag cgc ccc cta gac gca gtg gtg ccc ttc ctc ccg ctc cag cgg cac	284
Glu Arg Pro Leu Asp Ala Val Val Pro Phe Leu Pro Leu Gln Arg His	
3 8 13 18	
cac gtc cgg cac tgc gtg ctc aac gag ctg gcc cag ctg ggc ctg gag	332
His Val Arg His Cys Val Leu Asn Glu Leu Ala Gln Leu Gly Leu Glu	
19 24 29 34	
cca agg gat gag gtt gtc cag gct gtg ctg gac agc acc acc ttc ttc	380
Pro Arg Asp Glu Val Val Gln Ala Val Leu Asp Ser Thr Thr Phe Phe	

35	40	45	50	
cct gaa gac gag cag ctc ttc tcc tcc aac ggc tgc aag acc gtg gcc				428
Pro Glu Asp Glu Gln Leu Phe Ser Ser Asn Gly Cys Lys Thr Val Ala				
51	56	61	66	
tcc cga atc gcc ttc ttc ctc tga ctctctgagt ggtgtcctcg gccccctga				482
Ser Arg Ile Ala Phe Phe Leu *				
67	72			
tggccaggcc atgcaggaaa ggccaggggc ctctgtcaca ggaaccaga gcaccaagtg				542
agatgaacgg agtgtcggct agggcacggg acagatggcc aggaagggcc ctggcctcta				602
aactggctcg agagcatctt ggccccggcc accttcccca gggaaacccc tggtcacccc				662
agaacctcac tgagccttga cctccccctg cagcctgagc cttcttactg tgaattataa				722
ctcagggact gtggctcgtg gcggtgctcc ctctcagtc tgccaccctt gccccttgcc				782
tccttggtcg ggcaccatac ctctccccct ccaccccaca ccctgtgtcc atatcaagcc				842
aggtggagcc ttctcagttt ccagaaatgg agggactcaa gctgccactt gggcctgggt				902
ttagatgttt ttaattttgt aaaagaaaac aagtataata aactcagctg tgggaccaga				962
aaaaaaaa				970

<210> 105
 <211> 6813
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (102)..(3752)

<400> 105	
gaagcagaga agggaggccg cgccacgcgc tccgcgcccc gcgcagtgtc cccagtacat	60
ggcgcgctcg ccgagtcgac tcgaagccca gatgagccca g	113
	atg ccc ggg gct
	Met Pro Gly Ala
	1
caa ccc gga gtg cac gcc ttg caa ctc aag ccc gtg tgc gtg tcg gac	161
Gln Pro Gly Val His Ala Leu Gln Leu Lys Pro Val Cys Val Ser Asp	
5	10
	15
	20
agc ctc aag aag ggc acc aaa ttc gtc aag tgg gat gat gac tca act	209
Ser Leu Lys Lys Gly Thr Lys Phe Val Lys Trp Asp Asp Asp Ser Thr	
21	26
	31
	36
agt gtt act cca att att gtg agg act gac cct cag gga ttt ttc ttt	257
Ser Val Thr Pro Ile Ile Val Arg Thr Asp Pro Gln Gly Phe Phe Phe	

37	42	47	52	
tac tgg aca gat caa aac aag gag aca gag cta ctg gat ctc agc ctt				305
Tyr Trp Thr Asp Gln Asn Lys Glu Thr Glu Leu Leu Asp Leu Ser Leu				
53	58	63	68	
gtc aaa gat gcc aga tgt ggg aga cac gcc aaa gct ccc aag gac ccc				353
Val Lys Asp Ala Arg Cys Gly Arg His Ala Lys Ala Pro Lys Asp Pro				
69	74	79	84	
aaa tta cgt gaa ctt ttg gat gtg ggg aac atc ggg cgc ctg gag cag				401
Lys Leu Arg Glu Leu Leu Asp Val Gly Asn Ile Gly Arg Leu Glu Gln				
85	90	95	100	
cgc atg atc aca gtg gtg tat ggg cct gac ctc gtg aac atc tcc cat				449
Arg Met Ile Thr Val Val Tyr Gly Pro Asp Leu Val Asn Ile Ser His				
101	106	111	116	
ttg aat ctc gtg gct ttc caa gaa gaa gtg gcc aag gaa tgg aca aat				497
Leu Asn Leu Val Ala Phe Gln Glu Glu Val Ala Lys Glu Trp Thr Asn				
117	122	127	132	
gag gtt ttc agt ttg gca aca aac ctg ctg gcc caa aac atg tcc agg				545
Glu Val Phe Ser Leu Ala Thr Asn Leu Leu Ala Gln Asn Met Ser Arg				
133	138	143	148	
gat gca ttt ctg gaa aaa gcc tat act aaa ctt aag ctg caa gtc act				593
Asp Ala Phe Leu Glu Lys Ala Tyr Thr Lys Leu Lys Leu Gln Val Thr				
149	154	159	164	
cca gaa ggg cgt att cct ctc aaa aac ata tat cgc ttg ttt tca gca				641
Pro Glu Gly Arg Ile Pro Leu Lys Asn Ile Tyr Arg Leu Phe Ser Ala				
165	170	175	180	
gat cgg aag cga gtt gaa act gct tta gag gct tgt agt ctt cca tct				689
Asp Arg Lys Arg Val Glu Thr Ala Leu Glu Ala Cys Ser Leu Pro Ser				
181	186	191	196	
tca agg aat gat tca ata cct caa gaa gat ttc act cca gaa gtg tac				737
Ser Arg Asn Asp Ser Ile Pro Gln Glu Asp Phe Thr Pro Glu Val Tyr				
197	202	207	212	
aga gtt ttc ctc aac aac ctt tgc cct cga cct gaa att gat aac atc				785
Arg Val Phe Leu Asn Asn Leu Cys Pro Arg Pro Glu Ile Asp Asn Ile				
213	218	223	228	
ttt tca gaa ttt ggt gca aaa agc aaa cca tat ctt acc gtt gat cag				833
Phe Ser Glu Phe Gly Ala Lys Ser Lys Pro Tyr Leu Thr Val Asp Gln				
229	234	239	244	
atg atg gat ttt atc aac ctt aag cag cga gat cct cgg ctt aat gaa				881
Met Met Asp Phe Ile Asn Leu Lys Gln Arg Asp Pro Arg Leu Asn Glu				
245	250	255	260	
ata ctt tat cca cct cta aaa caa gag caa gtc caa gta ttg att gag				929
Ile Leu Tyr Pro Pro Leu Lys Gln Glu Gln Val Gln Val Leu Ile Glu				
261	266	271	276	

aag tat gaa ccc aac aac agc ctc gcc aga aaa gga caa ata tca gtg	977
Lys Tyr Glu Pro Asn Asn Ser Leu Ala Arg Lys Gly Gln Ile Ser Val	
277 282 287 292	
gat ggg ttc atg cgc tat ctg agt gga gaa gaa aac gga gtc gtt tca	1025
Asp Gly Phe Met Arg Tyr Leu Ser Gly Glu Glu Asn Gly Val Val Ser	
293 298 303 308	
cct gag aaa ctg gat ttg aat gaa gac atg tct cag ccc ctt tct cac	1073
Pro Glu Lys Leu Asp Leu Asn Glu Asp Met Ser Gln Pro Leu Ser His	
309 314 319 324	
tat ttc att aat tcc tcg cac aac acc tac ctc aca gct ggc caa ctg	1121
Tyr Phe Ile Asn Ser Ser His Asn Thr Tyr Leu Thr Ala Gly Gln Leu	
325 330 335 340	
gct gga aac tcc tct gtt gag atg tat cgc caa gtg ctc ctg tct ggt	1169
Ala Gly Asn Ser Ser Val Glu Met Tyr Arg Gln Val Leu Leu Ser Gly	
341 346 351 356	
tgt cgc tgt gtg gag ctg gac tgc tgg aag gga cgg act gca gaa gag	1217
Cys Arg Cys Val Glu Leu Asp Cys Trp Lys Gly Arg Thr Ala Glu Glu	
357 362 367 372	
gaa cct gtc atc acc cat ggc ttc acc atg aca act gaa ata tct ttc	1265
Glu Pro Val Ile Thr His Gly Phe Thr Met Thr Thr Glu Ile Ser Phe	
373 378 383 388	
aag gaa gtg ata gaa gca att gcg gag tgt gca ttt aag act tca cct	1313
Lys Glu Val Ile Glu Ala Ile Ala Glu Cys Ala Phe Lys Thr Ser Pro	
389 394 399 404	
ttt cca att ctc ctt tcg ttt gag aac cat gtg gat tcc cca aag cag	1361
Phe Pro Ile Leu Leu Ser Phe Glu Asn His Val Asp Ser Pro Lys Gln	
405 410 415 420	
caa gcc aag atg gcg gag tac tgc cga ctg atc ttt ggg gat gcc ctt	1409
Gln Ala Lys Met Ala Glu Tyr Cys Arg Leu Ile Phe Gly Asp Ala Leu	
421 426 431 436	
ctc atg gag ccc ctg gaa aaa tat cca ctg gaa tct gga gtt cct ctt	1457
Leu Met Glu Pro Leu Glu Lys Tyr Pro Leu Glu Ser Gly Val Pro Leu	
437 442 447 452	
cca agc cct atg gat tta atg tat aaa att ttg gtg aaa aat aag aag	1505
Pro Ser Pro Met Asp Leu Met Tyr Lys Ile Leu Val Lys Asn Lys Lys	
453 458 463 468	
aaa tca cac aag tca tca gaa gga agc ggc aaa aag aag ctc tca gaa	1553
Lys Ser His Lys Ser Ser Glu Gly Ser Gly Lys Lys Lys Leu Ser Glu	
469 474 479 484	
caa gcc tcc aac acc tac agt gac tcc tcc agc atg ttc gag ccc tca	1601
Gln Ala Ser Asn Thr Tyr Ser Asp Ser Ser Ser Met Phe Glu Pro Ser	
485 490 495 500	

tcc cca gga gcc gga gaa gct gat acg gaa agt gac gac gac gat gat Ser Pro Gly Ala Gly Glu Ala Asp Thr Glu Ser Asp Asp Asp Asp Asp 501 506 511 516	1649
gat gat gac tgt aaa aaa tct tca atg gat gag ggg act gct gga agt Asp Asp Asp Cys Lys Lys Ser Ser Met Asp Glu Gly Thr Ala Gly Ser 517 522 527 532	1697
gag gct atg gcc aca gaa gaa atg tct aat ctg gtg aac tat att cag Glu Ala Met Ala Thr Glu Glu Met Ser Asn Leu Val Asn Tyr Ile Gln 533 538 543 548	1745
cca gtc aag ttt gag tca ttt gaa att tca aaa aaa aga aat aaa agt Pro Val Lys Phe Glu Ser Phe Glu Ile Ser Lys Lys Arg Asn Lys Ser 549 554 559 564	1793
ttt gaa atg tct tcc ttc gtg gaa acc aaa gga ctt gaa caa ctc acc Phe Glu Met Ser Ser Phe Val Glu Thr Lys Gly Leu Glu Gln Leu Thr 565 570 575 580	1841
aag tct cca gtg gaa ttt gta gaa tat aac aaa atg cag ctt agc agg Lys Ser Pro Val Glu Phe Val Glu Tyr Asn Lys Met Gln Leu Ser Arg 581 586 591 596	1889
ata tat cca aaa gga aca cgt gtg gat tca tcc aac tat atg cct cag Ile Tyr Pro Lys Gly Thr Arg Val Asp Ser Ser Asn Tyr Met Pro Gln 597 602 607 612	1937
ctc ttc tgg aat gca ggt tgt cag atg gtg gca ctt aat ttc cag aca Leu Phe Trp Asn Ala Gly Cys Gln Met Val Ala Leu Asn Phe Gln Thr 613 618 623 628	1985
atg gac ctg gct atg caa ata aat atg ggg atg tat gaa tac aac ggg Met Asp Leu Ala Met Gln Ile Asn Met Gly Met Tyr Glu Tyr Asn Gly 629 634 639 644	2033
aag agt ggc tac aga ttg aag cca gag ttc atg agg agg cct gac aag Lys Ser Gly Tyr Arg Leu Lys Pro Glu Phe Met Arg Arg Pro Asp Lys 645 650 655 660	2081
cat ttt gat cca ttt act gaa ggc atc gta gat ggg ata gtg gca aac His Phe Asp Pro Phe Thr Glu Gly Ile Val Asp Gly Ile Val Ala Asn 661 666 671 676	2129
act ttg tct gtt aag att att tca ggt cag ttt ctt tct gat aag aaa Thr Leu Ser Val Lys Ile Ile Ser Gly Gln Phe Leu Ser Asp Lys Lys 677 682 687 692	2177
gtt ggg act tac gtg gaa gta gat atg ttt ggt ttg cct gtg gat aca Val Gly Thr Tyr Val Glu Val Asp Met Phe Gly Leu Pro Val Asp Thr 693 698 703 708	2225
agg agg aag gca ttt aag acc aaa aca tcc caa gga aat gct gtg aat Arg Arg Lys Ala Phe Lys Thr Lys Thr Ser Gln Gly Asn Ala Val Asn 709 714 719 724	2273
cct gtc tgg gaa gaa gaa cct att gtg ttc aaa aag gtg gtt ctt cct	2321

Pro Val Trp Glu Glu Glu Pro Ile Val Phe Lys Lys Val Val Leu Pro	
725 730 735 740	
act ctg gcc tgt ttg aga ata gca gtt tat gaa gaa gga ggt aaa ttc	2369
Thr Leu Ala Cys Leu Arg Ile Ala Val Tyr Glu Glu Gly Gly Lys Phe	
741 746 751 756	
att ggc cac cgt atc ttg cca gtg caa gcc att cgg cca ggc tat cac	2417
Ile Gly His Arg Ile Leu Pro Val Gln Ala Ile Arg Pro Gly Tyr His	
757 762 767 772	
tat atc tgt cta agg aat gaa agg aac cag cct ctg acg ctg cct gct	2465
Tyr Ile Cys Leu Arg Asn Glu Arg Asn Gln Pro Leu Thr Leu Pro Ala	
773 778 783 788	
gtc ttt gtc tac ata gaa gtg aaa gac tat gtg cca gac aca tat gca	2513
Val Phe Val Tyr Ile Glu Val Lys Asp Tyr Val Pro Asp Thr Tyr Ala	
789 794 799 804	
gat gtc atc gaa gct tta tca aac cca atc cga tat gtg aac ctg atg	2561
Asp Val Ile Glu Ala Leu Ser Asn Pro Ile Arg Tyr Val Asn Leu Met	
805 810 815 820	
gaa cag aga gct aag caa ttg gct gct ttg aca ctg gaa gat gaa gaa	2609
Glu Gln Arg Ala Lys Gln Leu Ala Ala Leu Thr Leu Glu Asp Glu Glu	
821 826 831 836	
gaa gta aag aaa gag gct gat cct gga gaa aca cca tca gag gct cca	2657
Glu Val Lys Lys Glu Ala Asp Pro Gly Glu Thr Pro Ser Glu Ala Pro	
837 842 847 852	
agt gaa gcg aga acg act cca gca gaa aat ggg gtg aat cac act aca	2705
Ser Glu Ala Arg Thr Thr Pro Ala Glu Asn Gly Val Asn His Thr Thr	
853 858 863 868	
acc ctg aca ccc aag cca ccc tcc cag gct ctc cac agc cag cca gct	2753
Thr Leu Thr Pro Lys Pro Pro Ser Gln Ala Leu His Ser Gln Pro Ala	
869 874 879 884	
cca ggt tct gta aag gca cct gcc aaa aca gaa gat ctt att cag agt	2801
Pro Gly Ser Val Lys Ala Pro Ala Lys Thr Glu Asp Leu Ile Gln Ser	
885 890 895 900	
gtc tta aca gaa gtg gaa gca cag acc atc gaa gaa cta aag caa cag	2849
Val Leu Thr Glu Val Glu Ala Gln Thr Ile Glu Glu Leu Lys Gln Gln	
901 906 911 916	
aaa tcg ttt gtg aaa ctt caa aag aaa cac tac aaa gaa atg aaa gac	2897
Lys Ser Phe Val Lys Leu Gln Lys Lys His Tyr Lys Glu Met Lys Asp	
917 922 927 932	
ctg gtt aag aga cac cac aag aaa acc act gac ctt atc aaa gaa cac	2945
Leu Val Lys Arg His His Lys Lys Thr Thr Asp Leu Ile Lys Glu His	
933 938 943 948	
act acc aag tat aat gaa att cag aat gac tac ttg aga agg aga gcc	2993
Thr Thr Lys Tyr Asn Glu Ile Gln Asn Asp Tyr Leu Arg Arg Arg Ala	

949	954	959	964	
gct ttg gaa aag tcc gcc aaa aag gac agt aag aaa aaa tcg gaa ccc				3041
Ala Leu Glu Lys Ser Ala Lys Lys Asp Ser Lys Lys Lys Ser Glu Pro				
965	970	975	980	
agc agc cct gat cat ggt tca tca acg att gag caa gac ctc gct gct				3089
Ser Ser Pro Asp His Gly Ser Ser Thr Ile Glu Gln Asp Leu Ala Ala				
981	986	991	996	
ctg gat gct gaa atg acc caa aag tta ata gac ttg aag gac aaa caa				3137
Leu Asp Ala Glu Met Thr Gln Lys Leu Ile Asp Leu Lys Asp Lys Gln				
997	1002	1007	1012	
cag cag cag ctg ctt aat ctt cgg caa gaa cag tat tat agt gaa aaa				3185
Gln Gln Gln Leu Leu Asn Leu Arg Gln Glu Gln Tyr Tyr Ser Glu Lys				
1013	1018	1023	1028	
tac cag aag cga gaa cat att aaa ctg ctt att caa aag ttg acg gat				3233
Tyr Gln Lys Arg Glu His Ile Lys Leu Leu Ile Gln Lys Leu Thr Asp				
1029	1034	1039	1044	
gtc gca gaa gag tgt cag aac aat cag tta aag aag ctc aaa gaa atc				3281
Val Ala Glu Glu Cys Gln Asn Asn Gln Leu Lys Lys Leu Lys Glu Ile				
1045	1050	1055	1060	
tgt gag aaa gaa aag aaa gaa tta aag aag aaa atg gat aaa aag agg				3329
Cys Glu Lys Glu Lys Lys Glu Leu Lys Lys Lys Met Asp Lys Lys Arg				
1061	1066	1071	1076	
cag gag aag ata aca gaa gct aaa tcc aaa gac aaa agt cag atg gaa				3377
Gln Glu Lys Ile Thr Glu Ala Lys Ser Lys Asp Lys Ser Gln Met Glu				
1077	1082	1087	1092	
gag gag aag aca gag atg atc cgg tca tat atc cag gaa gtg gtg cag				3425
Glu Glu Lys Thr Glu Met Ile Arg Ser Tyr Ile Gln Glu Val Val Gln				
1093	1098	1103	1108	
tat atc aag agg cta gaa gaa gcg caa agt aaa cgg caa gaa aaa ctc				3473
Tyr Ile Lys Arg Leu Glu Glu Ala Gln Ser Lys Arg Gln Glu Lys Leu				
1109	1114	1119	1124	
gta gag aaa cac aag gaa ata cgt cag cag atc ctg gat gaa aag ccc				3521
Val Glu Lys His Lys Glu Ile Arg Gln Gln Ile Leu Asp Glu Lys Pro				
1125	1130	1135	1140	
aag ctg cag gtg gag ctg gag caa gaa tac caa gac aaa ttc aaa aga				3569
Lys Leu Gln Val Glu Leu Glu Gln Glu Tyr Gln Asp Lys Phe Lys Arg				
1141	1146	1151	1156	
ctg ccc ctc gag att ttg gaa ttc gtg cag gaa gcc atg aaa gga aag				3617
Leu Pro Leu Glu Ile Leu Glu Phe Val Gln Glu Ala Met Lys Gly Lys				
1157	1162	1167	1172	
atc agt gaa gac agc aat cac ggt tct gcc cct ctc tcc ctg tcc tca				3665
Ile Ser Glu Asp Ser Asn His Gly Ser Ala Pro Leu Ser Leu Ser Ser				
1173	1178	1183	1188	

gac cct gga aaa gtg aac cac aag act ccc tcc agt gag gag ctg gga	3713
Asp Pro Gly Lys Val Asn His Lys Thr Pro Ser Ser Glu Glu Leu Gly	
1189 1194 1199 1204	
gga gac atc cca gga aaa gaa ttt gat act cct ctg tga atgctcctgc	3762
Gly Asp Ile Pro Gly Lys Glu Phe Asp Thr Pro Leu *	
1205 1210 1215	
caggccttca gaaattgcat ggccactcca gcgtcatcgg actctctcttt attacaaaga	3822
tcaactgccc ggaccatctt cccgagaagc atcccttagc ctaaaatcca caccaaaggg	3882
agagttccag aggaatccat gaagaattcc catgcccagg ctccatgtgt catgtggaaa	3942
cctccacagg tctgctagtg aagaatgcat gtatgtgaga tttttgtttt ctttccaata	4002
gcaaattcaa agcaagcaac ttgcaggctc catggaactt ttaatgaagg acagtgtctt	4062
ctttgaagaa aatcaagctc gtgtttttat tcgaagctct ggtgtaaaat atttcaaagt	4122
catagaaata gtttgagaaa tgcatagcat tatttaacac tattgaacag ccgactttga	4182
gcattgtttc ttctaactgc ccctcaacta ccattatctt caagtcaaca tgcataattac	4242
attttcatcc tttgctttgc aagcactggg ggcttgcagt ttgctaattt atttatcata	4302
gagtcaccaa tgtatttgtt gctgacatgg ttttattaga tactgtagtg attcaaataa	4362
gttttctatt tgaaaaaaaa aatcacttga ttgtatcctt gcccagtgaa gccatcctaa	4422
gacttagcaa tatggattgt acatttggct gcatgagcaa gtcggccgca cacttccaga	4482
cagtgtgctg tttgaattga ctatttgcac tcaaagctct ggtattcatt gggtattggc	4542
ctgaaatgat caaataacta caaatgatct gttgaataaa aatagttgag ctgatatatg	4602
ttaagcagat attcaatcag aatgaacagg ttccgggtggg tattttgccg tttgacattt	4662
tttatggttc atttattttt aatatagaga ggaagattga atatttatct agagaataca	4722
aagaccaca tgtaaatgat aggtattatc tccatgtata tatgtacca cttagtcatg	4782
taagtgcata tacacatata cacacatgag tgtagacatg tgtttattaa ttgacaatga	4842
cccaaattct ttccacaaga cttaaaacca aattcagggg caaatggata gagaagaaaa	4902
gggtcaaaca tcgagattac atggatgtta aattatatgg agacgctaag aaataattga	4962
tggagccatt gatgcaaacc gaagtagatt tagaacttat atgaatttga tttatatttt	5022
gcaagatcaa aaattagatg ttaagtatca gattttaagc ttgttttaat ggtcaaaaaa	5082
ttaggacaga aataatatgg acatttatta gtatcttcca taatttttaa gtctgacaca	5142
tttctatttt attctaacat aaaaaaactt ccattatata ttactaagt atatttaatt	5202

cacttaactc tgtctttata agttcctatt ttagatggaa taagagaaac aaattatatc	5262
aaggtaaaac tgatcaaaag cataattgaa agttctgaaa aaaaaaaaaat aataatatgt	5322
agaaaaatgt aacttagaga gtaacacatg aacattgaag ttaaaaccca gaagccagat	5382
gctcacagtt ttattttact ttaaaataaa cctgtctgac tgtagctttg cgaaatatct	5442
taaaacgcaa aaaccagttg tgtcctgaaa attgtttcaa gaatttaata tttttatgaa	5502
aattatttta tttaacttta agcaataact agagattaca attaaatttt aatcaaaatg	5562
aaggcttagt tcaaacataa ggaaacagtg tttgattaaa aaaaacacat ctagtaagac	5622
gtaaggggaa aatcacatcc tctttggaga tgattatatt ttgatctgaa ggggttgggg	5682
tgttcattag acacttaata aaacttaact tccaatgaaa aagaaatctt ttgtaaatca	5742
ttctactttt gcactttgaa agaaaggcgt taatcataaa gaagcaagaa tgggtcaaat	5802
cgaatgctgc atttttataa acaaaattac agactgtctg aaattgaaga agaatgaact	5862
aataatagca ttcataacca aacacaatga tgattattgc agaacattgt atcacatttt	5922
agtccagaga tagaataaag ttgaataacc ttgacttaca caaaactggt ttggtagttg	5982
gatttcatta tcttagtgaa tttagtcatt ttacaatatg tttgtatttg gccatttact	6042
gtaatcacat ttttatatct gtacaatgac actttttgca gttgtggggt agtgtgtaac	6102
actgtccatc ttgcatcatt gaaactacta caatgatact atcatttaat aatattaata	6162
ttacttgaaa tagactaaga taaagaaaag ggggtctgtat gatgtgcagt tttgtgcctt	6222
tatgtatttg ccttgttctt tgtcgaatgt gtgaaattct gtactgtggt ttttcctata	6282
atagaaagta gagctgtgta ttaaattaga ctgtgtctct ctgatacctt tacactactg	6342
agaatagcat ggttttggcc atgtaaacca attttcaaag ttctaatagac atagccatgt	6402
gtttttggtt ttttatattt cattttaaaa tttgagtatc accatacatt aattaatact	6462
cctgtagtag ataagctgtc attaagtaat tcccaaaaaa agggccattt gcttgcatta	6522
ctttgaattt aatggtgcgc ttgtgcactg tgtaaatatt gtttgtgatg gattggacgt	6582
tgtgactctt gccttttaag aagaaaaaaa agataggaca aagtatttga agctcttaaa	6642
atgtacatat tttggttctt ctatctcaaa ttatttaaaa tgcataatto acatttttgt	6702
aataattcta tgcaattttg tggcatgatg tttcttcac ttgtaatttt atgtgctttc	6762
atcacaaatc caaaggaaag aataaaaatt tcttaacaca aaaaaaaaaa a	6813

<210> 106
 <211> 911
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (357) .. (908)

```

<400> 106
cgtaatgggg ggggggaagg aaaaaatgat ttgcaagctg tacgcctgcc gtaccgggtcc      60

ggaattcccg ggtecgacgat ttcgtctgtc tctaaataaa taaataaaaa tattatagca      120

gtatactttg ttctatcaca ttatatgcaa gattattatt aaatcatgta cttgattaca      180

gatctgtcta acttgactag ctccctaagtt ttttggttaa ttgtggatca tgagtttctt      240

gagggcaaag cccatgtcta tctctagcac agtacaatgc ctggaacaca gtacatactt      300

ttcattttctg acttaattaa aaagaagggt cactcagctt ttccctgaat ctttaa      356
atg aaa ttt gat ttt tat tct ttc ttt gat ggt aca gca aag cgt aga      404
Met Lys Phe Asp Phe Tyr Ser Phe Phe Asp Gly Thr Ala Lys Arg Arg
  1             5             10             15

agg ttt tcc tcc aaa cca gtt gta ctc aca gaa gcc cag aaa caa ctt      452
Arg Phe Ser Ser Lys Pro Val Val Leu Thr Glu Ala Gln Lys Gln Leu
  17             22             27             32

atg ata tgc cac cta cct cag gtt ctc aga ctg cac ctc aaa cga ttc      500
Met Ile Cys His Leu Pro Gln Val Leu Arg Leu His Leu Lys Arg Phe
  33             38             43             48

agg tgg tca gga cgt aat aac cga gag aag att ggt gtt cat gtt ggc      548
Arg Trp Ser Gly Arg Asn Asn Arg Glu Lys Ile Gly Val His Val Gly
  49             54             59             64

ttt gag gaa atc tta aac atg gag ccc tat tgc tgc agg gag acc ctg      596
Phe Glu Glu Ile Leu Asn Met Glu Pro Tyr Cys Cys Arg Glu Thr Leu
  65             70             75             80

aaa tcc ctc aga cca gaa tgc ttt atc tat gac ttg tcc gcg gtg gtg      644
Lys Ser Leu Arg Pro Glu Cys Phe Ile Tyr Asp Leu Ser Ala Val Val
  81             86             91             96

atg cac cat ggg aaa gga ttt ggc tca ggg cac tac act gcc tac tgc      692
Met His His Gly Lys Gly Phe Gly Ser Gly His Tyr Thr Ala Tyr Cys
  97             102            107            112

tat aat tct gaa gga ggg ttc tgg gta cac tgc aat gat tcc aaa cta      740
Tyr Asn Ser Glu Gly Gly Phe Trp Val His Cys Asn Asp Ser Lys Leu
  113            118            123            128

agc atg tgc act atg gat gaa gta tgc aag gct caa gct tat atc ttg      788
Ser Met Cys Thr Met Asp Glu Val Cys Lys Ala Gln Ala Tyr Ile Leu
  129            134            139            144

```

ttt tat acc caa cga gtt act gag aat gga cat tct aaa ctt ttg cct	836
Phe Tyr Thr Gln Arg Val Thr Glu Asn Gly His Ser Lys Leu Leu Pro	
145 150 155 160	
cca gag ctc ctg ttg ggg agc caa cat ccc aat gaa gac gct gat acc	884
Pro Glu Leu Leu Leu Gly Ser Gln His Pro Asn Glu Asp Ala Asp Thr	
161 166 171 176	
tcg tct aat gaa atc ctt agc tga tcc	911
Ser Ser Asn Glu Ile Leu Ser *	
177 182	

<210> 107
 <211> 603
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (120)..(527)

<400> 107	
cacacctaca gtatagggaa tttgcgccct cgaggcaaag aattcggcac gagggttagg	60
ttcccggttg cgggacagtt tttttttctt ttttaaaaca gacacagcta ctgagtga	119
atg ccg cct cca cag aaa atc cca agc gtc aga ccc ttc aag cag agg	167
Met Pro Pro Pro Gln Lys Ile Pro Ser Val Arg Pro Phe Lys Gln Arg	
1 5 10 15	
aaa agc ttg gca atc aga caa gag gaa gtt gct gga atc cgg gca aag	215
Lys Ser Leu Ala Ile Arg Gln Glu Glu Val Ala Gly Ile Arg Ala Lys	
17 22 27 32	
ttc ccc aac aaa atc ccg gtg gta gtg gag cgc tac ccc agg gag acg	263
Phe Pro Asn Lys Ile Pro Val Val Val Glu Arg Tyr Pro Arg Glu Thr	
33 38 43 48	
ttc ctg ccc ccg ctg gac aaa acc aag ttc ctg gtc ccg cag gag ctg	311
Phe Leu Pro Pro Leu Asp Lys Thr Lys Phe Leu Val Pro Gln Glu Leu	
49 54 59 64	
acc atg acc cag ttc ctc agc atc atc ccg agc cgc atg gtc ctg aga	359
Thr Met Thr Gln Phe Leu Ser Ile Ile Arg Ser Arg Met Val Leu Arg	
65 70 75 80	
gcc acg gaa gcc ttt tac ttg ctg gtg aac aac aag agc ctg gtc agc	407
Ala Thr Glu Ala Phe Tyr Leu Leu Val Asn Asn Lys Ser Leu Val Ser	
81 86 91 96	
atg agc gca acc atg gca gag atc tac aga gac tgc atc cag cca tat	455
Met Ser Ala Thr Met Ala Glu Ile Tyr Arg Asp Cys Ile Gln Pro Tyr	
97 102 107 112	

aac cgt att cta aat aag aaa tgg ttg gct tgt gtg atg gtt ttg tgt 503
 Asn Arg Ile Leu Asn Lys Lys Trp Leu Ala Cys Val Met Val Leu Cys
 113 118 123 128

aat gag cta gag ata ata ttt taa gtgtcttctg tggatatatgt gggagggcca 557
 Asn Glu Leu Glu Ile Ile Phe *
 129 134

ttaaggagtg ggtttcactc cctgcatgtg ggcaggtgtc catcta 603

<210> 108
 <211> 1739
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (380)..(1654)

<400> 108
 agtccggaat tcccgggtcg acccacgcgt ccgccacgc gtccgataaa aaatgtttgt 60
 catctactat tcaagacaat cattatTTTT ctggaaattg tatctgtttt caaggttata 120
 tgtaaagtgt taagacaata tcctataaaa tgcattttta ggaagttttg cattactttc 180
 ttccctaagtc ttggtaaagt tatataatta gtaccttgaa aaaaataaag tgaaaagcct 240
 tttggggact ttagacttta gtgtttaaat gtaattatTT ttatttgttt ttggtttatt 300
 ttttattttt attttttttg gccgtgggta taatcttcag catctgcaag aaggacgaaa 360
 agctcaacaa tatcttgac atg tgc tgg aaa cag atg gat aat agt aaa aag 412
 Met Cys Trp Lys Gln Met Asp Asn Ser Lys Lys
 1 5

aag ttt gaa aga gaa tgt aga gag gca gaa aag gca caa cag agt tat 460
 Lys Phe Glu Arg Glu Cys Arg Glu Ala Glu Lys Ala Gln Gln Ser Tyr
 12 17 22 27

gaa aga ttg gat aat gat act aat gca acc aag gca gat gtt gaa aag 508
 Glu Arg Leu Asp Asn Asp Thr Asn Ala Thr Lys Ala Asp Val Glu Lys
 28 33 38 43

gcc aaa cag cag ttg aat ctg cgt acg cat atg gcc gat gaa aat aaa 556
 Ala Lys Gln Gln Leu Asn Leu Arg Thr His Met Ala Asp Glu Asn Lys
 44 49 54 59

aat gaa tat gct gca caa tta caa aac ttt aat gga gaa caa cat aaa 604
 Asn Glu Tyr Ala Ala Gln Leu Gln Asn Phe Asn Gly Glu Gln His Lys
 60 65 70 75

cat ttt tat gta gtg att cct cag att tac aag caa cta caa gaa atg 652
 His Phe Tyr Val Val Ile Pro Gln Ile Tyr Lys Gln Leu Gln Glu Met

76	81	86	91	
gac gaa cga agg act att aaa ctc agt gag tgt tac aga gga ttt gct				700
Asp Glu Arg Arg Thr Ile Lys Leu Ser Glu Cys Tyr Arg Gly Phe Ala				
92	97	102	107	
gac tca gaa cgc aaa gtt att ccc atc att tca aaa tgt ttg gaa gga				748
Asp Ser Glu Arg Lys Val Ile Pro Ile Ile Ser Lys Cys Leu Glu Gly				
108	113	118	123	
atg att ctt gca gca aaa tca gtt gat gaa aga aga gac tct caa atg				796
Met Ile Leu Ala Ala Lys Ser Val Asp Glu Arg Arg Asp Ser Gln Met				
124	129	134	139	
gtg gta gac tcc ttc aaa tct ggt ttt gaa cct cca gga gac ttt cca				844
Val Val Asp Ser Phe Lys Ser Gly Phe Glu Pro Pro Gly Asp Phe Pro				
140	145	150	155	
ttt gaa gat tac agt caa cat ata tat aga acc att tct gat ggg act				892
Phe Glu Asp Tyr Ser Gln His Ile Tyr Arg Thr Ile Ser Asp Gly Thr				
156	161	166	171	
atc agt gca tcc aaa cag gag agt ggg aag atg gat gcc aaa acc aca				940
Ile Ser Ala Ser Lys Gln Glu Ser Gly Lys Met Asp Ala Lys Thr Thr				
172	177	182	187	
gta gga aag gcc aag ggc aaa ttg tgg ctc ttt gga aag aag cca aag				988
Val Gly Lys Ala Lys Gly Lys Leu Trp Leu Phe Gly Lys Lys Pro Lys				
188	193	198	203	
ggc cca gca cta gaa gat ttc agt cat ctg cca cca gaa cag aga cgt				1036
Gly Pro Ala Leu Glu Asp Phe Ser His Leu Pro Pro Glu Gln Arg Arg				
204	209	214	219	
aaa aaa cta cag cag cgc att gat gaa ctt aac aga gaa cta cag aaa				1084
Lys Lys Leu Gln Gln Arg Ile Asp Glu Leu Asn Arg Glu Leu Gln Lys				
220	225	230	235	
gaa tca gac caa aaa gat gca ctc aac aaa atg aaa gat gta tat gag				1132
Glu Ser Asp Gln Lys Asp Ala Leu Asn Lys Met Lys Asp Val Tyr Glu				
236	241	246	251	
aag aat cca caa atg ggg gat cca ggg agt ttg cag cct aaa tta gca				1180
Lys Asn Pro Gln Met Gly Asp Pro Gly Ser Leu Gln Pro Lys Leu Ala				
252	257	262	267	
gag acc atg aat aac att gac cgc cta cga atg gaa atc cat aag aat				1228
Glu Thr Met Asn Asn Ile Asp Arg Leu Arg Met Glu Ile His Lys Asn				
268	273	278	283	
gag gct tgg ctc tct gaa gtc gaa ggc aaa aca ggt ggg aga gga gac				1276
Glu Ala Trp Leu Ser Glu Val Glu Gly Lys Thr Gly Gly Arg Gly Asp				
284	289	294	299	
aga aga cat agc agt gac ata aat cat ctt gta aca cag gga cga gaa				1324
Arg Arg His Ser Ser Asp Ile Asn His Leu Val Thr Gln Gly Arg Glu				
300	305	310	315	

Met Leu Glu Gln Ile Arg Asn
1 5

```

cct tca cca tgt ttt aaa gag gta ata cac aaa cat ttt tac ttg aaa      401
Pro Ser Pro Cys Phe Lys Glu Val Ile His Lys His Phe Tyr Leu Lys
  8          13          18          23

aga gtt gag ata atg gcc caa tgt gag gag tgg att gcg gat atc cag      449
Arg Val Glu Ile Met Ala Gln Cys Glu Glu Trp Ile Ala Asp Ile Gln
 24          29          34          39

cag tac agc agt gat aag cgg gta ggc agg act atg tct cac cat gca      497
Gln Tyr Ser Ser Asp Lys Arg Val Gly Arg Thr Met Ser His His Ala
 40          45          50          55

gca gct ctc aag cgt cac act gct cag ctc cgc gaa gag ttg ctg aaa      545
Ala Ala Leu Lys Arg His Thr Ala Gln Leu Arg Glu Glu Leu Leu Lys
 56          61          66          71

ctt ccc tgc cct gaa ggc ttg gat cct gac act gac gat gcc cca gag      593
Leu Pro Cys Pro Glu Gly Leu Asp Pro Asp Thr Asp Asp Ala Pro Glu
 72          77          82          87

gtg tgc aga gcc aca aca ggt gct gag gag act cta atg cat gat cag      641
Val Cys Arg Ala Thr Thr Gly Ala Glu Glu Thr Leu Met His Asp Gln
 88          93          98          103

gtt aaa ccc agc agc agc aaa gaa ctc ccc agt gac ttc cag tta tga      689
Val Lys Pro Ser Ser Ser Lys Glu Leu Pro Ser Asp Phe Gln Leu *
104          109          114          119

gctgcattga tgtggacttc atagacacaa aggcttcgaa gcacaagcca aatatgtcaa      749

tatttgatg taagaaacta attatgtaat aggtaatgaa actgaaacta tactatgccc      809

ttaaggagat ccagttaaat tcaaggatgat cttttatttta cctgtacagg agtgtaaact      869

tttttgctgct tttattttttc aattgtgaga accactgatt ggtatgttca acaaatttgt      929

gtatacaaag aaatggataa atcactgcta tataagggaa actaccttag gaaagaatgt      989

ttactgaatg tttatttttat tttttttttt ttttactata gaggtagggg ttgttaacaa     1049

agaatatata ttggtcattc ttacaactac tattttaaagt cagcaacttt tcactgaatt     1109

tgatagattt tatgtttggc catatcttca tgctcacatt tgatttctga agacctccta     1169

catacacttc aataaaaagtt aaatggacat aaaaaaaaaa aaa                        1212

```

<210> 110
<211> 4092
<212> DNA
<213> Homo sapiens

<220>
 <221> CDS
 <222> (465)..(2639)

<400> 110

```

ggatttttttc tgaaccagcc aggaaatacc ggaacccacc aaactttaaa caccagccta      60
aattattcct gttcttttaa gcaggcagca gaaatgacag aaacccgtta acagaaaaaa      120
aaaaaataat gcttttcatt tgaactcctg tgcattttct ttttaactta tatgtgttcc      180
taattttcct tactcttttt gtttgtttgt ttcttagtgt ggtttattga caatcattta      240
caatgccgaa gagtgctgta gtgagccagc acagtgggta acacagcaac ggagaacaga      300
tgcaggtttg aggaatttaa cttgctaaaa cttgtaactg aagtcttaga gattggaaca      360
tacggggttg tataaatagg cttttaagcc ctgtttgcaa tgggttactg ataggagaaa      420
cttgcttggtg gaatgtcagc tgcgtgagct cactgtcaga caag atg gaa gaa gaa      476
                               Met Glu Glu Glu
                               1

ggg ctg gag tgt cca aac tct tcc tct gaa aaa cgc tat ttt cct gaa      524
Gly Leu Glu Cys Pro Asn Ser Ser Ser Glu Lys Arg Tyr Phe Pro Glu
   5                               10                               15                               20

tcc ctg gat tcc agc gat ggg gat gag gaa gag gtt ttg gcc tgt gag      572
Ser Leu Asp Ser Ser Asp Gly Asp Glu Glu Val Leu Ala Cys Glu
  21                               26                               31                               36

gat ttg gaa ctt aac ccc ttt gat gga ttg cca tat tca tca cgt tat      620
Asp Leu Glu Leu Asn Pro Phe Asp Gly Leu Pro Tyr Ser Ser Arg Tyr
  37                               42                               47                               52

tat aaa ctt ctg aaa gaa aga gaa gat ctt cct ata tgg aaa gaa aaa      668
Tyr Lys Leu Leu Lys Glu Arg Glu Asp Leu Pro Ile Trp Lys Glu Lys
  53                               58                               63                               68

tac tcc ttt atg gag aac ctg ctt caa aat caa atc gtg att gtt tca      716
Tyr Ser Phe Met Glu Asn Leu Leu Gln Asn Gln Ile Val Ile Val Ser
  69                               74                               79                               84

gga gat gct aaa tgt ggt aag agc gct cag gtt cct cag tgg tgt gct      764
Gly Asp Ala Lys Cys Gly Lys Ser Ala Gln Val Pro Gln Trp Cys Ala
  85                               90                               95                               100

gaa tat tgt ctt tcc atc cac tac cag cac ggg ggc gtg ata tgc aca      812
Glu Tyr Cys Leu Ser Ile His Tyr Gln His Gly Gly Val Ile Cys Thr
 101                               106                               111                               116

cag gtc cac aag cag act atg gtc cag ctc gcc ctg cgg gtg gcg gat      860
Gln Val His Lys Gln Thr Met Val Gln Leu Ala Leu Arg Val Ala Asp
 117                               122                               127                               132

gaa atg gat gtt aac att ggt cat gag gtt ggc tac gtg atc cct ttc      908
Glu Met Asp Val Asn Ile Gly His Glu Val Gly Tyr Val Ile Pro Phe

```

133	138	143	148	
gag aac tgc tgt acc aac gaa aca atc ctg agg tat tgt act gat gat				956
Glu Asn Cys Cys Thr Asn Glu Thr Ile Leu Arg Tyr Cys Thr Asp Asp				
149	154	159	164	
atg ctg caa aga gaa atg atg tcc aat cct ttt ttg ggt agc tat ggg				1004
Met Leu Gln Arg Glu Met Met Ser Asn Pro Phe Leu Gly Ser Tyr Gly				
165	170	175	180	
gtc atc atc tta gat gat att cat gaa aga agc att gca acc gat gtg				1052
Val Ile Ile Leu Asp Asp Ile His Glu Arg Ser Ile Ala Thr Asp Val				
181	186	191	196	
tta ctt gga ctt ctt aaa gat gtt tta cta gca aga cca gaa ctg aag				1100
Leu Leu Gly Leu Leu Lys Asp Val Leu Leu Ala Arg Pro Glu Leu Lys				
197	202	207	212	
ctc ata att aac tcc tca cct cac ctg atc agc aaa ctc aat tct tat				1148
Leu Ile Ile Asn Ser Ser Pro His Leu Ile Ser Lys Leu Asn Ser Tyr				
213	218	223	228	
tat gga aac gtg cct gtc ata gaa gtg aaa aat aaa cac cct gtg gag				1196
Tyr Gly Asn Val Pro Val Ile Glu Val Lys Asn Lys His Pro Val Glu				
229	234	239	244	
gtt gtg tac ctt agt gag gct caa aag gat tct ttt gag tct att tta				1244
Val Val Tyr Leu Ser Glu Ala Gln Lys Asp Ser Phe Glu Ser Ile Leu				
245	250	255	260	
cgc ctt atc ttt gaa att cac cac tcg ggt gag aaa ggt gac att gta				1292
Arg Leu Ile Phe Glu Ile His His Ser Gly Glu Lys Gly Asp Ile Val				
261	266	271	276	
gtc ttt ctg gcc tgt gaa caa gat att gag aaa gtc tgt gaa act gtc				1340
Val Phe Leu Ala Cys Glu Gln Asp Ile Glu Lys Val Cys Glu Thr Val				
277	282	287	292	
tat caa gga tct aac cta aac cca gat ctt gga gaa ctg gtg gtt gtt				1388
Tyr Gln Gly Ser Asn Leu Asn Pro Asp Leu Gly Glu Leu Val Val Val				
293	298	303	308	
cct ttg tat cca aaa gag aaa tgt tca ttg ttc aag cca ctc gat gaa				1436
Pro Leu Tyr Pro Lys Glu Lys Cys Ser Leu Phe Lys Pro Leu Asp Glu				
309	314	319	324	
aca gaa aaa aga tgc caa gtt tat caa aga aga gtg gtg tta act act				1484
Thr Glu Lys Arg Cys Gln Val Tyr Gln Arg Arg Val Val Leu Thr Thr				
325	330	335	340	
agc tct gga gag ttt ttg atc tgg agc aac tca gtc aga ttt gtt atc				1532
Ser Ser Gly Glu Phe Leu Ile Trp Ser Asn Ser Val Arg Phe Val Ile				
341	346	351	356	
gat gtg ggt gtg gaa aga aga aag gtg tac aac ccg aga ata aga gca				1580
Asp Val Gly Val Glu Arg Arg Lys Val Tyr Asn Pro Arg Ile Arg Ala				
357	362	367	372	

aac Asn 373	tcg Ser	ctc Leu	gtc Val	atg Met	cag Gln 378	ccc Pro	atc Ile	agc Ser	cag Gln	agc Ser 383	cag Gln	gca Ala	gag Glu	ata Ile	cgc Arg 388	1628
aag Lys 389	cag Gln	att Ile	ctt Leu	ggc Gly	tca Ser 394	tct Ser	tct Ser	tca Ser	gga Gly	aaa Lys 399	ttt Phe	ttc Phe	tgc Cys	ctg Leu	tac Tyr 404	1676
act Thr 405	gaa Glu	gaa Glu	ttt Phe	gcc Ala	tcc Ser 410	aaa Lys	gac Asp	atg Met	acg Thr	cca Pro 415	ctg Leu	aag Lys	cca Pro	gca Ala	gaa Glu 420	1724
atg Met 421	cag Gln	gaa Glu	gcc Ala	aac Asn	cta Leu 426	aca Thr	agc Ser	atg Met	gtg Val	ctt Leu 431	ttt Phe	atg Met	aag Lys	agg Arg	ata Ile 436	1772
gac Asp 437	att Ile	gcg Ala	ggc Gly	cta Leu	ggc Gly 442	cac His	tgt Cys	gac Asp	ttc Phe	atg Met 447	aac Asn	aga Arg	cca Pro	gca Ala	cca Pro 452	1820
gaa Glu 453	agt Ser	ttg Leu	atg Met	cag Gln	gca Ala 458	ttg Leu	gaa Glu	gac Asp	tta Leu	gat Asp 463	tat Tyr	ctg Leu	gca Ala	gca Ala	ctg Leu 468	1868
gat Asp 469	aat Asn	gat Asp	gga Gly	aat Asn	ctt Leu 474	tct Ser	gaa Glu	ttt Phe	gga Gly	atc Ile 479	atc Ile	atg Met	tca Ser	gag Glu	ttt Phe 484	1916
cct Pro 485	ctt Leu	gat Asp	cca Pro	caa Gln	ctc Leu 490	tcg Ser	aag Lys	tct Ser	atc Ile	tta Leu 495	gcg Ala	tcc Ser	tgt Cys	gaa Glu	ttt Phe 500	1964
gac Asp 501	tgt Cys	gta Val	gat Asp	gaa Glu	gtg Val 506	cta Leu	aca Thr	atc Ile	gca Ala	gcc Ala 511	atg Met	gta Val	aca Thr	gct Ala	cca Pro 516	2012
aat Asn 517	tgc Cys	ttt Phe	tca Ser	cat His	gtg Val 522	cca Pro	cat His	gga Gly	gct Ala	gaa Glu 527	gag Glu	gct Ala	gcc Ala	ttg Leu	act Thr 532	2060
tgt Cys 533	tgg Trp	aag Lys	aca Thr	ttt Phe	tta Leu 538	cat His	ccc Pro	gaa Glu	gga Gly	gat Asp 543	cac His	ttt Phe	acc Thr	ctc Leu	atc Ile 548	2108
agc Ser 549	att Ile	tac Tyr	aag Lys	gct Ala	tac Tyr 554	caa Gln	gac Asp	aca Thr	act Thr	ctg Leu 559	aat Asn	tct Ser	agc Ser	agt Ser	gag Glu 564	2156
tac Tyr 565	tgt Cys	gtg Val	gaa Glu	aag Lys	tgg Trp 570	tgt Cys	cgt Arg	gat Asp	tac Tyr	ttc Phe 575	ctc Leu	aac Asn	tgt Cys	tca Ser	gca Ala 580	2204
ctc Leu 581	aga Arg	atg Met	gca Ala	gat Asp	gtt Val 586	att Ile	cga Arg	gct Ala	gaa Glu	ctc Leu 591	tta Leu	gaa Glu	att Ile	atc Ile	aag Lys 596	2252

cga atc gag ctt ccc tat gca gaa cct gct ttt ggc tcc aag gaa aac	2300
Arg Ile Glu Leu Pro Tyr Ala Glu Pro Ala Phe Gly Ser Lys Glu Asn	
597 602 607 612	
act cta aac ata aag aaa gct ctt ctg tcc ggt tac ttt atg cag att	2348
Thr Leu Asn Ile Lys Lys Ala Leu Leu Ser Gly Tyr Phe Met Gln Ile	
613 618 623 628	
gct cgg gat gtt gat gga tca ggt aac tac tta atg ctg aca cat aag	2396
Ala Arg Asp Val Asp Gly Ser Gly Asn Tyr Leu Met Leu Thr His Lys	
629 634 639 644	
cag gtt gct cag ctg cat ccc ctg tct ggt tac tca atc acc aag aag	2444
Gln Val Ala Gln Leu His Pro Leu Ser Gly Tyr Ser Ile Thr Lys Lys	
645 650 655 660	
atg cca gag tgg gtc ctc ttc cat aaa ttc agc att tct gag aac aac	2492
Met Pro Glu Trp Val Leu Phe His Lys Phe Ser Ile Ser Glu Asn Asn	
661 666 671 676	
tac atc agg att acc tca gaa atc tct cct gaa cta ttt atg cag ctg	2540
Tyr Ile Arg Ile Thr Ser Glu Ile Ser Pro Glu Leu Phe Met Gln Leu	
677 682 687 692	
gta cca caa tac tat ttc agt aat ctg cct cct agt gaa agt aag gac	2588
Val Pro Gln Tyr Tyr Phe Ser Asn Leu Pro Pro Ser Glu Ser Lys Asp	
693 698 703 708	
att cta cag caa gta gtg gga tca cct atc ccc tgt gtc aac aat gaa	2636
Ile Leu Gln Gln Val Val Gly Ser Pro Ile Pro Cys Val Asn Asn Glu	
709 714 719 724	
taa ggaa cagcaaatgt gtgagacgtg ccttgaaact gaacagagat gcactctcca	2693
* 725	
gtgactcccc agcaaacaca aggtgcagca ggggtcccaaa ggtagctgga tggctgaact	2753
gctggatatg ggagatacat gacgcgaaga cggatttcac atccacagga cggctcttgaa	2813
gaaaataaca ctgtgtatat tatttttaaaa taaaaaatag aagtttttat tgagttcttt	2873
aaattacgac tccatgcttt tcttcttctt ggaaaagttt ttaaatcaac cactcataat	2933
ttgaccaaaa ttttaaaaaa ctggtatttt gtaaagtgtg cagagacaca tgggacagaa	2993
ccctactttt tgtagaggaa cttaatctga ataaagtctg agtttttcag taaatctcca	3053
ctgagttttc tggtaatttt acaaaaaacaa gcccatcact gtccattgga aatggggttag	3113
acagatagat attctttcag tttatccatg atttcgttca tcttgctgcc tggaattaac	3173
atcacagttc gcaagggcgt cattggtacg tcatcaaaag accatttgcc tcccagacaa	3233
gtgtcgtctt cctcctgcac tgagtagttg aacttgagaa ttgccttctc atagaaaaat	3293
tcttcctctg catttgcaaa cattaacgca gctttctttt tgttgctagg tttctttttg	3353

```

gaattgtttt ttctgcttc cacaaatgtc ttactaatca gaaggtaaaa gtagcacttc 3413
ccacatggct tattggttct gtgtgcccc gccagttctt tctgaagctg ctggtacatg 3473
ggcagagcga tctgtggagg gacattaatg aatctttcac ttaggagaag gccacaggc 3533
ttggtggtgt catttaaaaa cttgtccagc tgttcaacca tgctcttttc acagttcttc 3593
tcacagaagc gtagaaccaa ctcttgaatt tgttcaacac actgggtacc ctttctttca 3653
gttaaattta aaaggcttat gaaacccaaa acctcatctt catccatata atcattgctg 3713
tcttctgaaa catccgtttg cttaatcaca ctcccaatat gggtctgttg aattaagaga 3773
tctgttagtt ctgcagtgtt cacaggagcc tttagaaaaa gctgctgcag taatttctta 3833
attccgtcat aatcattatc tgatagggaa taagcttcaa attcaatatt cacttcctcg 3893
tcaatgacct cgtcctcttc atccttttcc ttgtcactgt catcatcgtc ttcacacctca 3953
ttttcgactt ctttttcctc ttctcgtcg cgctggactg ggggatccgg cggctgcgga 4013
accccacttt ccacggcacg ccgcttagga aatcgtcgac ccgggaattc cggaccggtg 4073
cctgcaggcg taccagctt 4092

```

```

<210> 111
<211> 6103
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (238)..(5331)

```

```

<400> 111
ggctgaggcg gcgcggcgga gccctgagcg gctgtgacag gctacgcaac aggttcgcmg 60
gcggcggcct gacgaccaag ccagctgcag tggcggcgac ggcggcagag cagggctctcc 120
ccgcgcctgc ccgcgccag gctgccggtg ctgagggacg cggagtcgcmg ctgtgacgag 180

cgggaggcmg gcgcagggcg ccagatggct gagagctagc aaggaaaact caggacc 237
atg atg gct cag ttt ccc aca gct atg aat gga ggg cca aac atg tgg 285
Met Met Ala Gln Phe Pro Thr Ala Met Asn Gly Gly Pro Asn Met Trp
1 5 10 15

gct att acc tct gaa gaa cgt act aag cat gac agg cag ttt gat aac 333
Ala Ile Thr Ser Glu Glu Arg Thr Lys His Asp Arg Gln Phe Asp Asn
17 22 27 32

ctc aaa cct tca gga ggt tac ata aca ggt gat caa gca cgt aat ttt 381
Leu Lys Pro Ser Gly Gly Tyr Ile Thr Gly Asp Gln Ala Arg Asn Phe

```

33	38	43	48	
ttc cta caa tca ggt ctg ccg gcc cct gtt tta gct gaa ata tgg gct				429
Phe Leu Gln Ser Gly Leu Pro Ala Pro Val Leu Ala Glu Ile Trp Ala				
49	54	59	64	
tta tca gac cta aac aag gat ggg aag atg gat cag caa gag ttc tcc				477
Leu Ser Asp Leu Asn Lys Asp Gly Lys Met Asp Gln Gln Glu Phe Ser				
65	70	75	80	
ata gct atg aaa ctc atc aaa ctg aag ctt caa ggc caa cag ttg cct				525
Ile Ala Met Lys Leu Ile Lys Leu Lys Leu Gln Gly Gln Gln Leu Pro				
81	86	91	96	
gtg gtt ctc cct cct att atg aag caa ccc cct atg ttt tct cca tta				573
Val Val Leu Pro Pro Ile Met Lys Gln Pro Pro Met Phe Ser Pro Leu				
97	102	107	112	
att tct gct cgt ttt gga atg gga agc atg ccc aat ctg tcc att cct				621
Ile Ser Ala Arg Phe Gly Met Gly Ser Met Pro Asn Leu Ser Ile Pro				
113	118	123	128	
cag cca ttg cct cca gct gca cct ata aca tca ttg tct tct gcg act				669
Gln Pro Leu Pro Pro Ala Ala Pro Ile Thr Ser Leu Ser Ser Ala Thr				
129	134	139	144	
tca ggg acc aac ctt cct ccc tta atg atg ccc act ccc cta gtg cct				717
Ser Gly Thr Asn Leu Pro Pro Leu Met Met Pro Thr Pro Leu Val Pro				
145	150	155	160	
tct gtt agc aca tca tca tta cca aat gga acc gcc agt ctc att cag				765
Ser Val Ser Thr Ser Ser Leu Pro Asn Gly Thr Ala Ser Leu Ile Gln				
161	166	171	176	
cct tta ccc att cct tat tct tct tca aca ttg cct cat ggg tca tct				813
Pro Leu Pro Ile Pro Tyr Ser Ser Ser Thr Leu Pro His Gly Ser Ser				
177	182	187	192	
tat agt ctg atg atg gga gga ttt gga ggt gct agt ata cag aaa gcg				861
Tyr Ser Leu Met Met Gly Gly Phe Gly Gly Ala Ser Ile Gln Lys Ala				
193	198	203	208	
cag tct ctg att gat tta gga tct agt agc tca act tcc tcg act gct				909
Gln Ser Leu Ile Asp Leu Gly Ser Ser Ser Thr Ser Ser Thr Ala				
209	214	219	224	
tca ctc tca ggg aac tca ccc aag act ggg acc tca gag tgg gca gtt				957
Ser Leu Ser Gly Asn Ser Pro Lys Thr Gly Thr Ser Glu Trp Ala Val				
225	230	235	240	
cct cag cct aca aga tta aaa tat cgg caa aaa ttt aat act ctt gac				1005
Pro Gln Pro Thr Arg Leu Lys Tyr Arg Gln Lys Phe Asn Thr Leu Asp				
241	246	251	256	
aaa agt atg agt gga tat ctc tca ggt ttt caa gct aga aat gcc ctt				1053
Lys Ser Met Ser Gly Tyr Leu Ser Gly Phe Gln Ala Arg Asn Ala Leu				
257	262	267	272	

ctt cag tca aat ctt tct caa act cag ctg gct act att tgg act ctg	1101
Leu Gln Ser Asn Leu Ser Gln Thr Gln Leu Ala Thr Ile Trp Thr Leu	
273 278 283 288	
gct gac gtt gat ggt gat gga cag cta aaa gca gaa gag ttt att ctt	1149
Ala Asp Val Asp Gly Asp Gly Gln Leu Lys Ala Glu Glu Phe Ile Leu	
289 294 299 304	
gca atg cac ctt act gac atg gcc aaa gct gga cag cca tta cca ctg	1197
Ala Met His Leu Thr Asp Met Ala Lys Ala Gly Gln Pro Leu Pro Leu	
305 310 315 320	
act tta cct cct gag ctt gtt cct cca tct ttc aga gga gga aag caa	1245
Thr Leu Pro Pro Glu Leu Val Pro Pro Ser Phe Arg Gly Gly Lys Gln	
321 326 331 336	
att gat tcc att aat gga act ctg cct tca tat cag aaa atg caa gaa	1293
Ile Asp Ser Ile Asn Gly Thr Leu Pro Ser Tyr Gln Lys Met Gln Glu	
337 342 347 352	
gag gag cct cag aag aaa tta cca gtt act ttt gag gac aaa cgg aaa	1341
Glu Glu Pro Gln Lys Lys Leu Pro Val Thr Phe Glu Asp Lys Arg Lys	
353 358 363 368	
gcc aac tat gag cga ggg aac atg gag ctg gaa aag cga cgc caa gcc	1389
Ala Asn Tyr Glu Arg Gly Asn Met Glu Leu Glu Lys Arg Arg Gln Ala	
369 374 379 384	
ttg atg gag cag caa caa agg gag gca gaa cgt aaa gcc cag aaa gaa	1437
Leu Met Glu Gln Gln Gln Arg Glu Ala Glu Arg Lys Ala Gln Lys Glu	
385 390 395 400	
aag gaa gag tgg gaa cga aaa cag aga gaa tta caa gaa caa gaa tgg	1485
Lys Glu Glu Trp Glu Arg Lys Gln Arg Glu Leu Gln Glu Gln Glu Trp	
401 406 411 416	
aag aaa caa ctt gaa tta gaa aaa cgc tta gag aag caa cgg gaa ttg	1533
Lys Lys Gln Leu Glu Leu Glu Lys Arg Leu Glu Lys Gln Arg Glu Leu	
417 422 427 432	
gag aga caa cga gag gaa gaa agg aga aaa gac ata gaa aga cga gag	1581
Glu Arg Gln Arg Glu Glu Glu Arg Arg Lys Asp Ile Glu Arg Arg Glu	
433 438 443 448	
gca gca aaa cag gaa ctt gaa cga caa cgt cgc tta gaa tgg gag aga	1629
Ala Ala Lys Gln Glu Leu Glu Arg Gln Arg Arg Leu Glu Trp Glu Arg	
449 454 459 464	
att cgg cga cag gag ctt ctc aat caa aag aat aga gaa caa gaa gaa	1677
Ile Arg Arg Gln Glu Leu Leu Asn Gln Lys Asn Arg Glu Gln Glu Glu	
465 470 475 480	
att gtc agg tta aac tct aaa aag aag aat ctt cat ctt gag ttg gaa	1725
Ile Val Arg Leu Asn Ser Lys Lys Lys Asn Leu His Leu Glu Leu Glu	
481 486 491 496	

gca ctg aat ggc aaa cat cag cag atc tca ggc aga ctt cag gat gtc	1773
Ala Leu Asn Gly Lys His Gln Gln Ile Ser Gly Arg Leu Gln Asp Val	
497 502 507 512	
cga ctc aaa aag caa act caa aag act gag ctg gaa gtt ctg gat aag	1821
Arg Leu Lys Lys Gln Thr Gln Lys Thr Glu Leu Glu Val Leu Asp Lys	
513 518 523 528	
cag tgt gac ttg gaa att atg gaa atc aag caa ctt caa cag gaa ctt	1869
Gln Cys Asp Leu Glu Ile Met Glu Ile Lys Gln Leu Gln Gln Glu Leu	
529 534 539 544	
cag gaa tat cag aat aag ctt atc tat ctg gta cct gag aag caa tta	1917
Gln Glu Tyr Gln Asn Lys Leu Ile Tyr Leu Val Pro Glu Lys Gln Leu	
545 550 555 560	
tta aat gaa aga att aaa aac atg cag ttc agt aac aca cct gat tca	1965
Leu Asn Glu Arg Ile Lys Asn Met Gln Phe Ser Asn Thr Pro Asp Ser	
561 566 571 576	
ggg gtc agt tta ctt cat aaa aaa tca tta gaa aag gaa gaa tta tgc	2013
Gly Val Ser Leu Leu His Lys Lys Ser Leu Glu Lys Glu Glu Leu Cys	
577 582 587 592	
caa aga ctt aaa gaa cag tta gat gct ctt gaa aaa gaa act gca tct	2061
Gln Arg Leu Lys Glu Gln Leu Asp Ala Leu Glu Lys Glu Thr Ala Ser	
593 598 603 608	
aag ctg tca gaa atg gat tct ttt aac aat caa cta aag tgt ggg aat	2109
Lys Leu Ser Glu Met Asp Ser Phe Asn Asn Gln Leu Lys Cys Gly Asn	
609 614 619 624	
atg gat gac tct gtt ctt cag tgc ctt ttg tct ctg cta agc tgt ctc	2157
Met Asp Asp Ser Val Leu Gln Cys Leu Leu Ser Leu Leu Ser Cys Leu	
625 630 635 640	
aac aac ctc ttc ctc tta ctt aag gaa ctg aga gaa acc tac aac aca	2205
Asn Asn Leu Phe Leu Leu Leu Lys Glu Leu Arg Glu Thr Tyr Asn Thr	
641 646 651 656	
cag cag tta gcc ctt gaa cag ctt tat aag atc aaa cgt gac aag ttg	2253
Gln Gln Leu Ala Leu Glu Gln Leu Tyr Lys Ile Lys Arg Asp Lys Leu	
657 662 667 672	
aag gaa att gaa agg aaa aga tta gaa cta atg cag aaa aag aaa cta	2301
Lys Glu Ile Glu Arg Lys Arg Leu Glu Leu Met Gln Lys Lys Lys Leu	
673 678 683 688	
gaa gat gag gct gca agg aaa gca aag caa gga aaa gaa aac tta tgg	2349
Glu Asp Glu Ala Ala Arg Lys Ala Lys Gln Gly Lys Glu Asn Leu Trp	
689 694 699 704	
aaa gaa aat ctt aga aag gag gaa gaa gaa aaa caa aag cga ctc cag	2397
Lys Glu Asn Leu Arg Lys Glu Glu Glu Glu Lys Gln Lys Arg Leu Gln	
705 710 715 720	
gaa gaa aaa aca caa gaa aaa att caa gaa gag gaa cgg aaa gct gag	2445

Glu Glu Lys Thr Gln	Glu Lys Ile Gln Glu Glu Glu Arg Lys Ala Glu	
721	726	731 736
gag aaa caa cgt aag gat aag gat act ttg aaa gct gag gag aaa aaa		2493
Glu Lys Gln Arg Lys Asp Lys Asp Thr Leu Lys Ala Glu Glu Lys Lys		
737	742 747	752
cgt gag aca gct agt gtt ttg gtg aat tat aga gca tta tac ccc ttt		2541
Arg Glu Thr Ala Ser Val Leu Val Asn Tyr Arg Ala Leu Tyr Pro Phe		
753	758 763	768
gaa gca agg aac cat gat gag atg agt ttt aat tct gga gat ata att		2589
Glu Ala Arg Asn His Asp Glu Met Ser Phe Asn Ser Gly Asp Ile Ile		
769	774 779	784
cag gtt gat gaa aaa acc gta gga gaa cct ggt tgg ctt tat ggt agt		2637
Gln Val Asp Glu Lys Thr Val Gly Glu Pro Gly Trp Leu Tyr Gly Ser		
785	790 795	800
ttt caa gga aat ttt ggc tgg ttt cca tgc aat tat gta gaa aaa atg		2685
Phe Gln Gly Asn Phe Gly Trp Phe Pro Cys Asn Tyr Val Glu Lys Met		
801	806 811	816
cca tca agt gaa aat gaa aaa gct gta tct cca aag aag gcc tta ctt		2733
Pro Ser Ser Glu Asn Glu Lys Ala Val Ser Pro Lys Lys Ala Leu Leu		
817	822 827	832
cct cct aca gtt tct tta tct gct acc tca act tcc tct gaa cca ctt		2781
Pro Pro Thr Val Ser Leu Ser Ala Thr Ser Thr Ser Ser Glu Pro Leu		
833	838 843	848
tct tca aat caa cca gca tca gtg act gat tat caa aat gta tct ttt		2829
Ser Ser Asn Gln Pro Ala Ser Val Thr Asp Tyr Gln Asn Val Ser Phe		
849	854 859	864
tca aac cta act gta aat aca tca tgg cag aaa aaa tca gcc ttc act		2877
Ser Asn Leu Thr Val Asn Thr Ser Trp Gln Lys Lys Ser Ala Phe Thr		
865	870 875	880
cga act gtg tcc cct gga tct gta tca cct att cat gga cag gga caa		2925
Arg Thr Val Ser Pro Gly Ser Val Ser Pro Ile His Gly Gln Gly Gln		
881	886 891	896
gtg gta gaa aac tta aaa gca cag gcc ctt tgt tcc tgg act gca aag		2973
Val Val Glu Asn Leu Lys Ala Gln Ala Leu Cys Ser Trp Thr Ala Lys		
897	902 907	912
aaa gat aac cac ttg aac ttc tca aaa cat gac att att act gtc ttg		3021
Lys Asp Asn His Leu Asn Phe Ser Lys His Asp Ile Ile Thr Val Leu		
913	918 923	928
gag cag caa gaa aat tgg tgg ttt ggg gag gtg cat gga gga aga gga		3069
Glu Gln Gln Glu Asn Trp Trp Phe Gly Glu Val His Gly Gly Arg Gly		
929	934 939	944
tgg ttt ccc aaa tct tat gtc aag atc att cct ggg agt gaa gta aaa		3117
Trp Phe Pro Lys Ser Tyr Val Lys Ile Ile Pro Gly Ser Glu Val Lys		

945	950	955	960	
cgg gaa gaa cca gaa gct ttg tat gca gct gta aat aag aaa cct acc				3165
Arg Glu Glu Pro Glu Ala Leu Tyr Ala Ala Val Asn Lys Lys Pro Thr				
961	966	971	976	
tcg gca gcc tat tca gtt gga gaa gaa tat att gca ctt tat cca tat				3213
Ser Ala Ala Tyr Ser Val Gly Glu Glu Tyr Ile Ala Leu Tyr Pro Tyr				
977	982	987	992	
tca agt gtg gaa cct gga gat ttg act ttc aca gaa ggt gaa gaa ata				3261
Ser Ser Val Glu Pro Gly Asp Leu Thr Phe Thr Glu Gly Glu Glu Ile				
993	998	1003	1008	
ttg gtg acc cag aaa gat gga gag tgg tgg aca gga agt att gga gat				3309
Leu Val Thr Gln Lys Asp Gly Glu Trp Trp Thr Gly Ser Ile Gly Asp				
1009	1014	1019	1024	
aga agt gga att ttt cca tca aac tat gtc aaa cca aag gat caa gag				3357
Arg Ser Gly Ile Phe Pro Ser Asn Tyr Val Lys Pro Lys Asp Gln Glu				
1025	1030	1035	1040	
agt ttt ggg agt gct agc aag tct gga gca tca aat aaa aaa cct gag				3405
Ser Phe Gly Ser Ala Ser Lys Ser Gly Ala Ser Asn Lys Lys Pro Glu				
1041	1046	1051	1056	
att gct cag gta act tca gca tat gtt gct tct ggt tct gaa caa ctt				3453
Ile Ala Gln Val Thr Ser Ala Tyr Val Ala Ser Gly Ser Glu Gln Leu				
1057	1062	1067	1072	
agc ctt gca cca gga cag tta ata tta att cta aag aaa aat aca agt				3501
Ser Leu Ala Pro Gly Gln Leu Ile Leu Ile Leu Lys Lys Asn Thr Ser				
1073	1078	1083	1088	
ggg tgg tgg caa gga gag tta cag gcc aga gga aaa aag cga cag aaa				3549
Gly Trp Trp Gln Gly Glu Leu Gln Ala Arg Gly Lys Lys Arg Gln Lys				
1089	1094	1099	1104	
gga tgg ttt cct gcc agt cat gtt aaa ctt ttg ggt cca agt agt gaa				3597
Gly Trp Phe Pro Ala Ser His Val Lys Leu Leu Gly Pro Ser Ser Glu				
1105	1110	1115	1120	
aga gcc aca cct gcc ttt cat cct gta tgt cag gtg att gct atg tat				3645
Arg Ala Thr Pro Ala Phe His Pro Val Cys Gln Val Ile Ala Met Tyr				
1121	1126	1131	1136	
gac tat gca gca aat aat gaa gat gag ctc agt ttc tcc aag gga caa				3693
Asp Tyr Ala Ala Asn Asn Glu Asp Glu Leu Ser Phe Ser Lys Gly Gln				
1137	1142	1147	1152	
ctc att aat gtt atg aac aaa gat gat cct gat tgg tgg caa gga gag				3741
Leu Ile Asn Val Met Asn Lys Asp Asp Pro Asp Trp Trp Gln Gly Glu				
1153	1158	1163	1168	
atc aac ggg gtg act ggt ctc ttt cct tca aac tac gtt aag atg acg				3789
Ile Asn Gly Val Thr Gly Leu Phe Pro Ser Asn Tyr Val Lys Met Thr				
1169	1174	1179	1184	

aca gac tca gat cca agt caa cag tgg tgt gct gat ctg caa acc ctg	3837
Thr Asp Ser Asp Pro Ser Gln Gln Trp Cys Ala Asp Leu Gln Thr Leu	
1185 1190 1195 1200	
gac aca atg cag cca att gag agg aaa aga cag ggc tat att cat gag	3885
Asp Thr Met Gln Pro Ile Glu Arg Lys Arg Gln Gly Tyr Ile His Glu	
1201 1206 1211 1216	
ctg att cag acc gaa gag cgg tac atg gct gac ctt cag ctc gtc gtc	3933
Leu Ile Gln Thr Glu Arg Tyr Met Ala Asp Leu Gln Leu Val Val	
1217 1222 1227 1232	
gag gtt ttt cag aaa cgc atg gca gag tca ggc ttt ctc act gaa ggg	3981
Glu Val Phe Gln Lys Arg Met Ala Glu Ser Gly Phe Leu Thr Glu Gly	
1233 1238 1243 1248	
gag atg gcc ctg att ttt gtt aac tgg aag gag ctc atc atg tcc aac	4029
Glu Met Ala Leu Ile Phe Val Asn Trp Lys Glu Leu Ile Met Ser Asn	
1249 1254 1259 1264	
aca aag ctg ctg aag gct ttg cgg gtg cgg aag aag acc ggg ggc gag	4077
Thr Lys Leu Leu Lys Ala Leu Arg Val Arg Lys Lys Thr Gly Gly Glu	
1265 1270 1275 1280	
aag atg ccg gtg cag atg att ggg gac atc ctg gcc gct gag ctg tcc	4125
Lys Met Pro Val Gln Met Ile Gly Asp Ile Leu Ala Ala Glu Leu Ser	
1281 1286 1291 1296	
cac atg cag gct tac atc agg ttc tgc agc tgc cag ctt aat gga gca	4173
His Met Gln Ala Tyr Ile Arg Phe Cys Ser Cys Gln Leu Asn Gly Ala	
1297 1302 1307 1312	
gct ctg tta cag cag aag aca gat gaa gac aca gat ttc aaa gaa ttt	4221
Ala Leu Leu Gln Gln Lys Thr Asp Glu Asp Thr Asp Phe Lys Glu Phe	
1313 1318 1323 1328	
tta aag aag ctg gca tct gac ccg cgg tgt aaa gga atg ccc ctc tcc	4269
Leu Lys Lys Leu Ala Ser Asp Pro Arg Cys Lys Gly Met Pro Leu Ser	
1329 1334 1339 1344	
agc ttc ctg ctg aaa ccc atg cag agg atc acc cgc tac cca ctg ctc	4317
Ser Phe Leu Leu Lys Pro Met Gln Arg Ile Thr Arg Tyr Pro Leu Leu	
1345 1350 1355 1360	
atc aga agt att ctg gag aac acc ccg gag agc cat gca gac cat tcc	4365
Ile Arg Ser Ile Leu Glu Asn Thr Pro Glu Ser His Ala Asp His Ser	
1361 1366 1371 1376	
tcc cta aag ctg gcc ctc gag cgg gca gag gag ctg tgc tct caa gtg	4413
Ser Leu Lys Leu Ala Leu Glu Arg Ala Glu Glu Leu Cys Ser Gln Val	
1377 1382 1387 1392	
aat gag gga gtt cgg gag aag gaa aac tcg gac cga ctg gag tgg atc	4461
Asn Glu Gly Val Arg Glu Lys Glu Asn Ser Asp Arg Leu Glu Trp Ile	
1393 1398 1403 1408	

cag	gcg	cac	gtg	cag	tgt	gaa	ggc	ctc	gcg	gag	caa	ctt	att	ttc	aac	4509
Gln	Ala	His	Val	Gln	Cys	Glu	Gly	Leu	Ala	Glu	Gln	Leu	Ile	Phe	Asn	
1409					1414					1419					1424	
tct	ctc	acc	aac	tgc	ctg	ggg	ccc	cgg	aag	ctc	tta	cac	agt	ggg	aaa	4557
Ser	Leu	Thr	Asn	Cys	Leu	Gly	Pro	Arg	Lys	Leu	Leu	His	Ser	Gly	Lys	
1425					1430					1435					1440	
tta	tac	aag	acc	aag	agc	aac	aag	gaa	ctg	cac	gga	ttc	ctc	ttc	aat	4605
Leu	Tyr	Lys	Thr	Lys	Ser	Asn	Lys	Glu	Leu	His	Gly	Phe	Leu	Phe	Asn	
1441					1446					1451					1456	
gac	ttc	ctg	ctt	ctt	acc	tac	atg	gtc	aag	cag	ttt	gct	ggt	tcc	tct	4653
Asp	Phe	Leu	Leu	Leu	Thr	Tyr	Met	Val	Lys	Gln	Phe	Ala	Val	Ser	Ser	
1457					1462					1467					1472	
ggc	tct	gag	aaa	ctt	ttc	agc	tcg	aag	tcc	aat	gct	caa	ttc	aaa	atg	4701
Gly	Ser	Glu	Lys	Leu	Phe	Ser	Ser	Lys	Ser	Asn	Ala	Gln	Phe	Lys	Met	
1473					1478					1483					1488	
tat	aaa	acg	ccc	att	ttc	ctg	aat	gaa	gtc	ttg	gtg	aaa	ctg	ccc	aca	4749
Tyr	Lys	Thr	Pro	Ile	Phe	Leu	Asn	Glu	Val	Leu	Val	Lys	Leu	Pro	Thr	
1489					1494					1499					1504	
gac	cct	tcc	agc	gat	gag	cct	gtc	ttc	cac	att	tcc	cac	att	gat	cgg	4797
Asp	Pro	Ser	Ser	Asp	Glu	Pro	Val	Phe	His	Ile	Ser	His	Ile	Asp	Arg	
1505					1510					1515					1520	
gtc	tac	acc	ctc	cga	aca	gac	aac	att	aat	gag	agg	acc	acc	tgg	gtg	4845
Val	Tyr	Thr	Leu	Arg	Thr	Asp	Asn	Ile	Asn	Glu	Arg	Thr	Thr	Trp	Val	
1521					1526					1531					1536	
cag	aag	atc	aag	gcg	gcg	tct	gag	cag	tac	atc	gac	acc	gag	aag	aag	4893
Gln	Lys	Ile	Lys	Ala	Ala	Ser	Glu	Gln	Tyr	Ile	Asp	Thr	Glu	Lys	Lys	
1537					1542					1547					1552	
aag	cgt	gag	aaa	gct	tac	caa	gcc	cgc	tcc	caa	aag	act	tca	ggc	att	4941
Lys	Arg	Glu	Lys	Ala	Tyr	Gln	Ala	Arg	Ser	Gln	Lys	Thr	Ser	Gly	Ile	
1553					1558					1563					1568	
ggg	cgc	ctg	atg	gtg	cat	gtc	att	gaa	gct	aca	gaa	tta	aaa	gcc	tgc	4989
Gly	Arg	Leu	Met	Val	His	Val	Ile	Glu	Ala	Thr	Glu	Leu	Lys	Ala	Cys	
1569					1574					1579					1584	
aaa	cca	aat	gga	aag	agc	aac	cca	tac	tgt	gaa	atc	agc	atg	ggc	tcc	5037
Lys	Pro	Asn	Gly	Lys	Ser	Asn	Pro	Tyr	Cys	Glu	Ile	Ser	Met	Gly	Ser	
1585					1590					1595					1600	
cag	agc	tac	acc	acc	agg	acc	atc	cag	gac	aca	ctc	aat	ccc	aag	tgg	5085
Gln	Ser	Tyr	Thr	Thr	Arg	Thr	Ile	Gln	Asp	Thr	Leu	Asn	Pro	Lys	Trp	
1601					1606					1611					1616	
aat	ttt	aac	tgc	cag	ttc	ttt	att	aag</								

```

Cys Leu Thr Leu Phe Asp Arg Asp Gln Phe Ser Pro Asp Asp Phe Leu
1633                1638                1643                1648

ggg cgt act gaa att cca gtg gca aaa att cga aca gaa cag gaa agc      5229
Gly Arg Thr Glu Ile Pro Val Ala Lys Ile Arg Thr Glu Gln Glu Ser
1649                1654                1659                1664

aaa ggc cct atg acc cgc cga ctg ctg ctg cat gag gtc ccc acc ggg      5277
Lys Gly Pro Met Thr Arg Arg Leu Leu Leu His Glu Val Pro Thr Gly
1665                1670                1675                1680

gag gtc tgg gtc cgt ttt gac ctg cag ctt ttt gag caa aaa act ctc      5325
Glu Val Trp Val Arg Phe Asp Leu Gln Leu Phe Glu Gln Lys Thr Leu
1681                1686                1691                1696

ctg tag gggtttctaaa ggacagcacc agcgggacag cccacaaggc tggggctgga      5381
Leu *
1697

gaatgagaga ctgcgctctc ttggggctga gggagcacca tgcagcttca cccctcacia      5441

agccatgcac gctgggggct ctgttttctc gcacactaaa tagctagcaa tctatgcaaa      5501

cacctttccc ataaagaaac caaaccccat agtacagtgc cttgtcctag tggtcacatg      5561

ttcagctctg tttgtttaga tgccaagggt tccattttca gggctataaa aagtattact      5621

tggaatgag gcatcagacc accagatggt accgctcggg tgaatgtgtc caccgtggag      5681

tggtttggtg acgctgtaac cattccacgc cagtgcctc tgctgggtca cagccactca      5741

ggaggggaag ggtcaggatg agaggctgca gcctcgacac ttggcgcggc ctgatactga      5801

aatagcgtct actcgtgcac tgaataaaaa cagaaacttg atcattttat tcctgattag      5861

attttatcac tctctgctaa gacaatatag tctggagtat aagtgggaaa gcttgattta      5921

aatactgtga actctaataa tgtggaaaat atttttcaac tttaattttc tgaagtataa      5981

attatttatg taaattcatt gtttttgcac atttcttagg acatgcatct ttaagcttta      6041

tcattgccca tatgtacaga aagagaataa agacatatgt ttatggatgg aaaaaaaaaa      6101

aa                                                                    6103

```

```

<210> 112
<211> 1668
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (95)..(1432)

```

```

<400> 112
atttggccct cgaggccaag aattcggcac gagacactct tcagcgacca cgcaggcact      60

ttcccgggtcc ccagtatacc ataattgaag aaaa      atg atg gaa gag agt gga      112
                                         Met Met Glu Glu Ser Gly
                                         1

ata gag aca aca cca cct ggg act cct cca cca aat cct gca ggg ctg      160
Ile Glu Thr Thr Pro Pro Gly Thr Pro Pro Pro Asn Pro Ala Gly Leu
   7                12                17                22

gct gct act gct atg tct tct acc cct gtt cca tta gcg gca acc agt      208
Ala Ala Thr Ala Met Ser Ser Thr Pro Val Pro Leu Ala Ala Thr Ser
  23                28                33                38

tct ttt tct tct cca aat gta tcc tcc atg gag tcc ttc cca cca ctc      256
Ser Phe Ser Ser Pro Asn Val Ser Ser Met Glu Ser Phe Pro Pro Leu
  39                44                49                54

gca tac tct act cct cag ccg ccc ctt cct cct gtg agg cct tca gca      304
Ala Tyr Ser Thr Pro Gln Pro Pro Leu Pro Pro Val Arg Pro Ser Ala
  55                60                65                70

cca tta cct ttt gtg cct cct cct gca gtt cct tct gtc cca cca ctt      352
Pro Leu Pro Phe Val Pro Pro Pro Ala Val Pro Ser Val Pro Pro Leu
  71                76                81                86

gtt act tct atg cca cct cct gtt tct cca tca act gct gct gcc ttc      400
Val Thr Ser Met Pro Pro Pro Val Ser Pro Ser Thr Ala Ala Ala Phe
  87                92                97                102

ggg aat cct cct gta tct cac ttc cca cct tca act tct gcc cca aac      448
Gly Asn Pro Pro Val Ser His Phe Pro Pro Ser Thr Ser Ala Pro Asn
 103                108                113                118

act ctt tta cct gca ccc cct tcg ggt cct cct ata tca gga ttt tct      496
Thr Leu Leu Pro Ala Pro Pro Ser Gly Pro Pro Ile Ser Gly Phe Ser
 119                124                129                134

gtt ggt tca act tat gac att aca agg gga cat gct ggg aga gct ccc      544
Val Gly Ser Thr Tyr Asp Ile Thr Arg Gly His Ala Gly Arg Ala Pro
 135                140                145                150

cag aca ccc ctg atg cca tca ttt tct gca cct tca gga aca ggt ctt      592
Gln Thr Pro Leu Met Pro Ser Phe Ser Ala Pro Ser Gly Thr Gly Leu
 151                156                161                166

ttg cca act cct att act cag caa gcc agt ttg aca tct ctg gca cag      640
Leu Pro Thr Pro Ile Thr Gln Gln Ala Ser Leu Thr Ser Leu Ala Gln
 167                172                177                182

gga act gga acc aca tca gcc att act ttc cca gag gag caa gaa gac      688
Gly Thr Gly Thr Thr Ser Ala Ile Thr Phe Pro Glu Glu Gln Glu Asp
 183                188                193                198

cct aga att act aga ggt cag gat gaa gca tct gct ggt gga atc tgg      736
Pro Arg Ile Thr Arg Gly Gln Asp Glu Ala Ser Ala Gly Gly Ile Trp

```


199	204	209	214	
ggt ttt att aag ggt gtg gct ggg aat cct atg gtg aag tct gtg ctt				784
Gly Phe Ile Lys Gly Val Ala Gly Asn Pro Met Val Lys Ser Val Leu				
215	220	225	230	
gat aag aca aaa cat tca gta gaa agc atg att aca acg ctg gac cct				832
Asp Lys Thr Lys His Ser Val Glu Ser Met Ile Thr Thr Leu Asp Pro				
231	236	241	246	
ggc atg gct ccc tat atc aaa tct gga ggt gaa ctg gat att gta gtg				880
Gly Met Ala Pro Tyr Ile Lys Ser Gly Gly Glu Leu Asp Ile Val Val				
247	252	257	262	
acc tca aat aaa gaa gta aaa gtt gct gct gtc cga gat gcc ttc cag				928
Thr Ser Asn Lys Glu Val Lys Val Ala Ala Val Arg Asp Ala Phe Gln				
263	268	273	278	
gag gtc ttt ggc tta gct gtg gtt gta ggg gaa gct gga cag tcc aat				976
Glu Val Phe Gly Leu Ala Val Val Val Gly Glu Ala Gly Gln Ser Asn				
279	284	289	294	
att gcc cca caa cca gtg ggc tat gca gct gga tta aaa ggt gct cag				1024
Ile Ala Pro Gln Pro Val Gly Tyr Ala Ala Gly Leu Lys Gly Ala Gln				
295	300	305	310	
gaa cgg ata gat agc ttg cgt cga act ggg gtg atc cat gaa aaa cag				1072
Glu Arg Ile Asp Ser Leu Arg Arg Thr Gly Val Ile His Glu Lys Gln				
311	316	321	326	
aca gct gtg tca gta gaa aac ttc att gca gaa ttg ctg cct gac aaa				1120
Thr Ala Val Ser Val Glu Asn Phe Ile Ala Glu Leu Leu Pro Asp Lys				
327	332	337	342	
tgg ttt gac att ggt tgt ttg gtg gtt gaa gat cct gtc cat ggc att				1168
Trp Phe Asp Ile Gly Cys Leu Val Val Glu Asp Pro Val His Gly Ile				
343	348	353	358	
cat cta gaa aca ttt aca caa gcc aca cca gtg cct ttg gaa ttt gta				1216
His Leu Glu Thr Phe Thr Gln Ala Thr Pro Val Pro Leu Glu Phe Val				
359	364	369	374	
cag cag gct caa agt cta act ccc cag gac tat aat ctg agg tgg tca				1264
Gln Gln Ala Gln Ser Leu Thr Pro Gln Asp Tyr Asn Leu Arg Trp Ser				
375	380	385	390	
ggc ctt ttg gtg aca gtg ggt gaa gtc ctg gaa aag agt tta ctg aat				1312
Gly Leu Leu Val Thr Val Gly Glu Val Leu Glu Lys Ser Leu Leu Asn				
391	396	401	406	
gtc agc cgg act gat tgg cac atg gca ttt act ggg atg tcc cgt cgg				1360
Val Ser Arg Thr Asp Trp His Met Ala Phe Thr Gly Met Ser Arg Arg				
407	412	417	422	
cag atg atc tac agt gca gcc aga gcg ata gca ggc atg tat aaa cag				1408
Gln Met Ile Tyr Ser Ala Ala Arg Ala Ile Ala Gly Met Tyr Lys Gln				
423	428	433	438	

cgc ctg cca ccc agg aca gtg tga gaggagacct acctgggaga ctgagacttt 1462
 Arg Leu Pro Pro Arg Thr Val *
 439 444

ccccacttt tagcttgatg ttaaagaagt ggttgtagct tcctaaatcg aatagtctaa 1522

atgaatccag tagtttttat ctttttctg tagcctgcaa tttttctttc tctagaaagg 1582

catcatgtca ttccaggaga caaaaagaaa caaatccttt ttatagtcac accatttcac 1642

ctatcatagt actcaaaaaa aaaaaa 1668

<210> 113
 <211> 1350
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(1056)

<400> 113

atg gca ctc ccc ttt caa aaa gag ctg gag aaa tac aag aac att gat 48
 Met Ala Leu Pro Phe Gln Lys Glu Leu Glu Lys Tyr Lys Asn Ile Asp
 1 5 10

gaa gat gag ctt ctt ggc aaa ctc tca gaa gag gaa ctg aaa cag ttg 96
 Glu Asp Glu Leu Leu Gly Lys Leu Ser Glu Glu Glu Leu Lys Gln Leu
 17 22 27 32

gaa aat gtt cta gat gac cta gat cct gag agt gcc atg ctg cca gct 144
 Glu Asn Val Leu Asp Asp Leu Asp Pro Glu Ser Ala Met Leu Pro Ala
 33 38 43 48

gga ttt cga cag aaa gac cag aca cag aag gca gcc acc ggc ccc ttt 192
 Gly Phe Arg Gln Lys Asp Gln Thr Gln Lys Ala Ala Thr Gly Pro Phe
 49 54 59 64

gac cgc gag cac ctc ctc atg tac ctg gag aag gag gct ttg gaa cag 240
 Asp Arg Glu His Leu Leu Met Tyr Leu Glu Lys Glu Ala Leu Glu Gln
 65 70 75 80

aaa gac aga gag gac ttt gtg ccc ttc act gga gaa aag aaa ggg aga 288
 Lys Asp Arg Glu Asp Phe Val Pro Phe Thr Gly Glu Lys Lys Gly Arg
 81 86 91 96

gtc ttt atc cct aaa gaa aag cct ata gaa act cgt aaa gaa gaa aaa 336
 Val Phe Ile Pro Lys Glu Lys Pro Ile Glu Thr Arg Lys Glu Glu Lys
 97 102 107 112

gtg acc ctt gac cca gaa ctg gaa gaa gct ttg gcc agt gcc tct gac 384
 Val Thr Leu Asp Pro Glu Leu Glu Glu Ala Leu Ala Ser Ala Ser Asp
 113 118 123 128

acc Thr 129	gaa Glu	ctc Leu	tat Tyr	gat Asp	ctt Leu 134	gca Ala	gct Ala	gtc Val	ctt Leu	gga Gly 139	gta Val	cac His	aat Asn	ttg Leu	ctc Leu 144	432
aac Asn 145	aat Asn	cca Pro	aag Lys	ttc Phe	gat Asp 150	gaa Glu	gaa Glu	aca Thr	gcc Ala	aac Asn 155	aat Asn	aaa Lys	ggg Gly	ggc Gly	aaa Lys 160	480
gga Gly 161	cct Pro	gtc Val	aga Arg	aat Asn	gtt Val 166	gtc Val	aaa Lys	ggg Gly	gaa Glu	aaa Lys 171	gta Val	aag Lys	cca Pro	gta Val	ttt Phe 176	528
gag Glu 177	gaa Glu	cca Pro	cca Pro	aat Asn	ccc Pro 182	aca Thr	aat Asn	gtg Val	gaa Glu	ata Ile 187	agc Ser	ctg Leu	cag Gln	cag Gln	atg Met 192	576
aaa Lys 193	gcc Ala	aat Asn	gat Asp	cct Pro	agc Ser 198	ttg Leu	caa Gln	gaa Glu	gtc Val	aac Asn 203	ctc Leu	aac Asn	aac Asn	att Ile	aag Lys 208	624
aac Asn 209	att Ile	cca Pro	att Ile	cca Pro	acc Thr 214	ctg Leu	agg Arg	gaa Glu	ttt Phe	gca Ala 219	aag Lys	gct Ala	ctg Leu	gag Glu	acc Thr 224	672
aac Asn 225	act Thr	cac His	gtg Val	aag Lys	aag Lys 230	ttc Phe	agc Ser	ctg Leu	gcc Ala	gca Ala 235	act Thr	cgc Arg	agc Ser	aat Asn	gac Asp 240	720
cct Pro 241	gtg Val	gcc Ala	att Ile	gct Ala	ttt Phe 246	gca Ala	gac Asp	atg Met	ctg Leu	aaa Lys 251	gta Val	aac Asn	aag Lys	acc Thr	ttg Leu 256	768
aca Thr 257	agt Ser	cta Leu	aac Asn	ata Ile	gaa Glu 262	tcc Ser	aat Asn	ttt Phe	atc Ile	act Thr 267	gga Gly	act Thr	ggg Gly	atc Ile	ctg Leu 272	816
gcc Ala 273	ctg Leu	gta Val	gag Glu	gca Ala	ctg Leu 278	aaa Lys	gaa Glu	aat Asn	gac Asp	acc Thr 283	ttg Leu	aca Thr	gaa Glu	atc Ile	aag Lys 288	864
att Ile 289	gac Asp	aac Asn	cag Gln	agg Arg	cag Gln 294	cag Gln	ttg Leu	gga Gly	aca Thr	gct Ala 299	gta Val	gag Glu	atg Met	gaa Glu	att Ile 304	912
gcc Ala 305	cag Gln	atg Met	ctg Leu	gag Glu	gag Glu 310	aat Asn	tca Ser	agg Arg	atc Ile	ctc Leu 315	aag Lys	ttt Phe	gga Gly	tac Tyr	cag Gln 320	960
ttt Phe 321	acc Thr	aag Lys	caa Gln	ggg Gly	cca Pro 326	cga Arg	aca Thr	agg Arg	gtg Val	gca Ala 331	gct Ala	gcc Ala	atc Ile	aca Thr	aag Lys 336	1008
aat Asn 337	aat Asn	gac Asp	ctg Leu	gtt Val	cgt Arg 342	aag Lys	aag Lys	aga Arg	gtt Val	gaa Glu 347	gca Ala	gac Asp	cga Arg	agg Arg	taa * 352	1056

103	108	113	118	
gtc acc agg gag ctg gat gag cat gag cta gac tac gat gag gag gtt	558			
Val Thr Arg Glu Leu Asp Glu His Glu Leu Asp Tyr Asp Glu Glu Val				
119	124	129	134	
cct gag gag cca gct ccc gcc gtc cag gag gac gag gct gag aaa gcg	606			
Pro Glu Glu Pro Ala Pro Ala Val Gln Glu Asp Glu Ala Glu Lys Ala				
135	140	145	150	
ggg gct gag gat gat gag gag aag ggc gaa ggc act ccc agg gag gag	654			
Gly Ala Glu Asp Asp Glu Glu Lys Gly Glu Gly Thr Pro Arg Glu Glu				
151	156	161	166	
ggg aag gct ggt gtt cag agt gtg gga gaa aag gaa tcc ctg gag gct	702			
Gly Lys Ala Gly Val Gln Ser Val Gly Glu Lys Glu Ser Leu Glu Ala				
167	172	177	182	
gcc aag gag aaa aag aaa gag gac gat gat gga gaa atc gaa ttt agt	750			
Ala Lys Glu Lys Lys Lys Glu Asp Asp Asp Gly Glu Ile Glu Phe Ser				
183	188	193	198	
agt agt agg cgg ccg ctc tag ag gatccaagct tacgtacgcg tgcattgcgac	803			
Ser Ser Arg Arg Pro Leu *				
199	204			
gtcatagctc ttctatagtg tcacctaaat gcgattcact taccgctaca tc	855			
<210>	115			
<211>	1973			
<212>	DNA			
<213>	Homo sapiens			
<220>				
<221>	CDS			
<222>	(255) .. (1784)			
<400>	115			
cctgtattac gtagacccaa gctggctagc gtttaaactt aagcttggtta ccgagctcgg	60			
atccactagt ccagtgtggt ggaattcgat ggaggacgca gaggcacgct gttgccatgg	120			
cagtgtgggtc ctggctgccg cggaggcagg tgccgggggtc tcctttgcct caatgtgaag	180			
agcttaaaaaa gaggaggaga ggagaactcc cccggccatc tctgtgatcc cagccgccgc	240			
attttacaca gaaa atg aat gaa aat aaa gat act gat tca aag aaa agt	290			
Met Asn Glu Asn Lys Asp Thr Asp Ser Lys Lys Ser				
1	5	10		
gaa gaa tac gaa gat gac ttt gaa aag gac ctg gag tgg tta att aat	338			
Glu Glu Tyr Glu Asp Asp Phe Glu Lys Asp Leu Glu Trp Leu Ile Asn				
13	18	23	28	

gaa	aat	gaa	aaa	agt	gat	gcc	agc	ata	ata	gag	atg	gct	tgt	gag	aag	386
Glu	Asn	Glu	Lys	Ser	Asp	Ala	Ser	Ile	Ile	Glu	Met	Ala	Cys	Glu	Lys	
29					34					39					44	
gaa	gag	aat	att	aac	caa	gac	tta	aaa	gag	aat	gag	aca	gta	atg	gag	434
Glu	Glu	Asn	Ile	Asn	Gln	Asp	Leu	Lys	Glu	Asn	Glu	Thr	Val	Met	Glu	
45					50					55					60	
cac	acc	aaa	cgg	cat	tct	gat	cct	gac	aaa	tct	ttg	cag	gat	gag	gtc	482
His	Thr	Lys	Arg	His	Ser	Asp	Pro	Asp	Lys	Ser	Leu	Gln	Asp	Glu	Val	
61					66					71					76	
tca	cca	aga	aga	aat	gac	atc	att	tct	gta	cca	ggt	att	caa	cct	ttg	530
Ser	Pro	Arg	Arg	Asn	Asp	Ile	Ile	Ser	Val	Pro	Gly	Ile	Gln	Pro	Leu	
77					82					87					92	
gat	ccc	ata	tca	gat	tca	gat	agt	gaa	aac	tct	ttc	cag	gaa	tcc	aaa	578
Asp	Pro	Ile	Ser	Asp	Ser	Asp	Ser	Glu	Asn	Ser	Phe	Gln	Glu	Ser	Lys	
93					98					103					108	
cta	gaa	agc	cag	aaa	gac	ttg	gag	gag	gaa	gag	gat	gag	gaa	gta	agg	626
Leu	Glu	Ser	Gln	Lys	Asp	Leu	Glu	Glu	Glu	Glu	Asp	Glu	Glu	Val	Arg	
109					114					119					124	
aga	tat	att	atg	gag	aaa	att	gta	caa	gct	aac	aag	ctt	cta	cag	aat	674
Arg	Tyr	Ile	Met	Glu	Lys	Ile	Val	Gln	Ala	Asn	Lys	Leu	Leu	Gln	Asn	
125					130					135					140	
caa	gaa	ccg	gtg	aat	gat	aaa	agg	gag	cga	aaa	ctt	aag	ttc	aag	gac	722
Gln	Glu	Pro	Val	Asn	Asp	Lys	Arg	Glu	Arg	Lys	Leu	Lys	Phe	Lys	Asp	
141					146					151					156	
cag	tta	gtt	gat	ttg	gaa	gtt	cct	cca	cta	gaa	gac	act	act	act	ttt	770
Gln	Leu	Val	Asp	Leu	Glu	Val	Pro	Pro	Leu	Glu	Asp	Thr	Thr	Thr	Phe	
157					162					167					172	
aaa	aat	tat	ttt	gaa	aac	gaa	agg	aat	atg	ttt	ggg	aaa	ctg	tca	caa	818
Lys	Asn	Tyr	Phe	Glu	Asn	Glu	Arg	Asn	Met	Phe	Gly	Lys	Leu	Ser	Gln	
173					178					183					188	
tta	tgt	att	tcc	aat	gat	ttt	gga	caa	gaa	gat	gtg	ctc	ctg	tca	ctt	866
Leu	Cys	Ile	Ser	Asn	Asp	Phe	Gly	Gln	Glu	Asp	Val	Leu	Leu	Ser	Leu	
189					194					199					204	
act	aat	gga	agc	tgt	gaa	gaa	aac	aag	gat	agg	aca	ata	ctg	gta	gag	914
Thr	Asn	Gly	Ser	Cys	Glu	Glu	Asn	Lys	Asp	Arg	Thr	Ile	Leu	Val	Glu	
205					210					215					220	
aga	gat	gga	aaa	ttt	gaa	ctt	ctg	aat	tta	caa	gac	att	gcc	agt	cag	962
Arg	Asp	Gly	Lys	Phe	Glu	Leu	Leu	Asn	Leu	Gln	Asp	Ile	Ala	Ser	Gln	
221					226					231					236	
ggg	ttt	ttg	cct	ccc	att	aat	aat	gca	aat	agt	aca	gaa	aat	gac	cct	1010
Gly	Phe	Leu	Pro	Pro	Ile	Asn	Asn	Ala	Asn	Ser	Thr	Glu	Asn	Asp	Pro	
237					242					247					252	
cag	cag	ttg	tta	ccc	aga	tct	tcc	aac	tcc	tct	gtc	agt	ggc	acc	aag	1058

Gln Gln Leu Leu Pro Arg Ser Ser Asn Ser Ser Val Ser Gly Thr Lys	
253 258 263 268	
aaa gaa gat tct aca gca aag att cat gct gtc act cac tca tca aca	1106
Lys Glu Asp Ser Thr Ala Lys Ile His Ala Val Thr His Ser Ser Thr	
269 274 279 284	
gga gag ccg ctg gct tat atc gct cag cca cca ctc aac cgc aag act	1154
Gly Glu Pro Leu Ala Tyr Ile Ala Gln Pro Pro Leu Asn Arg Lys Thr	
285 290 295 300	
tgt cca agc tct gct gtc aac tca gat cga agt aaa ggg aat ggg aaa	1202
Cys Pro Ser Ser Ala Val Asn Ser Asp Arg Ser Lys Gly Asn Gly Lys	
301 306 311 316	
tct aat cac agg aca cag tct gca cat atc tca cca gtg act tca aca	1250
Ser Asn His Arg Thr Gln Ser Ala His Ile Ser Pro Val Thr Ser Thr	
317 322 327 332	
tac tgt ctt tcc cct cga cag aaa gaa cta caa aaa caa cta gaa gaa	1298
Tyr Cys Leu Ser Pro Arg Gln Lys Glu Leu Gln Lys Gln Leu Glu Glu	
333 338 343 348	
aag aga gaa aaa ctg aaa aga gag gaa gag cga cga aaa ata gaa gaa	1346
Lys Arg Glu Lys Leu Lys Arg Glu Glu Glu Arg Arg Lys Ile Glu Glu	
349 354 359 364	
gag aaa gaa aaa aag aga gag aat gac ata gta ttt aaa gcg tgg ttg	1394
Glu Lys Glu Lys Lys Arg Glu Asn Asp Ile Val Phe Lys Ala Trp Leu	
365 370 375 380	
caa aag aaa aga gag cag gtc tta gaa atg agg aga att cag cga gca	1442
Gln Lys Lys Arg Glu Gln Val Leu Glu Met Arg Arg Ile Gln Arg Ala	
381 386 391 396	
aag gaa att gaa gac atg aac agt aga cag gaa aac aga gat cca caa	1490
Lys Glu Ile Glu Asp Met Asn Ser Arg Gln Glu Asn Arg Asp Pro Gln	
397 402 407 412	
caa gct ttt cga tta tgg ctt aaa aaa aag cac gaa gag cag atg aaa	1538
Gln Ala Phe Arg Leu Trp Leu Lys Lys Lys His Glu Glu Gln Met Lys	
413 418 423 428	
gaa aga cag aca gaa gaa cta aga aag caa gag gaa tgt tta ttc ttc	1586
Glu Arg Gln Thr Glu Glu Leu Arg Lys Gln Glu Glu Cys Leu Phe Phe	
429 434 439 444	
ctt aaa gga aca gaa ggc cgg gaa agg gcc ttt aaa caa tgg tta aga	1634
Leu Lys Gly Thr Glu Gly Arg Glu Arg Ala Phe Lys Gln Trp Leu Arg	
445 450 455 460	
agg aaa cgg atg gaa aaa atg gca gag caa caa gct gtc aga gag aga	1682
Arg Lys Arg Met Glu Lys Met Ala Glu Gln Gln Ala Val Arg Glu Arg	
461 466 471 476	
act aga cag ctc cga cta gaa gct aag cgt tct aaa cag tta cag cac	1730
Thr Arg Gln Leu Arg Leu Glu Ala Lys Arg Ser Lys Gln Leu Gln His	

477	482	487	492	
cac cta tat atg tca gaa gcc aaa cct ttt cgt ttt act gat cat tat				1778
His Leu Tyr Met Ser Glu Ala Lys Pro Phe Arg Phe Thr Asp His Tyr				
493	498	503	508	
aac tga aagtttctat taaatatttc agtgggcagc tgctatcaaa attttggata				1834
Asn *				
509				
tgatttctta gggctctgtgt actttggttg tattctaaat tatggaaatg gtattttatct				1894
tttattgaca gtgaatttgt ttttttaata ctagaacaaa ataaattttt ttctcacagt				1954
gttgtaaaaa aaaaaaaaaa				1973

<210> 116
 <211> 951
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (620)..(859)

<400> 116	
atgctgctcc atgaggtggg gattttgtct gcttggtcac tgctgtgtgc ccagggccca	60
cgacagtgcc cgatacagca ggcgctcaat aagtggcgaa tgaaagacag ggcaaggcgg	120
agagagaaga aacagaaagg gaaagagaaa gcccggggccg ccagagcgct taatcacacc	180
tggtcaggc tccacactgg tcttcagct cctttttctc agcgatggac tcacagcccc	240
acccggagcg ctggagcgcg gacgcggtca ctgctgctgc gcctcaccgc gctggcacc	300
cggcctggca gcctttgggg acctgaacca gctgctgctg cgcaggtgga acgggtggaa	360
cgggtggggg agcggacagt cgaacggcct gagagggctc agctggtccg gggctgcggc	420
gcctttgtga gcgcggccgc cggccaggat cgagccctgg cccggggcct ggcccagccc	480
cggcctcaa ggaccgcgcc gaaggaggtg cccactggag ggaggaggcg ctcgactttc	540
tcaggatact gtccctctcc cacagaggag ctgaaggagt aggacagaag aactgtcaaa	600
ttctggaatc cttaaagcc atg tcc aag gat ttg gtg aca ttt ggg gat gtg	652
Met Ser Lys Asp Leu Val Thr Phe Gly Asp Val	
1 5	
gct gta aat ttc tct caa gag gaa tgg gaa tgg ctg aac cct gct cag	700
Ala Val Asn Phe Ser Gln Glu Glu Trp Glu Trp Leu Asn Pro Ala Gln	
12 17 22 27	


```

agg aat ttg tac agg aaa gtg atg ttg gag aac tac agg agc ttg gta      748
Arg Asn Leu Tyr Arg Lys Val Met Leu Glu Asn Tyr Arg Ser Leu Val
 28                      33                      38                      43

tca ttg gga gtt tct gtt tct aag cca gat gtg atc tca tta ttg gag      796
Ser Leu Gly Val Ser Val Ser Lys Pro Asp Val Ile Ser Leu Leu Glu
 44                      49                      54                      59

caa gga aaa gag ccc tgg atg gtg aag aag gag gga aca aga ggc cca      844
Gln Gly Lys Glu Pro Trp Met Val Lys Lys Glu Gly Thr Arg Gly Pro
 60                      65                      70                      75

tgc cct ggt gag tga gagagaaata gggagacaga agccattgcc aggaagagct      899
Cys Pro Gly Glu  *
 76

cagcaatttc tgaagatttc agttcataat tgacgtttcg tgggtagctc tt      951

<210> 117
<211> 508
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (116)..(328)

<400> 117
aaaatgtatg cggtagctagc tggttagcgt ttaaacttaa gcttggtacc gagctcggat      60

ccactagtcc agtgtggtgg aattcgcgtt ttcggcgggc ttcccgggta caaaa atg      118
                                   Met
                                   1

gct gtg gct agc gat ttc tac ctg cgc tac tac gta ggg cac aag ggc      166
Ala Val Ala Ser Asp Phe Tyr Leu Arg Tyr Tyr Val Gly His Lys Gly
 2                      7                      12                      17

aag ttt ggg cac gag ttt ctg gag ttc gaa ttt cgg ccg gac ggt gag      214
Lys Phe Gly His Glu Phe Leu Glu Phe Glu Phe Arg Pro Asp Gly Glu
 18                      23                      28                      33

aag agg ccc acg gca cgc ggt gct ggg aaa ggg gag cga gac cga gag      262
Lys Arg Pro Thr Ala Arg Gly Ala Gly Lys Gly Glu Arg Asp Arg Glu
 34                      39                      44                      49

gcc ggg tgg tgt gga ggg tac agg cgg cgg agg cca ctg ctt ccc tcg      310
Ala Gly Trp Cys Gly Gly Tyr Arg Arg Arg Arg Pro Leu Leu Pro Ser
 50                      55                      60                      65

aag gaa ata gga gct taa gaatag aggaggcata agttgggttt ataaatgaaa      364
Lys Glu Ile Gly Ala  *
 66                      71

```

gagaattaat tgcaataaat taaagctaata cctgtcacaa actgaaaagt tgaacctaca 424
gtaatcagaa ttctgtaaca gtgcaccaga agggactcta gatcgtcgcc ctgattgaaa 484
atgctagcac ttttttgaaa accg 508

<210> 118
<211> 792
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (122)..(751)

<400> 118
cactgagtcc ctcgtacggg cggaggaaga cctccgcgga cagacattgc aagacacccc 60
tgctcctcgt tggcaagccg ccccatgatg aaggcctaca cctggtcacg gagacttttg 120
g atg cag cct tta acg aag gac gca ggc atg agc ctg tcc tct gtg 166
Met Gln Pro Leu Thr Lys Asp Ala Gly Met Ser Leu Ser Ser Val
1 5 10
acg ctg gcc agc gcc cta cag gtc agg ggt gaa gct ctg tct gag gag 214
Thr Leu Ala Ser Ala Leu Gln Val Arg Gly Glu Ala Leu Ser Glu Glu
16 21 26 31
gaa atc tgg tcc ctc ctg ttc ctg gcc gct gag cag ctc ctg gaa gac 262
Glu Ile Trp Ser Leu Leu Phe Leu Ala Ala Glu Gln Leu Leu Glu Asp
32 37 42 47
ctc cgc aac gat tcc tcg gac tat gtg gtt tgc ccc tgg tca gcc ctg 310
Leu Arg Asn Asp Ser Ser Asp Tyr Val Val Cys Pro Trp Ser Ala Leu
48 53 58 63
ctt tct gca gct gga agc ctt tct ttc caa ggc cgt gtt tct cat ata 358
Leu Ser Ala Ala Gly Ser Leu Ser Phe Gln Gly Arg Val Ser His Ile
64 69 74 79
gag gct gct cct ttc aag gcc cct gaa ctg cta cag gga cag agt gag 406
Glu Ala Ala Pro Phe Lys Ala Pro Glu Leu Leu Gln Gly Gln Ser Glu
80 85 90 95
gat gag cag cct gat gca tct cag atg cat gtc tat tct tta gga atg 454
Asp Glu Gln Pro Asp Ala Ser Gln Met His Val Tyr Ser Leu Gly Met
96 101 106 111
acc ctc tac tgg tca gca ggg ttt cat gtt ccg cca cat cag ccc ctg 502
Thr Leu Tyr Trp Ser Ala Gly Phe His Val Pro Pro His Gln Pro Leu
112 117 122 127
cag ctc tgc gag ccc ctg cac tcc atc ctg ctg acc atg tgt gaa gac 550
Gln Leu Cys Glu Pro Leu His Ser Ile Leu Leu Thr Met Cys Glu Asp

128	133	138	143	
cag cct cac agg cgg tgc acg ttg cag tcg gtt ctg gaa gct tgt cgg				598
Gln Pro His Arg Arg Cys Thr Leu Gln Ser Val Leu Glu Ala Cys Arg				
144	149	154	159	
ggt cat gag aaa gaa gtg tct gtc tac cca gcc cct gct ggt ctc cac				646
Val His Glu Lys Glu Val Ser Val Tyr Pro Ala Pro Ala Gly Leu His				
160	165	170	175	
atc aga agg ctg gtt ggc ttg gtt ctg ggt acc att tct gag gtc agt				694
Ile Arg Arg Leu Val Gly Leu Val Leu Gly Thr Ile Ser Glu Val Ser				
176	181	186	191	
aga gaa ccg tgc ttt tca agc agt agc tgc tgg tca tgt gtg gct att				742
Arg Glu Pro Cys Phe Ser Ser Ser Ser Cys Trp Ser Cys Val Ala Ile				
192	197	202	207	
aaa att tga attagttata ttatcattaa ctaaaataaa ataaaaaaaa a				792
Lys Ile *				
208				

<210> 119
 <211> 2136
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (309)..(1625)

<400> 119	
aatgcaggac cgggtccggaa ttcccgggtc gacgatttcg tcgagggggg gttaaaggcc	60
cccaaaacat gcacacatga aaagggcaaa aagtaaccgt ccttgacagg gagtcttaac	120
tagagaagga aacggaacta aactggcggg ctccgtggaa gcgtggccgg cagcgtccccg	180
gacgaggaga gacagcgtct tgctcagtca cccaggctgg agtgcagtga tcatagctca	240
tcgcacacctt gaactcctgg gcttaagcta tcctcccgcc ttagcctcct gaatagctgg	300
gaccacag atg tct ttg gtg gac ttg gga aag agg ttg cta gaa gca gca	350
Met Ser Leu Val Asp Leu Gly Lys Arg Leu Leu Glu Ala Ala	
1 5 10	
aga aaa ggc caa gat gat gaa gtg aga acg ttg atg gca aat ggc gcc	398
Arg Lys Gly Gln Asp Asp Glu Val Arg Thr Leu Met Ala Asn Gly Ala	
15 20 25 30	
cca ttc acc aca gac tgg ttt tcc aaa ttg aga gtc tcc tgt gga tat	446
Pro Phe Thr Thr Asp Trp Phe Ser Lys Leu Arg Val Ser Cys Gly Tyr	
31 36 41 46	

ata Ile 47	ggg Gly	gat Asp	aat Asn	tgt Cys	aag Lys 52	aat Asn	ggg Gly	gca Ala	gat Asp	gtg Val 57	aat Asn	gcc Ala	aag Lys	gac Asp	atg Met 62	494
ctg Leu 63	aag Lys	atg Met	aca Thr	gct Ala	ttg Leu 68	cat His	tgg Trp	gcc Ala	aca Thr	gag Glu 73	cgc Arg	cac His	cat His	cga Arg	gat Asp 78	542
gtc Val 79	gta Val	gag Glu	tta Leu	ctt Leu	atc Ile 84	aaa Lys	tat Tyr	gga Gly	gct Ala	gat Asp 89	gtc Val	cat His	gct Ala	ttc Phe	agc Ser 94	590
aaa Lys 95	ttt Phe	gat Asp	aaa Lys	tca Ser	gcc Ala 100	ttt Phe	gac Asp	ata Ile	gct Ala	ctg Leu 105	gag Glu	aaa Lys	aac Asn	aat Asn	gct Ala 110	638
gag Glu 111	att Ile	ttg Leu	gtc Val	atc Ile	ctc Leu 116	cag Gln	gaa Glu	gca Ala	atg Met	cag Gln 121	aat Asn	cag Gln	gtg Val	aat Asn	gtt Val 126	686
aat Asn 127	cca Pro	gag Glu	aga Arg	gcc Ala	aac Asn 132	cct Pro	gtg Val	act Thr	gac Asp	cct Pro 137	gtg Val	agt Ser	atg Met	gct Ala	gct Ala 142	734
cca Pro 143	ttc Phe	atc Ile	ttc Phe	acg Thr	tcg Ser 148	ggg Gly	gag Glu	gtt Val	gtt Val	aac Asn 153	ctc Leu	gca Ala	agc Ser	ctt Leu	att Ile 158	782
tct Ser 159	tca Ser	acc Thr	aac Asn	acc Thr	aaa Lys 164	aca Thr	acc Thr	tca Ser	ggg Gly	gac Asp 169	ccc Pro	cat His	gcc Ala	tca Ser	aca Thr 174	830
gta Val 175	cag Gln	ttt Phe	tca Ser	aat Asn	tct Ser 180	acc Thr	acc Thr	tca Ser	gtg Val	ctg Leu 185	gct Ala	acc Thr	ctt Leu	gca Ala	gct Ala 190	878
ctt Leu 191	gct Ala	gag Glu	gca Ala	tca Ser	gtc Val 196	ccc Pro	ctc Leu	tcc Ser	aac Asn	tca Ser 201	cac His	aga Arg	gcc Ala	aca Thr	gcc Ala 206	926
aat Asn 207	aca Thr	gag Glu	gaa Glu	att Ile	ata Ile 212	gaa Glu	gga Gly	aat Asn	tcc Ser	gtt Val 217	gac Asp	tca Ser	tca Ser	atc Ile	cag Gln 222	974
caa Gln 223	gta Val	atg Met	ggg Gly	agt Ser	gga Gly 228	ggc Gly	cag Gln	agg Arg	gtc Val	atc Ile 233	acc Thr	ata Ile	gtg Val	act Thr	gat Asp 238	1022
gga Gly 239	gtc Val	cct Pro	ctg Leu	ggg Gly	aat Asn 244	atc Ile	caa Gln	act Thr	tca Ser	atc Ile 249	cct Pro	act Thr	gga Gly	ggc Gly	att Ile 254	1070
ggc Gly 255	cag Gln	cca Pro	ttt Phe	att Ile	gta Val 260	act Thr	gtg Val	caa Gln	gat Asp	gga Gly 265	cag Gln	caa Gln	gtt Val	cta Leu	act Thr 270	1118

gta cct gct ggt aag ggt gca gag gag act gta att aaa gag gaa gaa	1166
Val Pro Ala Gly Lys Gly Ala Glu Glu Thr Val Ile Lys Glu Glu Glu	
271 276 281 286	
gaa gag aag ttg cca cta aca aag aaa cca agg ata gga gag aag aca	1214
Glu Glu Lys Leu Pro Leu Thr Lys Lys Pro Arg Ile Gly Glu Lys Thr	
287 292 297 302	
aac agt gtg gag gaa agc aag gaa ggc aat gaa aga gag cta cta cag	1262
Asn Ser Val Glu Glu Ser Lys Glu Gly Asn Glu Arg Glu Leu Leu Gln	
303 308 313 318	
caa caa ctc cag gag gcc aat cga aga gcc cag gaa tac cga cac cag	1310
Gln Gln Leu Gln Glu Ala Asn Arg Arg Ala Gln Glu Tyr Arg His Gln	
319 324 329 334	
ctc cta aag aaa gag cag gaa gca gaa cag tac cgt ctt aag ctg gag	1358
Leu Leu Lys Lys Glu Gln Glu Ala Glu Gln Tyr Arg Leu Lys Leu Glu	
335 340 345 350	
gcc ata gcc cga cag cag ccc aat gga gtt gat ttc acc atg gtt gaa	1406
Ala Ile Ala Arg Gln Gln Pro Asn Gly Val Asp Phe Thr Met Val Glu	
351 356 361 366	
gag gtg gct gag gta gat gct gta gta gtc aca gag ggg gag ttg gaa	1454
Glu Val Ala Glu Val Asp Ala Val Val Val Thr Glu Gly Glu Leu Glu	
367 372 377 382	
gag aga gag aca aaa gtg act ggg tca gca ggg gcc acg gag cct cac	1502
Glu Arg Glu Thr Lys Val Thr Gly Ser Ala Gly Ala Thr Glu Pro His	
383 388 393 398	
act aga ggt ttc cat ggc aac tgt ttc atc tta ata tgc aag ggc cac	1550
Thr Arg Gly Phe His Gly Asn Cys Phe Ile Leu Ile Cys Lys Gly His	
399 404 409 414	
aat ttg cac tgt gtt cat att aat cct ctt tta aaa aag gaa ata tac	1598
Asn Leu His Cys Val His Ile Asn Pro Leu Leu Lys Lys Glu Ile Tyr	
415 420 425 430	
aga aga caa aca ttg tat aaa aac taa gagtg tctttaagaa gaaaactata	1650
Arg Arg Gln Thr Leu Tyr Lys Asn *	
431 436	
gcagggtaca atgcttgggc tcaggaagtt tctctgtgca actagaaaat tcaaagccat	1710
atttagggaa cattttttct gaggggccaa aagaataaag gaccaaattt cttagctcat	1770
atcattgctt taaacataga agtaaaagaa tactgcatgt tgtggggttga tttttttttt	1830
ttaaataact gactttctca caaaagattt taagataaca tttctaatat atatgcacca	1890
atatatatgc ctttaataat tataccatca agtgacctga aaatgccctt tagatttatg	1950
atgcgatatct gttggaaaaa ccaattggaa gggaagttag acaagctttg gggaagagaa	2010
aaggaatata gtccatttcc aaaggagcag gaactcccaa ccttaagtta atttcactga	2070

agagaatttt cccttttttt tttttttttg gaaacaaagg ggattttaac ttcaaaaaaa 2130
aaaaaa 2136

<210> 120
<211> 1335
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1335)

<400> 120

atg att gaa gac aat aag gag aac aaa gac cat tcc tta gaa agg gga 48
Met Ile Glu Asp Asn Lys Glu Asn Lys Asp His Ser Leu Glu Arg Gly
1 5 10

aga gca agt ctc att ttt tcc tta aag aat gaa gtt gga gga ctt ata 96
Arg Ala Ser Leu Ile Phe Ser Leu Lys Asn Glu Val Gly Gly Leu Ile
17 22 27 32

aaa gcc ctg aaa atc ttt cag gag aag cat gtg aat ctg tta cat atc 144
Lys Ala Leu Lys Ile Phe Gln Glu Lys His Val Asn Leu Leu His Ile
33 38 43 48

gag tcc cga aaa tca aaa aga aga aac tca gaa ttt gag att ttt gtt 192
Glu Ser Arg Lys Ser Lys Arg Arg Asn Ser Glu Phe Glu Ile Phe Val
49 54 59 64

gac tgt gac atc aac aga gaa caa ttg aat gat att ttt cat ctg ctg 240
Asp Cys Asp Ile Asn Arg Glu Gln Leu Asn Asp Ile Phe His Leu Leu
65 70 75 80

aag tct cat acc aat gtt ctc tct gtg aat cta cca gat aat ttt act 288
Lys Ser His Thr Asn Val Leu Ser Val Asn Leu Pro Asp Asn Phe Thr
81 86 91 96

ttg aag gaa gat ggt atg gaa act gtt cct tgg ttt cca aag aag att 336
Leu Lys Glu Asp Gly Met Glu Thr Val Pro Trp Phe Pro Lys Lys Ile
97 102 107 112

tct gac ctg gac cat tgt gcc aac aga gtt ctg atg tat gga tct gaa 384
Ser Asp Leu Asp His Cys Ala Asn Arg Val Leu Met Tyr Gly Ser Glu
113 118 123 128

cta gat gca gac cat cct ggc ttc aaa gac aat gtc tac cgt aaa cgt 432
Leu Asp Ala Asp His Pro Gly Phe Lys Asp Asn Val Tyr Arg Lys Arg
129 134 139 144

cga aag tat ttt gcg gac ttg gct atg aac tat aaa cat gga gac ccc 480
Arg Lys Tyr Phe Ala Asp Leu Ala Met Asn Tyr Lys His Gly Asp Pro
145 150 155 160

att cca aag gtt gaa ttc act gaa gag gag att aag acc tgg gga acc	528
Ile Pro Lys Val Glu Phe Thr Glu Glu Glu Ile Lys Thr Trp Gly Thr	
161 166 171 176	
gta ttc caa gag ctc aac aaa ctc tac cca acc cat gct tgc aga gag	576
Val Phe Gln Glu Leu Asn Lys Leu Tyr Pro Thr His Ala Cys Arg Glu	
177 182 187 192	
tat ctc aaa aac tta cct ttg ctt tct aaa tat tgt gga tat cgg gag	624
Tyr Leu Lys Asn Leu Pro Leu Leu Ser Lys Tyr Cys Gly Tyr Arg Glu	
193 198 203 208	
gat aat atc cca caa ttg gaa gat gtc tcc aac ttt tta aaa gag cgt	672
Asp Asn Ile Pro Gln Leu Glu Asp Val Ser Asn Phe Leu Lys Glu Arg	
209 214 219 224	
aca ggt ttt tcc atc cgt cct gtg gct ggt tac tta tca cca aga gat	720
Thr Gly Phe Ser Ile Arg Pro Val Ala Gly Tyr Leu Ser Pro Arg Asp	
225 230 235 240	
ttc tta tca ggt tta gcc ttt cga gtt ttt cac tgc act caa tat gtg	768
Phe Leu Ser Gly Leu Ala Phe Arg Val Phe His Cys Thr Gln Tyr Val	
241 246 251 256	
aga cac agt tca gac ccc ttc tat acc cca gag ccg gat acc tgc cat	816
Arg His Ser Ser Asp Pro Phe Tyr Thr Pro Glu Pro Asp Thr Cys His	
257 262 267 272	
gaa ctc tta ggt cac gtt ccc ctt ttg gct gag cca agt ttt gct cag	864
Glu Leu Leu Gly His Val Pro Leu Leu Ala Glu Pro Ser Phe Ala Gln	
273 278 283 288	
ttc tcc caa gaa att ggc ctg gct tcc ctt gga gct tca gag gag gct	912
Phe Ser Gln Glu Ile Gly Leu Ala Ser Leu Gly Ala Ser Glu Glu Ala	
289 294 299 304	
gtt caa aaa ctg gca acg tgc tac ttt ttc act gtg gag ttt ggt cta	960
Val Gln Lys Leu Ala Thr Cys Tyr Phe Phe Thr Val Glu Phe Gly Leu	
305 310 315 320	
tgt aaa caa gac gga cag tta cga gtc ttc ggc gct ggc tta ctt tct	1008
Cys Lys Gln Asp Gly Gln Leu Arg Val Phe Gly Ala Gly Leu Leu Ser	
321 326 331 336	
tct atc agt gaa ctc aaa cat gtg ctt tct gga cat gcc aaa gta aag	1056
Ser Ile Ser Glu Leu Lys His Val Leu Ser Gly His Ala Lys Val Lys	
337 342 347 352	
cct ttt gat ccc aag att acc tgc aaa caa gaa tgc ctc atc aca act	1104
Pro Phe Asp Pro Lys Ile Thr Cys Lys Gln Glu Cys Leu Ile Thr Thr	
353 358 363 368	
ttt cag gat gtc tac ttt gta tct gaa agt ttt gaa gat gca aag gag	1152
Phe Gln Asp Val Tyr Phe Val Ser Glu Ser Phe Glu Asp Ala Lys Glu	
369 374 379 384	

aag atg aga gaa ttt acc aaa aca att aag cgt ccc ttt gga gtg aaa	1200
Lys Met Arg Glu Phe Thr Lys Thr Ile Lys Arg Pro Phe Gly Val Lys	
385 390 395 400	
tat aat ccc tac aca cga agc att cag atc ctg aaa gac gcc aaa agc	1248
Tyr Asn Pro Tyr Thr Arg Ser Ile Gln Ile Leu Lys Asp Ala Lys Ser	
401 406 411 416	
ata acg aat gcc atg aac gag ctg cgg cat gat ctt gac gtt gtc agc	1296
Ile Thr Asn Ala Met Asn Glu Leu Arg His Asp Leu Asp Val Val Ser	
417 422 427 432	
gac gcc ctt ggg aag gtc agc agg aag ccg agt atc taa	1335
Asp Ala Leu Gly Lys Val Ser Arg Lys Pro Ser Ile *	
433 438 443	

<210> 121
 <211> 3266
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (166)..(2742)

<400> 121	
atcgattgca atagctatct attcgatgat gaagataccc caccaaacc aaaaaaagag	60
atctctcgag gatccgaatt cgcggtcgcg tccgcgtcgc cgccatcctc ggcgcgactc	120
gcttctttcg gttctacctg ggagaatcca ccgccatccg ccacc atg gtg aac	174
	Met Val Asn
	1
ttc acg gta gac cag atc cgc gcc atc atg gac aag aag gcc aac atc	222
Phe Thr Val Asp Gln Ile Arg Ala Ile Met Asp Lys Lys Ala Asn Ile	
4 9 14 19	
cgc aac atg tct gtc atc gcc cac gtg gac cat ggc aag tcc acg ctg	270
Arg Asn Met Ser Val Ile Ala His Val Asp His Gly Lys Ser Thr Leu	
20 25 30 35	
aca gac tcc ctg gtg tgc aag gcg ggc atc atc gcc tcg gcc cgg gcc	318
Thr Asp Ser Leu Val Cys Lys Ala Gly Ile Ile Ala Ser Ala Arg Ala	
36 41 46 51	
ggg gag aca cgc ttc act gat acc cgg aag gac gag cag gag cgt tgc	366
Gly Glu Thr Arg Phe Thr Asp Thr Arg Lys Asp Glu Gln Glu Arg Cys	
52 57 62 67	
atc acc atc aag tca act gcc atc tcc ctc ttc tac gag ctc tcg gag	414
Ile Thr Ile Lys Ser Thr Ala Ile Ser Leu Phe Tyr Glu Leu Ser Glu	
68 73 78 83	

aat gac ttg aac ttc atc aag cag agc aag gac ggt gcc ggc ttc ctc Asn Asp Leu Asn Phe Ile Lys Gln Ser Lys Asp Gly Ala Gly Phe Leu 84 89 94 99	462
atc aac ctc att gac tcc ccc ggg cat gtc gac ttc tcc tcg gag gtg Ile Asn Leu Ile Asp Ser Pro Gly His Val Asp Phe Ser Ser Glu Val 100 105 110 115	510
act gct gcc ctc cga gtc acc gat ggc gca ttg gtg gtg gtg gac tgc Thr Ala Ala Leu Arg Val Thr Asp Gly Ala Leu Val Val Val Asp Cys 116 121 126 131	558
gtg tca ggc gtg tgc gtg cag acg gag aca gtg ctg cgg cag gcc att Val Ser Gly Val Cys Val Gln Thr Glu Thr Val Leu Arg Gln Ala Ile 132 137 142 147	606
gcc gag cgc atc aag cct gtg ctg atg atg aac aag atg gac cgc gcc Ala Glu Arg Ile Lys Pro Val Leu Met Met Asn Lys Met Asp Arg Ala 148 153 158 163	654
ctg ctg gag ctg cag ctg gag ccc gag gag ctc tac cag act ttc cag Leu Leu Glu Leu Gln Leu Glu Pro Glu Glu Leu Tyr Gln Thr Phe Gln 164 169 174 179	702
cgc atc gtg gag aac gtg aac gtc atc atc tcc acc tac ggc gag ggc Arg Ile Val Glu Asn Val Asn Val Ile Ile Ser Thr Tyr Gly Glu Gly 180 185 190 195	750
gag agc ggc ccc atg ggc aac atc atg atc gat cct gtc ctc ggt acc Glu Ser Gly Pro Met Gly Asn Ile Met Ile Asp Pro Val Leu Gly Thr 196 201 206 211	798
gtg ggc ttt ggg tct ggc ctc cac ggg tgg gcc ttc acc ctg aag cag Val Gly Phe Gly Ser Gly Leu His Gly Trp Ala Phe Thr Leu Lys Gln 212 217 222 227	846
ttt gcc gag atg tat gtg gcc aag ttc gcc gcc aag ggg gag ggc cag Phe Ala Glu Met Tyr Val Ala Lys Phe Ala Ala Lys Gly Glu Gly Gln 228 233 238 243	894
ttg ggg cct gcc gag cgg gcc aag aaa gta gag gac atg atg aag aag Leu Gly Pro Ala Glu Arg Ala Lys Lys Val Glu Asp Met Met Lys Lys 244 249 254 259	942
ctg tgg ggt gac agg tac ttt gac cca gcc aac ggc aag ttc agc aag Leu Trp Gly Asp Arg Tyr Phe Asp Pro Ala Asn Gly Lys Phe Ser Lys 260 265 270 275	990
tca gcc acc agc ccc gaa ggg aag aag ctg cca cgc acc ttc tgc cag Ser Ala Thr Ser Pro Glu Gly Lys Lys Leu Pro Arg Thr Phe Cys Gln 276 281 286 291	1038
ctg atc ctg gac ccc atc ttc aag gtg ttt gat gcg atc atg aat ttc Leu Ile Leu Asp Pro Ile Phe Lys Val Phe Asp Ala Ile Met Asn Phe 292 297 302 307	1086

aag aaa gag gag aca gca aaa ctg ata gag aaa ctg gac atc aaa ctg Lys Lys Glu Glu Thr Ala Lys Leu Ile Glu Lys Leu Asp Ile Lys Leu 308 313 318 323	1134
gac agc gag gac aag gac aaa gaa ggc aaa ccc ctg ctg aag gct gtg Asp Ser Glu Asp Lys Asp Lys Glu Gly Lys Pro Leu Leu Lys Ala Val 324 329 334 339	1182
atg cgc cgc tgg ctg cct gcc gga gac gcc ttg ttg cag atg atc acc Met Arg Arg Trp Leu Pro Ala Gly Asp Ala Leu Leu Gln Met Ile Thr 340 345 350 355	1230
atc cac ctg ccc tcc cct gtg acg gcc cag aag tac cgc tgc gag ctc Ile His Leu Pro Ser Pro Val Thr Ala Gln Lys Tyr Arg Cys Glu Leu 356 361 366 371	1278
ctg tac gag ggg ccc ccg gac gac gag gct gcc atg ggc att aaa agc Leu Tyr Glu Gly Pro Pro Asp Asp Glu Ala Ala Met Gly Ile Lys Ser 372 377 382 387	1326
tgt gac ccc aaa ggc cct ctt atg atg tat att tcc aaa atg gtg cca Cys Asp Pro Lys Gly Pro Leu Met Met Tyr Ile Ser Lys Met Val Pro 388 393 398 403	1374
acc tcc gac aaa ggt cgg ttc tac gcc ttt gga cga gtc ttc tcg ggg Thr Ser Asp Lys Gly Arg Phe Tyr Ala Phe Gly Arg Val Phe Ser Gly 404 409 414 419	1422
ctg gtc tcc act ggc ctg aag gtc agg atc atg ggg ccc aac tat acc Leu Val Ser Thr Gly Leu Lys Val Arg Ile Met Gly Pro Asn Tyr Thr 420 425 430 435	1470
cct ggg aag aag gag gac ctc tac ctg aag cca atc cag aga aca atc Pro Gly Lys Lys Glu Asp Leu Tyr Leu Lys Pro Ile Gln Arg Thr Ile 436 441 446 451	1518
ttg atg atg ggc cgc tac gtg gag ccc atc gag gat gtg cct tgt ggg Leu Met Met Gly Arg Tyr Val Glu Pro Ile Glu Asp Val Pro Cys Gly 452 457 462 467	1566
aac att gtg ggc ctc gtg ggc gtg gac cag ttc ctg gtg aag acg ggc Asn Ile Val Gly Leu Val Gly Val Asp Gln Phe Leu Val Lys Thr Gly 468 473 478 483	1614
acc atc acc acc ttc gag cac gcg cac aac atg cgg gtg atg aag ttc Thr Ile Thr Thr Phe Glu His Ala His Asn Met Arg Val Met Lys Phe 484 489 494 499	1662
agc gtc agc cct gtt gtc aga gtg gcc gtg gag gcc aag aac ccg gct Ser Val Ser Pro Val Val Arg Val Ala Val Glu Ala Lys Asn Pro Ala 500 505 510 515	1710
gac ctg ccc aag ctg gtg gag ggg ctg aag cgg ctg gcc aag tcc gag Asp Leu Pro Lys Leu Val Glu Gly Leu Lys Arg Leu Ala Lys Ser Asp 516 521 526 531	1758
ccc atg gtg cag tgc atc atc gag gag tcg gga gag cac atc atc gcg	1806

756											761											766											771											
gag	gag	tcc	cag	gtg	gcc	ggc	acc	ccc	atg	ttt	gtg	gtc	aag	gcc	tat	2526																												
Glu	Glu	Ser	Gln	Val	Ala	Gly	Thr	Pro	Met	Phe	Val	Val	Lys	Ala	Tyr																													
772											777											782											787											
ctg	ccc	gtc	aac	gag	tcc	ttt	ggc	ttc	acc	gct	gac	ctg	agg	tcc	aac	2574																												
Leu	Pro	Val	Asn	Glu	Ser	Phe	Gly	Phe	Thr	Ala	Asp	Leu	Arg	Ser	Asn																													
788											793											798											803											
acg	ggc	ggc	cag	gcg	ttc	ccc	cag	tgt	gtg	ttt	gac	cac	tgg	cag	atc	2622																												
Thr	Gly	Gly	Gln	Ala	Phe	Pro	Gln	Cys	Val	Phe	Asp	His	Trp	Gln	Ile																													
804											809											814											819											
ctg	ccc	gga	gac	ccc	ttc	gac	aac	agc	agc	cgc	ccc	agc	cag	gtg	gtg	2670																												
Leu	Pro	Gly	Asp	Pro	Phe	Asp	Asn	Ser	Ser	Arg	Pro	Ser	Gln	Val	Val																													
820											825											830											835											
gcg	gag	acc	cgc	aag	cgc	aag	ggc	ctg	aaa	gaa	ggc	atc	cct	gcc	ctg	2718																												
Ala	Glu	Thr	Arg	Lys	Arg	Lys	Gly	Leu	Lys	Glu	Gly	Ile	Pro	Ala	Leu																													
836											841											846											851											
gac	aac	ttc	ctg	gac	aaa	ttg	tag	gcggcccttc	ctgcagcgcc	tgccgccccg						2772																												
Asp	Asn	Phe	Leu	Asp	Lys	Leu	*																																					
852											857																																	
gggactcgca	gcacccacag	caccacgtcc	tcgaattctc	agacgacacc	tgagactgt											2832																												
cccgacacag	cgacgctccc	ctgagaggtt	tctggggccc	gctgcgtgcc	atcactcaac											2892																												
cataacactt	gatgccgttt	ctttcaatat	ttatttccag	agtccggagg	cagcagacac											2952																												
gccctcttag	tagggactta	atgggccggt	cggggagggg	gaggcgggat	gggacaccca											3012																												
acactttttc	catttcttca	gagggaaact	cagatgtcca	aactaatattt	tcaaaaccta											3072																												
attttaacaa	acgcattaag	aggtttatatt	gggtacatgg	cccgcagtgg	cttttgcccc											3132																												
agaaagggga	aaggaacacg	cgggtagatg	atttctagca	ggcaggaagt	cctgtgcggt											3192																												
gtcaccatga	gcacctccag	ctgtactagt	gccattggaa	taataaatatt	gataagggtg											3252																												
tgaaaaaaaa	aaaa														3266																													

```
<210> 122
<211> 833
<212> DNA
<213> Homo sapiens
```

<400> 122

ctcgtagccg gtcgcctgcg gtaccgggtcc ggaattcccc ggtcgaccca cgcgtccgct																60
cttcaaccag gagccgagat ttctgttgct ctgaagccat ccaggggtct ttaaccagaa																120
gagagaggag agcctcagga gttaggacca gaagaagcca gggaagcagt gca atg Met 1																176
gct tca aaa atc ttg ctt aac gta caa gag gag gtg acc tgt ccc atc Ala Ser Lys Ile Leu Leu Asn Val Gln Glu Glu Val Thr Cys Pro Ile 2 7 12 17																224
tgc ctg gag ctg ttg aca gaa ccc ttg agt cta gac tgt ggc cac agc Cys Leu Glu Leu Leu Thr Glu Pro Leu Ser Leu Asp Cys Gly His Ser 18 23 28 33																272
ctc tgc cga gcc tgc atc act gtg agc aac aag gag gca gtg acc agc Leu Cys Arg Ala Cys Ile Thr Val Ser Asn Lys Glu Ala Val Thr Ser 34 39 44 49																320
atg gga gga aaa agc agc tgt cct gtg tgt ggt atc agt tac tca ttt Met Gly Gly Lys Ser Ser Cys Pro Val Cys Gly Ile Ser Tyr Ser Phe 50 55 60 65																368
gaa cat cta cag gct aat cag cat ctg gcc aac ata gtg gag aga ctc Glu His Leu Gln Ala Asn Gln His Leu Ala Asn Ile Val Glu Arg Leu 66 71 76 81																416
aag gag gtc aag ttg agc cca gac aat ggg aag aag aga gat ctc tgt Lys Glu Val Lys Leu Ser Pro Asp Asn Gly Lys Lys Arg Asp Leu Cys 82 87 92 97																464
gat cat cat gga gag aaa ctc cta ctc ttc tgt aag gag gat agg aaa Asp His His Gly Glu Lys Leu Leu Leu Phe Cys Lys Glu Asp Arg Lys 98 103 108 113																512
gtc att tgc tgg ctt tgt gag cgg tct cag gag cac cgt ggt cac cac Val Ile Cys Trp Leu Cys Glu Arg Ser Gln Glu His Arg Gly His His 114 119 124 129																560
aca gtc ctc acg gag gaa gta ttc aag gaa tgt cag gag aaa ctc cag Thr Val Leu Thr Glu Glu Val Phe Lys Glu Cys Gln Glu Lys Leu Gln 130 135 140 145																608
gca gtc ctc aag agg ctg aag aag gaa gag gag gaa gct gag aag ctg Ala Val Leu Lys Arg Leu Lys Lys Glu Glu Glu Glu Ala Glu Lys Leu 146 151 156 161																656
gaa gct gac atc aga gaa gag aaa act tcc tgg aag tat cag gta caa Glu Ala Asp Ile Arg Glu Glu Lys Thr Ser Trp Lys Tyr Gln Val Gln 162 167 172 177																704
act gag aga caa agg ata caa aca gaa ttt gat cag ctt aga agc atc Thr Glu Arg Gln Arg Ile Gln Thr Glu Phe Asp Gln Leu Arg Ser Ile 178 183 188 193																752
cta aat aat gag gag cag aga gag ctg caa aga ttg gaa aaa aaa aaa																800

Leu Asn Asn Glu Glu Gln Arg Glu Leu Gln Arg Leu Glu Lys Lys Lys
 194 199 204 209

aaa aag atc ttt aat taa gcggccgcaa gctta 833
 Lys Lys Ile Phe Asn *
 210 215

<210> 123
 <211> 2385
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (103)..(1935)

<400> 123
 attccgagag agagacgccc tggaaggtct gtatcagcgt ctgtcgcgct gggaccaca 60
 ctggctttta aggaggacac ccggacacct ggaagctggg aa atg gac tca gtg 114
 Met Asp Ser Val
 1
 gcc ttt gaa gat gtg gct gtg aac ttc aca caa gag gag tgg gct ttg 162
 Ala Phe Glu Asp Val Ala Val Asn Phe Thr Gln Glu Glu Trp Ala Leu
 5 10 15 20
 ctg ggt cca tca cag aag agt ctc tac aga aat gtc atg cag gaa acc 210
 Leu Gly Pro Ser Gln Lys Ser Leu Tyr Arg Asn Val Met Gln Glu Thr
 21 26 31 36
 att agg aac ctg gac tgt ata gaa atg aaa tgg gag gac cag aac att 258
 Ile Arg Asn Leu Asp Cys Ile Glu Met Lys Trp Glu Asp Gln Asn Ile
 37 42 47 52
 gga gat cag tgc caa aat gcc aag aga aat cta aga agt cat aca tgt 306
 Gly Asp Gln Cys Gln Asn Ala Lys Arg Asn Leu Arg Ser His Thr Cys
 53 58 63 68
 gaa att aaa gat gac agt caa tgt gga gaa act ttt ggc cag att cca 354
 Glu Ile Lys Asp Asp Ser Gln Cys Gly Glu Thr Phe Gly Gln Ile Pro
 69 74 79 84
 gat agt att gtg aac aag aac act cct cga gta aat cca tgt gac agt 402
 Asp Ser Ile Val Asn Lys Asn Thr Pro Arg Val Asn Pro Cys Asp Ser
 85 90 95 100
 ggt gag tgt gga gaa gtc gtc ttg ggt cat tcg tct ctt aat tgc aac 450
 Gly Glu Cys Gly Glu Val Val Leu Gly His Ser Ser Leu Asn Cys Asn
 101 106 111 116
 atc aga gtt gac act gga cac aaa tca tgt gag cat cag gaa tat gga 498
 Ile Arg Val Asp Thr Gly His Lys Ser Cys Glu His Gln Glu Tyr Gly

117					122					127					132	
gag	aag	cca	tat	aca	cat	aaa	caa	cgt	ggg	aaa	gcc	atc	agt	cat	cag	546
Glu	Lys	Pro	Tyr	Thr	His	Lys	Gln	Arg	Gly	Lys	Ala	Ile	Ser	His	Gln	
133					138					143					148	
cac	tcc	ttc	cag	aca	cat	gaa	agg	ccc	ccc	acc	gga	aag	aaa	ccc	ttc	594
His	Ser	Phe	Gln	Thr	His	Glu	Arg	Pro	Pro	Thr	Gly	Lys	Lys	Pro	Phe	
149					154					159					164	
gat	tgt	aaa	gaa	tgt	gca	aaa	acc	ttt	agt	tct	ctt	gga	aac	ctc	cga	642
Asp	Cys	Lys	Glu	Cys	Ala	Lys	Thr	Phe	Ser	Ser	Leu	Gly	Asn	Leu	Arg	
165					170					175					180	
aga	cac	atg	gcg	gca	cac	cat	gga	gat	gga	cct	tat	aaa	tgt	aag	ttg	690
Arg	His	Met	Ala	Ala	His	His	Gly	Asp	Gly	Pro	Tyr	Lys	Cys	Lys	Leu	
181					186					191					196	
tgt	ggg	aaa	gcc	ttt	gtt	tgg	ccc	agt	tta	ttt	cat	ttg	cac	gaa	aga	738
Cys	Gly	Lys	Ala	Phe	Val	Trp	Pro	Ser	Leu	Phe	His	Leu	His	Glu	Arg	
197					202					207					212	
aca	cac	act	gga	gag	aaa	ccg	tat	gaa	tgt	aag	cag	tgt	tct	aaa	gcc	786
Thr	His	Thr	Gly	Glu	Lys	Pro	Tyr	Glu	Cys	Lys	Gln	Cys	Ser	Lys	Ala	
213					218					223					228	
ttt	cct	ttt	tac	agt	tcc	tat	cta	aga	cat	gaa	aga	atc	cac	acg	gga	834
Phe	Pro	Phe	Tyr	Ser	Ser	Tyr	Leu	Arg	His	Glu	Arg	Ile	His	Thr	Gly	
229					234					239					244	
gag	aaa	gcg	tat	gaa	tgt	aag	cag	tgt	tcc	aaa	gcc	ttt	cct	gat	tac	882
Glu	Lys	Ala	Tyr	Glu	Cys	Lys	Gln	Cys	Ser	Lys	Ala	Phe	Pro	Asp	Tyr	
245					250					255					260	
agt	acc	tat	cta	aga	cat	gag	aga	act	cac	acc	gga	gag	aaa	ccc	tat	930
Ser	Thr	Tyr	Leu	Arg	His	Glu	Arg	Thr	His	Thr	Gly	Glu	Lys	Pro	Tyr	
261					266					271					276	
aaa	tgt	aca	caa	tgt	ggg	aaa	gcc	ttc	agc	tgt	tac	tat	tac	act	cga	978
Lys	Cys	Thr	Gln	Cys	Gly	Lys	Ala	Phe	Ser	Cys	Tyr	Tyr	Tyr	Thr	Arg	
277					282					287					292	
cta	cat	gaa	agg	act	cac	acg	gga	gaa	caa	ccc	tat	gca	tgt	aag	caa	1026
Leu	His	Glu	Arg	Thr	His	Thr	Gly	Glu	Gln	Pro	Tyr	Ala	Cys	Lys	Gln	
293					298					303					308	
tgt	ggg	aaa	acg	ttt	tat	cat	cac	aca	agc	ttt	cga	aga	cac	atg	ata	1074
Cys	Gly	Lys	Thr	Phe	Tyr	His	His	Thr	Ser	Phe	Arg	Arg	His	Met	Ile	
309					314					319					324	
agg	cac	act	gga	gac	gga	cca	cat	aaa	tgt	aag	ata	tgt	ggg	aaa	ggc	1122
Arg	His	Thr	Gly	Asp	Gly	Pro	His	Lys	Cys	Lys	Ile	Cys	Gly	Lys	Gly	
325					330					335					340	
ttt	gat	tgt	cct	agt	tca	gtt	cga	aat	cat	gaa	act	act	cac	act	gga	1170
Phe	Asp	Cys	Pro	Ser	Ser	Val	Arg	Asn	His	Glu	Thr	Thr	His	Thr	Gly	
341					346					351					356	

gag Glu 357	aaa Lys	ccc Pro	tat Tyr	gaa Glu	tgt Cys 362	aag Lys	cag Gln	tgt Cys	ggg Gly	aaa Lys 367	gtg Val	tta Leu	tct Ser	cat His	agc Ser 372	1218
tcg Ser 373	agc Ser	ttt Phe	cga Arg	agt Ser	cac His 378	atg Met	ata Ile	aca Thr	cac His	aca Thr 383	gga Gly	gat Asp	gga Gly	ccc Pro	cag Gln 388	1266
aaa Lys 389	tgc Cys	aag Lys	ata Ile	tgt Cys	ggg Gly 394	aaa Lys	gcc Ala	ttt Phe	ggg Gly	tgt Cys 399	ccc Pro	agt Ser	tta Leu	ttt Phe	caa Gln 404	1314
aga Arg 405	cat His	gaa Glu	agg Arg	act Thr	cac His 410	act Thr	gga Gly	gag Glu	aaa Lys	ccc Pro 415	tat Tyr	caa Gln	tgt Cys	aaa Lys	caa Gln 420	1362
tgt Cys 421	ggg Gly	aaa Lys	gcc Ala	ttc Phe	agt Ser 426	ctt Leu	gcc Ala	ggg Gly	tcc Ser	ctt Leu 431	cga Arg	aga Arg	cat His	gaa Glu	gca Ala 436	1410
act Thr 437	cac His	act Thr	gga Gly	gtg Val	aaa Lys 442	ccc Pro	tat Tyr	aaa Lys	tgt Cys	cag Gln 447	tgt Cys	ggg Gly	aaa Lys	gcc Ala	ttt Phe 452	1458
agt Ser 453	gat Asp	ctc Leu	tct Ser	tcc Ser	ttt Phe 458	caa Gln	aat Asn	cat His	gag Glu	aca Thr 463	act Thr	cac His	act Thr	gga Gly	gag Glu 468	1506
aag Lys 469	cca Pro	tat Tyr	gag Glu	tgt Cys	aag Lys 474	gaa Glu	tgt Cys	ggg Gly	aaa Lys	gca Ala 479	ttc Phe	agt Ser	tgt Cys	ttc Phe	aaa Lys 484	1554
tac Tyr 485	ctt Leu	tct Ser	caa Gln	cat His	aaa Lys 490	agg Arg	acc Thr	cac His	aca Thr	gta Val 495	gaa Glu	aaa Lys	cct Pro	tat Tyr	gag Glu 500	1602
tgt Cys 501	aaa Lys	aca Thr	tgt Cys	aga Arg	aaa Lys 506	gcc Ala	ttc Phe	agt Ser	cat His	ttc Phe 511	agt Ser	aac Asn	tta Leu	aaa Lys	gtc Val 516	1650
cat His 517	gaa Glu	agg Arg	att Ile	cac His	tct Ser 522	gga Gly	gag Glu	aag Lys	cca Pro	tat Tyr 527	gaa Glu	tgt Cys	aag Lys	gaa Glu	tgt Cys 532	1698
gga Gly 533	aaa Lys	gca Ala	ttc Phe	tct Ser	tgg Trp 538	ctc Leu	act Thr	tgc Cys	ctt Leu	cta Leu 543	cga Arg	cat His	gaa Glu	aga Arg	att Ile 548	1746
cac His 549	act Thr	gga Gly	gag Glu	aaa Lys	ccc Pro 554	tat Tyr	gaa Glu	tgt Cys	cta Leu	caa Gln 559	tgt Cys	ggg Gly	aaa Lys	gcc Ala	ttc Phe 564	1794
act Thr 565	cgt Arg	tcc Ser	cgt Arg	ttc Phe	ctt Leu 570	cga Arg	gga Gly	cat His	gaa Glu	aaa Lys 575	act Thr	cac His	act Thr	gga Gly	gag Glu 580	1842

aag ctg tat gaa tgt aag gaa tgt ggg aaa gca ttg agt tct ctc cgt 1890
 Lys Leu Tyr Glu Cys Lys Glu Cys Gly Lys Ala Leu Ser Ser Leu Arg
 581 586 591 596

tcc ttg cat aga cat aaa agg act cac tgg aaa gat act ctc taa atg 1938
 Ser Leu His Arg His Lys Arg Thr His Trp Lys Asp Thr Leu *
 597 602 607

tatggaatgt gggaaaacat tcagtacttt aatttcagaa acttgaaaga actcactttg 1998

gagatagacc ctatgaatgt aaacatggga taaagcctta agtagtttca attttttttaa 2058

atacagttat cccccaatat attgcagggg attggttcca gcaccctcta aatccacaga 2118

tgccaagtcc tttgttatat ggcataatttg catgtaacct atgcatatcc tccagtatac 2178

tgtgtaaadc atctctagat gacttttaaat acctcatgca ttgtaaaagc tatgtaaata 2238

gttgtttgat tgtattgttt agagaatcat gacaagaaaa atagtctcta catgttcgat 2298

gcagacacaa ccattgcagg cccacctacg tggatatatgt caccagaaac attaaaattt 2358

gttttaacat tcaaaaaaaaa aaaaaaa 2385

<210> 124

<211> 1045

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (302)..(889)

<400> 124

gaaggcagct cgtggcgact gtccgtggtg ctgagcgccg gcgagagctg gcgcgagagcg 60

gctgatcggc tccctcgaac tggggagggtc cagtgggggtc gcttagggcc caaagccccc 120

acccggctcc aaaagctccc agggcctccc caggcaccgg tgctcggccc ttccttcggt 180

cagaaagtcg cccctcgggg gcagttcgtc ccaaaggggt tccctcgaag aatctgagag 240

ggcgagctcc ttgaccgagg gaatctctct gtgtagcctt ggaagccgcc agccccagaa 300

g atg cct gcc ttc aat aga ttg ttt ccc ctg gct tct ctc gtg ctt 346
 Met Pro Ala Phe Asn Arg Leu Phe Pro Leu Ala Ser Leu Val Leu
 1 5 10

atc tac tgg gtc agt gtc tgc ttc cct gtg tgt gtg gaa gtg ccc tcg 394
 Ile Tyr Trp Val Ser Val Cys Phe Pro Val Cys Val Glu Val Pro Ser
 16 21 26 31

gag acg gag gcc gtg cag ggc aac ccc atg aag ctg cgc tgc atc tcc 442
 Glu Thr Glu Ala Val Gln Gly Asn Pro Met Lys Leu Arg Cys Ile Ser

32	37	42	47	
tgc atg aag aga gag gag gtg gag gcc acc acg gtg gtg gaa tgg ttc				490
Cys Met Lys Arg Glu Glu Val Glu Ala Thr Thr Val Val Glu Trp Phe				
48	53	58	63	
tac agg ccc gag ggc ggt aaa gat ttc ctt att tac gag tat cgg aat				538
Tyr Arg Pro Glu Gly Gly Lys Asp Phe Leu Ile Tyr Glu Tyr Arg Asn				
64	69	74	79	
ggc cac cag gag gtg gag agc ccc ttt cag ggg cgc ctg cag tgg aat				586
Gly His Gln Glu Val Glu Ser Pro Phe Gln Gly Arg Leu Gln Trp Asn				
80	85	90	95	
ggc agc aag gac ctg cag gac gtg tcc atc act gtg ctc aac gtc act				634
Gly Ser Lys Asp Leu Gln Asp Val Ser Ile Thr Val Leu Asn Val Thr				
96	101	106	111	
ctg aac gac tct ggc ctc tac acc tgc aat gtg tcc cgg gag ttt gag				682
Leu Asn Asp Ser Gly Leu Tyr Thr Cys Asn Val Ser Arg Glu Phe Glu				
112	117	122	127	
ttt gag gcg cat cgg ccc ttt gtg aag acg acg cgg ctg atc ccc cta				730
Phe Glu Ala His Arg Pro Phe Val Lys Thr Thr Arg Leu Ile Pro Leu				
128	133	138	143	
aga gtc acc gag gag gct gga gag gac ttc acc tct gtg gtc tca gaa				778
Arg Val Thr Glu Glu Ala Gly Glu Asp Phe Thr Ser Val Val Ser Glu				
144	149	154	159	
atc atg atg tac atc ctt ctg gtc ttc ctc acc ttg tgg ctg ctc atc				826
Ile Met Met Tyr Ile Leu Leu Val Phe Leu Thr Leu Trp Leu Leu Ile				
160	165	170	175	
gag atg ata tat tgc tac aga aag gtc tca aaa gcc gaa gag gca gcc				874
Glu Met Ile Tyr Cys Tyr Arg Lys Val Ser Lys Ala Glu Glu Ala Ala				
176	181	186	191	
caa gaa aac gcg taa gtccagagat gccaaagtaa taatgaaagc tagcaccttc				929
Gln Glu Asn Ala *				
192				
agaatgcttg ctctcacagg tgagggtgcta agcagtttac attcatccgg acgcgtgggt				989
cgacccggga attccggacc ggtacctgca ggcgtacgag cttcagtaat tcaaaa				1045

<210> 125
 <211> 936
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (7)..(594)

```

<400> 125
aggctg   atg tat ata act atc tat tcg atg atg aag ata ccc cac caa   48
          Met Tyr Ile Thr Ile Tyr Ser Met Met Lys Ile Pro His Gln
            1             5             10

acc caa aaa aag aga tct ctc gag gat ccg aat tcg cgg ccg cgt cga   96
Thr Gln Lys Lys Arg Ser Leu Glu Asp Pro Asn Ser Arg Pro Arg Arg
  15             20             25             30

cct ttc ttt aaa agt gtg aag gaa gaa gtg ttc tgg agg aac tac ttt   144
Pro Phe Phe Lys Ser Val Lys Glu Glu Val Phe Trp Arg Asn Tyr Phe
  31             36             41             46

tac cgc gtc tcc ctg att aag cag tca gcc cag ctc acg gcc ctg gct   192
Tyr Arg Val Ser Leu Ile Lys Gln Ser Ala Gln Leu Thr Ala Leu Ala
  47             52             57             62

gcc caa cag cag gcc gca ggg aag gag gag aag agc aat ggc aga gag   240
Ala Gln Gln Gln Ala Ala Gly Lys Glu Glu Lys Ser Asn Gly Arg Glu
  63             68             73             78

caa gat ttg ccg ctg gca gag gca gta cgg ccc aaa acg cca ccc gtt   288
Gln Asp Leu Pro Leu Ala Glu Ala Val Arg Pro Lys Thr Pro Pro Val
  79             84             89             94

gta atc aaa tct cag ctt aaa act caa gag gat gag gaa gaa att tct   336
Val Ile Lys Ser Gln Leu Lys Thr Gln Glu Asp Glu Glu Glu Ile Ser
  95             100            105            110

act agc cca ggt gtt tct gag ttt gtc agt gat gcc ttc gat gcc tgt   384
Thr Ser Pro Gly Val Ser Glu Phe Val Ser Asp Ala Phe Asp Ala Cys
 111             116            121            126

aac cta aat cag gaa gat cta agg aaa gaa atg gag caa cta gtg ctt   432
Asn Leu Asn Gln Glu Asp Leu Arg Lys Glu Met Glu Gln Leu Val Leu
 127             132            137            142

gac aaa aag caa gag gag aca gcc gta ctg gaa gag gat tct gca gat   480
Asp Lys Lys Gln Glu Glu Thr Ala Val Leu Glu Glu Asp Ser Ala Asp
 143             148            153            158

tgg gaa aaa gaa ctg cag cag gaa ctt caa gaa tat gaa gtg gtg aca   528
Trp Glu Lys Glu Leu Gln Gln Glu Leu Gln Glu Tyr Glu Val Val Thr
 159             164            169            174

gaa tct gaa aaa cga gat gaa aac tgg gat aag gaa ata gag aaa atg   576
Glu Ser Glu Lys Arg Asp Glu Asn Trp Asp Lys Glu Ile Glu Lys Met
 175             180            185            190

ctt caa gag gaa aat tag ctgttc ctgaaataga agaataatcc ttaacagtct   630
Leu Gln Glu Glu Asn *
 191             196

gcaaactgac attaaattct agatgttgac aattactgaa tcagaaggca tgaaagagta   690

taattttatg aaattcaaaa ttattctttt ttcaagttga aacttgccctc ttctacttta   750

```

aaaaagtata tagaacagtt acttctaata atcagaaaga gatgttttat agaacatttc 810
 tttaatataa agttagagat gtcttcatag gcagtatggc tatctttgcc acagaaacat 870
 aagtaaaatt ttagagttct gttttccatg aggtcaaaaa tataatttat tcctcaaaaa 930
 aaaaaa 936

<210> 126
 <211> 2124
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (235)..(1980)

<400> 126
 ggagttgaga attagggagg aggtggtaga gtccgggtag tgagcggagg gacaggaagg 60
 gtagggcaag aaagggagag gggacaggag ggaaggggtgg gccaaagcgg tgagaaagga 120
 gggccagcca gttgggtggg ggagagggcc gagggccggg ggcaggagtg cagggctctg 180
 aggcgggggag aggagaggag agaagagccg cgggggggcc agcccggagc cagg atg 237
 Met
 1
 ccc gcg ccg cgc gcc cgg gag cag ccc cgc gtg ccc ggg gag cgc cag 285
 Pro Ala Pro Arg Ala Arg Glu Gln Pro Arg Val Pro Gly Glu Arg Gln
 2 7 12 17
 ccg ctg ctg cct cgc ggt gcg cgg ggc cct cga cgg tgg cgg cgg gcg 333
 Pro Leu Leu Pro Arg Gly Ala Arg Gly Pro Arg Arg Trp Arg Arg Ala
 18 23 28 33
 gcg ggc gcg gcc gtg ctg ctg gtg gag atg ctg gag cgc gcc gcc ttc 381
 Ala Gly Ala Ala Val Leu Leu Val Glu Met Leu Glu Arg Ala Ala Phe
 34 39 44 49
 ttc ggc gtc acc gcc aac ctc gtg ctg tac ctc aac agc acc aac ttc 429
 Phe Gly Val Thr Ala Asn Leu Val Leu Tyr Leu Asn Ser Thr Asn Phe
 50 55 60 65
 aac tgg acc ggc gag cag gcg acg cgc gcc gcg ctg gta ttc ctg ggc 477
 Asn Trp Thr Gly Glu Gln Ala Thr Arg Ala Ala Leu Val Phe Leu Gly
 66 71 76 81
 gcc tcc tac ctg ctg gcg ccc gtg ggc ggc tgg ctg gcc gac gtg tac 525
 Ala Ser Tyr Leu Leu Ala Pro Val Gly Gly Trp Leu Ala Asp Val Tyr
 82 87 92 97
 ctg ggc cgc tac cgc gcg gtc gcg ctc agc ctg ctg ctc tac ctg gcc 573

Leu	Gly	Arg	Tyr	Arg	Ala	Val	Ala	Leu	Ser	Leu	Leu	Leu	Tyr	Leu	Ala	
98					103					108					113	
gcc	tcg	ggc	ctg	ctg	ccc	gcc	acc	gcc	ttc	ccc	gac	ggc	cgc	agc	tcc	621
Ala	Ser	Gly	Leu	Leu	Pro	Ala	Thr	Ala	Phe	Pro	Asp	Gly	Arg	Ser	Ser	
114					119					124					129	
ttc	tgc	gga	gag	atg	ccc	gcg	tcg	ccg	ctg	gga	cct	gcc	tgc	ccc	tcg	669
Phe	Cys	Gly	Glu	Met	Pro	Ala	Ser	Pro	Leu	Gly	Pro	Ala	Cys	Pro	Ser	
130					135					140					145	
gcc	ggc	tgc	ccg	cgc	tcc	tcg	ccc	agc	ccc	tac	tgc	gcg	ccc	gtc	ctc	717
Ala	Gly	Cys	Pro	Arg	Ser	Ser	Pro	Ser	Pro	Tyr	Cys	Ala	Pro	Val	Leu	
146					151					156					161	
tac	gcg	ggc	ctg	ctg	cta	ctc	ggc	ctg	gcc	gcc	agc	tcc	gtc	cgg	agc	765
Tyr	Ala	Gly	Leu	Leu	Leu	Leu	Gly	Leu	Ala	Ala	Ser	Ser	Val	Arg	Ser	
162					167					172					177	
aac	ctc	acc	tcc	ttc	ggt	gcc	gac	cag	gtg	atg	gat	ctc	ggc	cgc	gac	813
Asn	Leu	Thr	Ser	Phe	Gly	Ala	Asp	Gln	Val	Met	Asp	Leu	Gly	Arg	Asp	
178					183					188					193	
gcc	acc	cgc	cgc	ttc	ttc	aac	tgg	ttt	tac	tgg	agc	atc	aac	ctg	ggt	861
Ala	Thr	Arg	Arg	Phe	Phe	Asn	Trp	Phe	Tyr	Trp	Ser	Ile	Asn	Leu	Gly	
194					199					204					209	
gct	gtg	ctg	tcg	ctg	ctg	gtg	gtg	gcg	ttt	att	cag	cag	aac	atc	agc	909
Ala	Val	Leu	Ser	Leu	Leu	Val	Val	Ala	Phe	Ile	Gln	Gln	Asn	Ile	Ser	
210					215					220					225	
ttc	ctg	ctg	ggc	tac	agc	atc	cct	gtg	ggc	tgt	gtg	ggc	ctg	gca	ttt	957
Phe	Leu	Leu	Gly	Tyr	Ser	Ile	Pro	Val	Gly	Cys	Val	Gly	Leu	Ala	Phe	
226					231					236					241	
ttc	atc	ttc	ctc	ttt	gcc	acc	ccc	gtc	ttc	atc	acc	aag	ccc	ccg	atg	1005
Phe	Ile	Phe	Leu	Phe	Ala	Thr	Pro	Val	Phe	Ile	Thr	Lys	Pro	Pro	Met	
242					247					252					257	
ggc	agc	caa	gtg	tcc	tct	atg	ctt	aag	ctc	gct	ctc	caa	aac	tgc	tgc	1053
Gly	Ser	Gln	Val	Ser	Ser	Met	Leu	Lys	Leu	Ala	Leu	Gln	Asn	Cys	Cys	
258					263					268					273	
ccc	cag	ctg	tgg	caa	cga	cac	tcg	gcc	aga	gac	cgt	caa	tgt	gcc	cgc	1101
Pro	Gln	Leu	Trp	Gln	Arg	His	Ser	Ala	Arg	Asp	Arg	Gln	Cys	Ala	Arg	
274					279					284					289	
gtg	ctg	gcc	gac	gag	agg	tct	ccc	cag	cca	ggg	gct	tcc	ccg	caa	gag	1149
Val	Leu	Ala	Asp	Glu	Arg	Ser	Pro	Gln	Pro	Gly	Ala	Ser	Pro	Gln	Glu	
290					295					300					305	
gac	atc	gcc	aac	ttc	cag	gtg	ctg	gtg	aag	atc	ttg	ccc	gtc	atg	gtg	1197
Asp	Ile	Ala	Asn	Phe	Gln	Val	Leu	Val	Lys	Ile	Leu	Pro	Val	Met	Val	
306					311					316					321	
acc	ctg	gtg	ccc	tac	tgg	atg	gtc	tac	ttc	cag	atg	cag	tcc	acc	tat	1245
Thr	Leu	Val	Pro	Tyr	Trp	Met	Val	Tyr	Phe	Gln	Met	Gln	Ser	Thr	Tyr	

322	327	332	337	
gtc ctg cag ggt ctt cac ctc cac atc cca aac att ttc cca gcc aac				1293
Val Leu Gln Gly Leu His Leu His Ile Pro Asn Ile Phe Pro Ala Asn				
338	343	348	353	
ccg gcc aac atc tct gtg gcc ctg aga gcc cag ggc agc agc tac acg				1341
Pro Ala Asn Ile Ser Val Ala Leu Arg Ala Gln Gly Ser Ser Tyr Thr				
354	359	364	369	
atc ccg gaa gcc tgg ctc ctc ctg gcc aat gtt gtg gtg gtg ctg att				1389
Ile Pro Glu Ala Trp Leu Leu Leu Ala Asn Val Val Val Val Leu Ile				
370	375	380	385	
ctg gtc cct ctg aag gac cgc ttg atc gac cct tta ctg ctg cgg tgc				1437
Leu Val Pro Leu Lys Asp Arg Leu Ile Asp Pro Leu Leu Leu Arg Cys				
386	391	396	401	
aag ctg ctt ccc tct gct ctg cag aag atg gcg ctg ggg atg ttc ttt				1485
Lys Leu Leu Pro Ser Ala Leu Gln Lys Met Ala Leu Gly Met Phe Phe				
402	407	412	417	
ggt ttt acc tcc gtc att gtg gca gga gtc ctg gag atg gag cgc tta				1533
Gly Phe Thr Ser Val Ile Val Ala Gly Val Leu Glu Met Glu Arg Leu				
418	423	428	433	
cac tac atc cac cac aac gag acc gtg tcc cag cag att ggg gag gtc				1581
His Tyr Ile His His Asn Glu Thr Val Ser Gln Gln Ile Gly Glu Val				
434	439	444	449	
ctg tac aac gcg gca cca ctg tcc atc tgg tgg cag atc cct cag tac				1629
Leu Tyr Asn Ala Ala Pro Leu Ser Ile Trp Trp Gln Ile Pro Gln Tyr				
450	455	460	465	
ctg ctc att ggg atc agt gag atc ttt gcc agc atc cca ggc ctg gag				1677
Leu Leu Ile Gly Ile Ser Glu Ile Phe Ala Ser Ile Pro Gly Leu Glu				
466	471	476	481	
ttt gcc tac tca gag gcc ccg cgc tcc atg cag ggc gcc atc atg ggc				1725
Phe Ala Tyr Ser Glu Ala Pro Arg Ser Met Gln Gly Ala Ile Met Gly				
482	487	492	497	
atc ttc ttc tgc ctg tgc ggg gtg ggc tca ctg ttg ggc tcc agc cta				1773
Ile Phe Phe Cys Leu Ser Gly Val Gly Ser Leu Leu Gly Ser Ser Leu				
498	503	508	513	
gtg gca ctg ctg tcc ttg ccc ggg ggc tgg ctg cac tgc ccc aag gac				1821
Val Ala Leu Leu Ser Leu Pro Gly Gly Trp Leu His Cys Pro Lys Asp				
514	519	524	529	
ttt ggg aac atc aac aat tgc cgg atg gac ctc tac ttc ttc ctg ctg				1869
Phe Gly Asn Ile Asn Asn Cys Arg Met Asp Leu Tyr Phe Phe Leu Leu				
530	535	540	545	
gct ggc att cag gcc gtc acg gct ctc cta ttt gtc tgg atc gct gga				1917
Ala Gly Ile Gln Ala Val Thr Ala Leu Leu Phe Val Trp Ile Ala Gly				
546	551	556	561	

Thr Gly Lys Tyr Val His Asn His Asn Thr Tyr Thr Asn Asn Glu Asn	
97 102 107 112	
tgc tcc tcg ccc tcc tgg cag gca cag cac gag agc cgc acc ttt gcc	564
Cys Ser Ser Pro Ser Trp Gln Ala Gln His Glu Ser Arg Thr Phe Ala	
113 118 123 128	
gtg tac ctc aat agc act ggc tac cgg aca gct ttc ttc ggg aag tat	612
Val Tyr Leu Asn Ser Thr Gly Tyr Arg Thr Ala Phe Phe Gly Lys Tyr	
129 134 139 144	
ctt aat gaa tac aac ggc tcc tac gtg cca ccc ggc tgg aag gag tgg	660
Leu Asn Glu Tyr Asn Gly Ser Tyr Val Pro Pro Gly Trp Lys Glu Trp	
145 150 155 160	
gtc gga ctc ctt aaa aac tcc cgc ttt tat aac tac acg ctg tgt cgg	708
Val Gly Leu Leu Lys Asn Ser Arg Phe Tyr Asn Tyr Thr Leu Cys Arg	
161 166 171 176	
aac ggg gtg aaa gag aag cac ggc tcc gac tac tcc aag gat tac ctc	756
Asn Gly Val Lys Glu Lys His Gly Ser Asp Tyr Ser Lys Asp Tyr Leu	
177 182 187 192	
aca gac ctc atc acc aat gac agc gtg agc ttc ttc cgc acg tcc aag	804
Thr Asp Leu Ile Thr Asn Asp Ser Val Ser Phe Phe Arg Thr Ser Lys	
193 198 203 208	
aag atg tac ccg cac agg cca gtc ctc atg gtc atc agc cat gca gcc	852
Lys Met Tyr Pro His Arg Pro Val Leu Met Val Ile Ser His Ala Ala	
209 214 219 224	
ccc cac ggc cct gag gat tca gcc cca caa tat tca cgc ctc ttc cca	900
Pro His Gly Pro Glu Asp Ser Ala Pro Gln Tyr Ser Arg Leu Phe Pro	
225 230 235 240	
aac gca tct cag cac atc acg ccg agc tac aac tac gcg ccc aac ccg	948
Asn Ala Ser Gln His Ile Thr Pro Ser Tyr Asn Tyr Ala Pro Asn Pro	
241 246 251 256	
gac aaa cac tgg atc atg cgc tac acg ggg ccc atg aag ccc atc cac	996
Asp Lys His Trp Ile Met Arg Tyr Thr Gly Pro Met Lys Pro Ile His	
257 262 267 272	
atg gaa ttc acc aac atg ctc cag cgg aag cgc ttg cag acc ctc atg	1044
Met Glu Phe Thr Asn Met Leu Gln Arg Lys Arg Leu Gln Thr Leu Met	
273 278 283 288	
tcg gtg gac gac tcc atg gag acg att tac aac atg ctg gtt gag acg	1092
Ser Val Asp Asp Ser Met Glu Thr Ile Tyr Asn Met Leu Val Glu Thr	
289 294 299 304	
ggc gag ctg gac aac acg tac atc gta tac acc gcc gac cac ggt tac	1140
Gly Glu Leu Asp Asn Thr Tyr Ile Val Tyr Thr Ala Asp His Gly Tyr	
305 310 315 320	
cac atc ggc cag ttt ggc ctg gtg aaa ggg aaa tcc atg cca tat gag	1188
His Ile Gly Gln Phe Gly Leu Val Lys Gly Lys Ser Met Pro Tyr Glu	

321	326	331	336	
ttt gac atc agg gtc ccg ttc tac gtg agg ggc ccc aac gtg gaa gcc				1236
Phe Asp Ile Arg Val Pro Phe Tyr Val Arg Gly Pro Asn Val Glu Ala				
337	342	347	352	
ggc tgt ctg aat ccc cac atc gtc ctc aac att gac ctg gcc ccc acc				1284
Gly Cys Leu Asn Pro His Ile Val Leu Asn Ile Asp Leu Ala Pro Thr				
353	358	363	368	
atc ctg gac att gca ggc ctg gac ata cct gcg gat atg gac ggg aaa				1332
Ile Leu Asp Ile Ala Gly Leu Asp Ile Pro Ala Asp Met Asp Gly Lys				
369	374	379	384	
tcc atc ctc aag ctg ctg gac acg gag cgg ccg gtg aat cgg ttt cac				1380
Ser Ile Leu Lys Leu Leu Asp Thr Glu Arg Pro Val Asn Arg Phe His				
385	390	395	400	
ttg aaa aag aag atg agg gtc tgg cgg gac tcc ttc ttg gtg gag aga				1428
Leu Lys Lys Lys Met Arg Val Trp Arg Asp Ser Phe Leu Val Glu Arg				
401	406	411	416	
ggc aag ctg cta cac aag aga gac aat gac aag gtg gac gcc cag gag				1476
Gly Lys Leu Leu His Lys Arg Asp Asn Asp Lys Val Asp Ala Gln Glu				
417	422	427	432	
gag aac ttt ctg ccc aag tac cag cgt gtg aag gac ctg tgt cag cgt				1524
Glu Asn Phe Leu Pro Lys Tyr Gln Arg Val Lys Asp Leu Cys Gln Arg				
433	438	443	448	
gct gag tac cag acg gcg tgt gag cag ctg gga cag aag tgg cag tgt				1572
Ala Glu Tyr Gln Thr Ala Cys Glu Gln Leu Gly Gln Lys Trp Gln Cys				
449	454	459	464	
gtg gag gac gcc acg ggg aag ctg aag ctg cat aag tgc aag ggc ccc				1620
Val Glu Asp Ala Thr Gly Lys Leu Lys Leu His Lys Cys Lys Gly Pro				
465	470	475	480	
atg cgg ctg ggc ggc agc aga gcc ctc tcc aac ctc gtg ccc aag tac				1668
Met Arg Leu Gly Gly Ser Arg Ala Leu Ser Asn Leu Val Pro Lys Tyr				
481	486	491	496	
tac ggg cag ggc agc gag gcc tgc acc tgt gac agc ggg gac tac aag				1716
Tyr Gly Gln Gly Ser Glu Ala Cys Thr Cys Asp Ser Gly Asp Tyr Lys				
497	502	507	512	
ctc agc ctg gcc gga cgc cgg aaa aaa ctc ttc aag aag aag tac aag				1764
Leu Ser Leu Ala Gly Arg Arg Lys Lys Leu Phe Lys Lys Lys Tyr Lys				
513	518	523	528	
gcc agc tat gtc cgc agt cgc tcc atc cgc tca gtg gcc atc gag gtg				1812
Ala Ser Tyr Val Arg Ser Arg Ser Ile Arg Ser Val Ala Ile Glu Val				
529	534	539	544	
gac ggc agg gtg tac cac gta ggc ctg ggt gat gcc gcc cag ccc cga				1860
Asp Gly Arg Val Tyr His Val Gly Leu Gly Asp Ala Ala Gln Pro Arg				
545	550	555	560	

aac ctc acc aag cgg cac tgg cca ggg gcc cct gag gac caa gat gac Asn Leu Thr Lys Arg His Trp Pro Gly Ala Pro Glu Asp Gln Asp Asp 561 566 571 576	1908
aag gat ggt ggg gac ttc agt ggc act gga ggc ctt ccc gac tac tca Lys Asp Gly Gly Asp Phe Ser Gly Thr Gly Gly Leu Pro Asp Tyr Ser 577 582 587 592	1956
gcc gcc aac ccc att aaa gtg aca cat cgg tgc tac atc cta gag aac Ala Ala Asn Pro Ile Lys Val Thr His Arg Cys Tyr Ile Leu Glu Asn 593 598 603 608	2004
gac aca gtc cag tgt gac ctg gac ctg tac aag tcc ctg cag gcc tgg Asp Thr Val Gln Cys Asp Leu Asp Leu Tyr Lys Ser Leu Gln Ala Trp 609 614 619 624	2052
aaa gac cac aag ctg cac atc gac cac gag att gaa acc ctg cag aac Lys Asp His Lys Leu His Ile Asp His Glu Ile Glu Thr Leu Gln Asn 625 630 635 640	2100
aaa att aag aac ctg agg gaa gtc cga ggt cac ctg aag aaa aag cgg Lys Ile Lys Asn Leu Arg Glu Val Arg Gly His Leu Lys Lys Lys Arg 641 646 651 656	2148
cca gaa gaa tgt gac tgt cac aaa atc agc tac cac acc cag cac aaa Pro Glu Glu Cys Asp Cys His Lys Ile Ser Tyr His Thr Gln His Lys 657 662 667 672	2196
ggc cgc ctc aag cac aga ggc tcc agt ctg cat cct ttc agg aag ggc Gly Arg Leu Lys His Arg Gly Ser Ser Leu His Pro Phe Arg Lys Gly 673 678 683 688	2244
ctg caa gag aag gac aag gtg tgg ctg ttg cgg gag cag aag cgc aag Leu Gln Glu Lys Asp Lys Val Trp Leu Leu Arg Glu Gln Lys Arg Lys 689 694 699 704	2292
aag aaa ctc cgc aag ctg ctc aag cgc ctg cag aac aac gac acg tgc Lys Lys Leu Arg Lys Leu Leu Lys Arg Leu Gln Asn Asn Asp Thr Cys 705 710 715 720	2340
agc atg cca ggc ctc acg tgc ttc acc cac gac aac cag cac tgg cag Ser Met Pro Gly Leu Thr Cys Phe Thr His Asp Asn Gln His Trp Gln 721 726 731 736	2388
acg gcg cct ttc tgg aca ctg ggg cct ttc tgt gcc tgc acc agc gcc Thr Ala Pro Phe Trp Thr Leu Gly Pro Phe Cys Ala Cys Thr Ser Ala 737 742 747 752	2436
aac aat aac acg tac tgg tgc atg agg acc atc aat gag act cac aat Asn Asn Asn Thr Tyr Trp Cys Met Arg Thr Ile Asn Glu Thr His Asn 753 758 763 768	2484
ttc ctc ttc tgt gaa ttt gca act ggc ttc cta gag tac ttt gat ctc Phe Leu Phe Cys Glu Phe Ala Thr Gly Phe Leu Glu Tyr Phe Asp Leu 769 774 779 784	2532

aac aca gac ccc tac cag ctg atg aat gca gtg aac aca ctg gac agg	2580
Asn Thr Asp Pro Tyr Gln Leu Met Asn Ala Val Asn Thr Leu Asp Arg	
785 790 795 800	
gat gtc ctc aac cag cta cac gta cag ctc atg gag ctg agg agc tgc	2628
Asp Val Leu Asn Gln Leu His Val Gln Leu Met Glu Leu Arg Ser Cys	
801 806 811 816	
aag ggt tac aag cag tgt aac ccc cgg act cga aac atg gac ctg gga	2676
Lys Gly Tyr Lys Gln Cys Asn Pro Arg Thr Arg Asn Met Asp Leu Gly	
817 822 827 832	
ctt aaa gat gga gga agc tat gag caa tac agg cag ttt cag cgt cga	2724
Leu Lys Asp Gly Gly Ser Tyr Glu Gln Tyr Arg Gln Phe Gln Arg Arg	
833 838 843 848	
aag tgg cca gaa atg aag aga cct tct tcc aaa tca ctg gga caa ctg	2772
Lys Trp Pro Glu Met Lys Arg Pro Ser Ser Lys Ser Leu Gly Gln Leu	
849 854 859 864	
tgg gaa ggc tgg gaa ggt taa ga aacaacagag gtggacctcc aaaaacatag	2825
Trp Glu Gly Trp Glu Gly *	
865 870	
aggcatcacc tgactgcaca ggcaatgaaa aaccatgtgg gtgatttcca gcagacctgt	2885
gctattggcc aggaggcctg agaaagcaag cacgcactct cagtcaacat gacagattct	2945
ggaggataac cagcaggagc agagataact tcaggaagtc catttttgcc cctgcttttg	3005
ctttggatta tacctcacca gctgcacaaa atgcattttt tcgtatcaaa aagtcaccac	3065
taaccctccc ccagaagctc acaaaggaaa acggagagag cgagcgagag agatttcctt	3125
ggaaatttct cccaagggcg aaagtcattg gaatttttaa atcatagggg aaaagcagtc	3185
ctgttctaaa tcctcttatt cttttggttt gtcacaaaga aggaactaag aagcaggaca	3245
gaggcaacgt ggagaggctg aaaacagtgc agagacgttt gacaatgagt cagtagcaca	3305
aaagagatga catttaccta gcactataaa ccttggttgc ctctgaagaa actgccttca	3365
ttgtatatat gtgactatct acatgtaatc aacatgggaa cttttagggg aacctaataa	3425
gaaatcccaa ttttcaggag tgggtggtgtc aataaacgct ctgtggccag tgtaaaagaa	3485
aaaaaaaaa	3495

<210> 128

<211> 3435

<212> DNA

<213> Homo sapiens

<220>

<221> CDS
 <222> (181)..(2733)

<400> 128

```

ccgggaaccg agttcgtggc tgcggctgag gcggcgccgg cgccccgctt ctgttgaggt      60

tgccggggcc gcgcgcgctg atctgcgagt gaagagggac gagggaaaag aaacaaagcc      120

acagacgcaa cttgagactc ccgcatccca aaagaagcac cagatcagca aaaaaagaag      180

atg ggc ccc ccg agc ctc gtg ctg tgc ttg ctg tcc gca act gtg ttc      228
Met Gly Pro Pro Ser Leu Val Leu Cys Leu Leu Ser Ala Thr Val Phe
  1             5             10             15

tcc ctg ctg ggt gga agc tcg gcc ttc ctg tcg cac cac cgc ctg aaa      276
Ser Leu Leu Gly Gly Ser Ser Ala Phe Leu Ser His His Arg Leu Lys
  17             22             27             32

ggc agg ttt cag agg gac cgc agg aac atc cgc ccc aac atc atc ctg      324
Gly Arg Phe Gln Arg Asp Arg Arg Asn Ile Arg Pro Asn Ile Ile Leu
  33             38             43             48

gtg ctg acg gac gac cag gat gtg gag ctg ggt tcc atg cag gtg atg      372
Val Leu Thr Asp Asp Gln Asp Val Glu Leu Gly Ser Met Gln Val Met
  49             54             59             64

aac aag acc cgg cgc atc atg gag cag ggc ggg gcg cac ttc atc aac      420
Asn Lys Thr Arg Arg Ile Met Glu Gln Gly Gly Ala His Phe Ile Asn
  65             70             75             80

gcc ttc gtg acc aca ccc atg tgc tgc ccc tca cgc tcc tcc atc ctc      468
Ala Phe Val Thr Thr Pro Met Cys Cys Pro Ser Arg Ser Ser Ile Leu
  81             86             91             96

acc ggc aag tac gtc cac aac cac aac acc tac acc aac aat gag aac      516
Thr Gly Lys Tyr Val His Asn His Asn Thr Tyr Thr Asn Asn Glu Asn
  97             102            107            112

tgc tcc tcg ccc tcc tgg cag gca cag cac gag agc cgc acc ttt gcc      564
Cys Ser Ser Pro Ser Trp Gln Ala Gln His Glu Ser Arg Thr Phe Ala
  113            118            123            128

gtg tac ctc aat agc act ggc tac cgg aca gct ttc ttc ggg aag tat      612
Val Tyr Leu Asn Ser Thr Gly Tyr Arg Thr Ala Phe Phe Gly Lys Tyr
  129            134            139            144

ctt aat gaa tac aac ggc tcc tac gtg cca ccc ggc tgg aag gag tgg      660
Leu Asn Glu Tyr Asn Gly Ser Tyr Val Pro Pro Gly Trp Lys Glu Trp
  145            150            155            160

gtc gga ctc ctt aaa aac tcc cgc ttt tat aac tac acg ctg tgt cgg      708
Val Gly Leu Leu Lys Asn Ser Arg Phe Tyr Asn Tyr Thr Leu Cys Arg
  161            166            171            176

aac ggg gtg aaa gag aag cac ggc tcc gac tac tcc aag gat tac ctc      756
Asn Gly Val Lys Glu Lys His Gly Ser Asp Tyr Ser Lys Asp Tyr Leu
  177            182            187            192

```

aca gac ctc atc acc aat gac agc gtg agc ttc ttc cgc acg tcc aag Thr Asp Leu Ile Thr Asn Asp Ser Val Ser Phe Phe Arg Thr Ser Lys 193 198 203 208	804
aag atg tac ccg cac agg cca gtc ctc atg gtc atc agc cat gca gcc Lys Met Tyr Pro His Arg Pro Val Leu Met Val Ile Ser His Ala Ala 209 214 219 224	852
ccc cac ggc cct gag gat tca gcc cca caa tat tca cgc ctc ttc cca Pro His Gly Pro Glu Asp Ser Ala Pro Gln Tyr Ser Arg Leu Phe Pro 225 230 235 240	900
aac gca tct cag cac atc acg ccg agc tac aac tac gcg ccc aac ccg Asn Ala Ser Gln His Ile Thr Pro Ser Tyr Asn Tyr Ala Pro Asn Pro 241 246 251 256	948
gac aaa cac tgg atc atg cgc tac acg ggg ccc atg aag ccc atc cac Asp Lys His Trp Ile Met Arg Tyr Thr Gly Pro Met Lys Pro Ile His 257 262 267 272	996
atg gaa ttc acc aac atg ctc cag cgg aag cgc ttg cag acc ctc atg Met Glu Phe Thr Asn Met Leu Gln Arg Lys Arg Leu Gln Thr Leu Met 273 278 283 288	1044
tcg gtg gac gac tcc atg gag acg att tac aac atg ctg gtt gag acg Ser Val Asp Asp Ser Met Glu Thr Ile Tyr Asn Met Leu Val Glu Thr 289 294 299 304	1092
ggc gag ctg gac aac acg tac atc gta tac acc gcc gac cac ggt tac Gly Glu Leu Asp Asn Thr Tyr Ile Val Tyr Thr Ala Asp His Gly Tyr 305 310 315 320	1140
cac atc ggc cag ttt ggc ctg gtg aaa ggg aaa tcc atg cca tat gag His Ile Gly Gln Phe Gly Leu Val Lys Gly Lys Ser Met Pro Tyr Glu 321 326 331 336	1188
ttt gac atc agg gtc ccg ttc tac gtg agg ggc ccc aac gtg gaa gcc Phe Asp Ile Arg Val Pro Phe Tyr Val Arg Gly Pro Asn Val Glu Ala 337 342 347 352	1236
ggc tgt ctg aat ccc cac atc gtc ctc aac att gac ctg gcc ccc acc Gly Cys Leu Asn Pro His Ile Val Leu Asn Ile Asp Leu Ala Pro Thr 353 358 363 368	1284
atc ctg gac att gca ggc ctg gac ata cct gcg gat atg gac ggg aaa Ile Leu Asp Ile Ala Gly Leu Asp Ile Pro Ala Asp Met Asp Gly Lys 369 374 379 384	1332
tcc atc ctc aag ctg ctg gac acg gag cgg ccg gtg aat cgg ttt cac Ser Ile Leu Lys Leu Leu Asp Thr Glu Arg Pro Val Asn Arg Phe His 385 390 395 400	1380
ttg aaa aag aag atg agg gtc tgg cgg gac tcc ttc ttg gtg gag aga Leu Lys Lys Lys Met Arg Val Trp Arg Asp Ser Phe Leu Val Glu Arg 401 406 411 416	1428

ggc aag ctg cta cac aag aga gac aat gac aag gtg gac gcc cag gag Gly Lys Leu Leu His Lys Arg Asp Asn Asp Lys Val Asp Ala Gln Glu 417 422 427 432	1476
gag aac ttt ctg ccc aag tac cag cgt gtg aag gac ctg tgt cag cgt Glu Asn Phe Leu Pro Lys Tyr Gln Arg Val Lys Asp Leu Cys Gln Arg 433 438 443 448	1524
gct gag tac cag acg gcg tgt gag cag ctg gga cag aag tgg cag tgt Ala Glu Tyr Gln Thr Ala Cys Glu Gln Leu Gly Gln Lys Trp Gln Cys 449 454 459 464	1572
gtg gag gac gcc acg ggg aag ctg aag ctg cat aag tgc aag ggc ccc Val Glu Asp Ala Thr Gly Lys Leu Lys Leu His Lys Cys Lys Gly Pro 465 470 475 480	1620
atg cgg ctg ggc ggc agc aga gcc ctc tcc aac ctc gtg ccc aag tac Met Arg Leu Gly Gly Ser Arg Ala Leu Ser Asn Leu Val Pro Lys Tyr 481 486 491 496	1668
tac ggg cag ggc agc gag gcc tgc acc tgt gac agc ggg gac tac aag Tyr Gly Gln Gly Ser Glu Ala Cys Thr Cys Asp Ser Gly Asp Tyr Lys 497 502 507 512	1716
ctc agc ctg gcc gga cgc cgg aaa aaa ctc ttc aag aag aag tac aag Leu Ser Leu Ala Gly Arg Arg Lys Lys Leu Phe Lys Lys Lys Tyr Lys 513 518 523 528	1764
gcc agc tat gtc cgc agt cgc tcc atc cgc tca gtg gcc atc gag gtg Ala Ser Tyr Val Arg Ser Arg Ser Ile Arg Ser Val Ala Ile Glu Val 529 534 539 544	1812
gac ggc agg gtg tac cac gta ggc ctg ggt gat gcc gcc cag ccc cga Asp Gly Arg Val Tyr His Val Gly Leu Gly Asp Ala Ala Gln Pro Arg 545 550 555 560	1860
aac ctc acc aag cgg cac tgg cca ggg gcc cct gag gac caa gat gac Asn Leu Thr Lys Arg His Trp Pro Gly Ala Pro Glu Asp Gln Asp Asp 561 566 571 576	1908
aag gat ggt ggg gac ttc agt ggc act gga ggc ctt ccc gac tac tca Lys Asp Gly Gly Asp Phe Ser Gly Thr Gly Gly Leu Pro Asp Tyr Ser 577 582 587 592	1956
gcc gcc aac ccc att aaa gtg aca cat cgg tgc tac atc cta gag aac Ala Ala Asn Pro Ile Lys Val Thr His Arg Cys Tyr Ile Leu Glu Asn 593 598 603 608	2004
gac aca gtc cag tgt gac ctg gac ctg tac aag tcc ctg cag gcc tgg Asp Thr Val Gln Cys Asp Leu Asp Leu Tyr Lys Ser Leu Gln Ala Trp 609 614 619 624	2052
aaa gac cac aag ctg cac atc gac cac gag att gaa acc ctg cag aac Lys Asp His Lys Leu His Ile Asp His Glu Ile Glu Thr Leu Gln Asn 625 630 635 640	2100
aaa att aag aac ctg agg gaa gtc cga ggt cac ctg aag aaa aag cgg	2148

Lys Ile Lys Asn Leu Arg Glu Val Arg Gly His Leu Lys Lys Lys Arg	
641 646 651 656	
cca gaa gaa tgt gac tgt cac aaa atc agg aag ggc ctg caa gag aag	2196
Pro Glu Glu Cys Asp Cys His Lys Ile Arg Lys Gly Leu Gln Glu Lys	
657 662 667 672	
gac aag gtg tgg ctg ttg cgg gag cag aag cgc aag aag aaa ctc cgc	2244
Asp Lys Val Trp Leu Leu Arg Glu Gln Lys Arg Lys Lys Lys Leu Arg	
673 678 683 688	
aag ctg ctc aag cgc ctg cag aac aac gac acg tgc agc atg cca ggc	2292
Lys Leu Leu Lys Arg Leu Gln Asn Asn Asp Thr Cys Ser Met Pro Gly	
689 694 699 704	
ctc acg tgc ttc acc cac gac aac cag cac tgg cag acg gcg cct ttc	2340
Leu Thr Cys Phe Thr His Asp Asn Gln His Trp Gln Thr Ala Pro Phe	
705 710 715 720	
tgg aca ctg ggg cct ttc tgt gcc tgc acc agc gcc aac aat aac acg	2388
Trp Thr Leu Gly Pro Phe Cys Ala Cys Thr Ser Ala Asn Asn Asn Thr	
721 726 731 736	
tac tgg tgc atg agg acc atc aat gag act cac aat ttc ctc ttc tgt	2436
Tyr Trp Cys Met Arg Thr Ile Asn Glu Thr His Asn Phe Leu Phe Cys	
737 742 747 752	
gaa ttt gca act ggc ttc cta gag tac ttt gat ctc aac aca gac ccc	2484
Glu Phe Ala Thr Gly Phe Leu Glu Tyr Phe Asp Leu Asn Thr Asp Pro	
753 758 763 768	
tac cag ctg atg aat gca gtg aac aca ctg gac agg gat gtc ctc aac	2532
Tyr Gln Leu Met Asn Ala Val Asn Thr Leu Asp Arg Asp Val Leu Asn	
769 774 779 784	
cag cta cac gta cag ctc atg gag ctg agg agc tgc aag ggt tac aag	2580
Gln Leu His Val Gln Leu Met Glu Leu Arg Ser Cys Lys Gly Tyr Lys	
785 790 795 800	
cag tgt aac ccc cgg act cga aac atg gac ctg gga ctt aaa gat gga	2628
Gln Cys Asn Pro Arg Thr Arg Asn Met Asp Leu Gly Leu Lys Asp Gly	
801 806 811 816	
gga agc tat gag caa tac agg cag ttt cag cgt cga aag tgg cca gaa	2676
Gly Ser Tyr Glu Gln Tyr Arg Gln Phe Gln Arg Arg Lys Trp Pro Glu	
817 822 827 832	
atg aag aga cct tct tcc aaa tca ctg gga caa ctg tgg gaa ggc tgg	2724
Met Lys Arg Pro Ser Ser Lys Ser Leu Gly Gln Leu Trp Glu Gly Trp	
833 838 843 848	
gaa ggt taa gaaacaa cagaggtgga cctccaaaaa catagaggca tcacctgact	2780
Glu Gly *	
849	
gcacaggcaa tgaaaaacca tgtgggtgat ttccagcaga cctgtgctat tggccaggag	2840

```

gcctgagaaa gcaagcacgc actctcagtc aacatgacag attctggagg ataaccagca 2900
ggagcagaga taacttcagg aagtccattt ttgcccctgc ttttgctttg gattatacct 2960
caccagctgc acaaaatgca ttttttcgta tcaaaaagtc accactaacc ctccccaga 3020
agctcacaaa ggaaaacgga gagagcgagc gagagagatt tccttggaag tttctcccaa 3080
gggcgaaagt cattggaatt tttaaactcat aggggaaaag cagtctgtt ctaaactctc 3140
ttattctttt ggtttgtcac aaagaaggaa ctaagaagca ggacagaggc aacgtggaga 3200
ggctgaaaac agtgcagaga cgtttgacaa tgagtcagta gcacaaaaga gatgacattt 3260
acctagcact ataaaccctg gttgcctctg aagaaactgc cttcattgta tatatgtgac 3320
tatttacatg taatcaacat gggaactttt aggggaacct aataagaaat cccaattttc 3380
aggagtggtg gtgtcaataa acgctctgtg gccagtgtaa aagaaaaaaaa aaaaa 3435

```

```

<210> 129
<211> 1260
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (1)..(1260)

```

```

<400> 129

```

```

atg gtc ttc tcg gca gtg ttg act gcg ttc cat acc ggg aca tcc aac 48
Met Val Phe Ser Ala Val Leu Thr Ala Phe His Thr Gly Thr Ser Asn
  1             5             10

aca aca ttt gtc gtg tat gaa aac acc tac atg aat att aca ctc cct 96
Thr Thr Phe Val Val Tyr Glu Asn Thr Tyr Met Asn Ile Thr Leu Pro
 17             22             27             32

cca cca ttc cag cat cct gac ctc agt cca ttg ctt aga tat agt ttt 144
Pro Pro Phe Gln His Pro Asp Leu Ser Pro Leu Leu Arg Tyr Ser Phe
 33             38             43             48

gaa acc atg gct ccc act ggt ttg agt tcc ttg acc gtg aat agt aca 192
Glu Thr Met Ala Pro Thr Gly Leu Ser Ser Leu Thr Val Asn Ser Thr
 49             54             59             64

gct gtg ccc aca aca cca gca gca ttt aag agc cta aac ttg cct ctt 240
Ala Val Pro Thr Thr Pro Ala Ala Phe Lys Ser Leu Asn Leu Pro Leu
 65             70             75             80

cag atc acc ctt tct gct ata atg ata ttc att ctg ttt gtg tct ttt 288
Gln Ile Thr Leu Ser Ala Ile Met Ile Phe Ile Leu Phe Val Ser Phe
 81             86             91             96

```


ctt ggg aac ttg gtt gtt tgc ctc atg gtt tac caa aaa gct gcc atg Leu Gly Asn Leu Val Val Cys Leu Met Val Tyr Gln Lys Ala Ala Met 97 102 107 112	336
agg tct gca att aac atc ctc ctt gcc agc cta gct ttt gca gac atg Arg Ser Ala Ile Asn Ile Leu Leu Ala Ser Leu Ala Phe Ala Asp Met 113 118 123 128	384
ttg ctt gca gtg ctg aac atg ccc ttt gcc ctg gta act att ctt act Leu Leu Ala Val Leu Asn Met Pro Phe Ala Leu Val Thr Ile Leu Thr 129 134 139 144	432
acc cga tgg att ttt ggg aaa ttc ttc tgt agg gta tct gct atg ttt Thr Arg Trp Ile Phe Gly Lys Phe Phe Cys Arg Val Ser Ala Met Phe 145 150 155 160	480
ttc tgg tta ttt gtg ata gaa gga gta gcc atc ctg ctc atc att agc Phe Trp Leu Phe Val Ile Glu Gly Val Ala Ile Leu Leu Ile Ile Ser 161 166 171 176	528
ata gat agg ttc ctt att ata gtc cag agg cag gat aag cta aac cca Ile Asp Arg Phe Leu Ile Ile Val Gln Arg Gln Asp Lys Leu Asn Pro 177 182 187 192	576
tat aga gct aag gtt ctg att gca gtt tct tgg gca act tcc ttt tgt Tyr Arg Ala Lys Val Leu Ile Ala Val Ser Trp Ala Thr Ser Phe Cys 193 198 203 208	624
gta gct ttt cct tta gcc gta gga aac ccc gac ctg cag ata cct tcc Val Ala Phe Pro Leu Ala Val Gly Asn Pro Asp Leu Gln Ile Pro Ser 209 214 219 224	672
cga gct ccc cag tgt gtg ttt ggg tac aca acc aat cca ggc tac cag Arg Ala Pro Gln Cys Val Phe Gly Tyr Thr Thr Asn Pro Gly Tyr Gln 225 230 235 240	720
gct tat gtg att ttg att tct ctc att tct ttc ttc ata ccc ttc ctg Ala Tyr Val Ile Leu Ile Ser Leu Ile Ser Phe Phe Ile Pro Phe Leu 241 246 251 256	768
gta ata ctg tac tca ttt atg ggc ata ctc aac acc ctt cgg cac aat Val Ile Leu Tyr Ser Phe Met Gly Ile Leu Asn Thr Leu Arg His Asn 257 262 267 272	816
gcc ttg agg atc cat agc tac cct gaa ggt ata tgc ctc agc cag gcc Ala Leu Arg Ile His Ser Tyr Pro Glu Gly Ile Cys Leu Ser Gln Ala 273 278 283 288	864
agc aaa ctg ggt ctc atg agt ctg cag aga cct ttc cag atg agc att Ser Lys Leu Gly Leu Met Ser Leu Gln Arg Pro Phe Gln Met Ser Ile 289 294 299 304	912
gac atg ggc ttt aaa aca cgt gcc ttc acc act att ttg att ctc ttt Asp Met Gly Phe Lys Thr Arg Ala Phe Thr Thr Ile Leu Ile Leu Phe 305 310 315 320	960
gct gtc ttc att gtc tgc tgg gcc cca ttc acc act tac agc ctt gtg	1008

Ala Val Phe Ile Val Cys Trp Ala Pro Phe Thr Thr Tyr Ser Leu Val	
321 326 331 336	
gca aca ttc agt aag cac ttt tac tat cag cac aac ttt ttt gag att	1056
Ala Thr Phe Ser Lys His Phe Tyr Tyr Gln His Asn Phe Phe Glu Ile	
337 342 347 352	
agc acc tgg cta ctg tgg ctc tgc tac ctc aag tct gca ttg aat ccg	1104
Ser Thr Trp Leu Leu Trp Leu Cys Tyr Leu Lys Ser Ala Leu Asn Pro	
353 358 363 368	
ctg atc tac tac tgg agg att aag aaa ttc cat gat gct tgc ctg gac	1152
Leu Ile Tyr Tyr Trp Arg Ile Lys Lys Phe His Asp Ala Cys Leu Asp	
369 374 379 384	
atg atg cct aag tcc ttc aag ttt ttg ccg cag ctc cct ggt cac aca	1200
Met Met Pro Lys Ser Phe Lys Phe Leu Pro Gln Leu Pro Gly His Thr	
385 390 395 400	
aag cga cgg ata cgt cct agt gct gtc tat gtg tgt ggg gaa cat cgg	1248
Lys Arg Arg Ile Arg Pro Ser Ala Val Tyr Val Cys Gly Glu His Arg	
401 406 411 416	
acg gtg gtg tga	1260
Thr Val Val *	
417	
<210> 130	
<211> 3836	
<212> DNA	
<213> Homo sapiens	
<220>	
<221> CDS	
<222> (1)..(2835)	
<400> 130	
atg gcg gcg gta gcg gca gtg gcg gcg cgt agg agg cgg tct tgg gcg	48
Met Ala Ala Val Ala Ala Val Ala Ala Arg Arg Arg Ser Trp Ala	
1 5 10	
tct ttg gta ctg gct ttt tta ggg gtc tgc ctg ggg att acc ctt gct	96
Ser Leu Val Leu Ala Phe Leu Gly Val Cys Leu Gly Ile Thr Leu Ala	
17 22 27 32	
gtg gat aga agc aac ttt aag acc tgt gaa gag agt tct ttc tgc aag	144
Val Asp Arg Ser Asn Phe Lys Thr Cys Glu Glu Ser Ser Phe Cys Lys	
33 38 43 48	
cga cag aga agc ata cgg cca ggc ctc tct cca tac cga gcc ttg ctg	192
Arg Gln Arg Ser Ile Arg Pro Gly Leu Ser Pro Tyr Arg Ala Leu Leu	
49 54 59 64	

gac tct cta cag ctt ggt cct gat tcc ctc acg gtc cat ctg atc cat	240
Asp Ser Leu Gln Leu Gly Pro Asp Ser Leu Thr Val His Leu Ile His	
65 70 75 80	
gag gtc acc aag gtg ttg ctg gtg cta gag ctt cag ggg ctt caa aag	288
Glu Val Thr Lys Val Leu Leu Val Leu Glu Leu Gln Gly Leu Gln Lys	
81 86 91 96	
aac atg act cgg ttc agg att gat gag ctg gag cct cgg cga ccc cga	336
Asn Met Thr Arg Phe Arg Ile Asp Glu Leu Glu Pro Arg Arg Pro Arg	
97 102 107 112	
tac cgt gta cca gat gtt ttg gtg gct gat cca cca ata gcc cgg ctt	384
Tyr Arg Val Pro Asp Val Leu Val Ala Asp Pro Pro Ile Ala Arg Leu	
113 118 123 128	
tct gtc tct ggt cgt gat gag aac agt gtg gag tta acc atg gct gag	432
Ser Val Ser Gly Arg Asp Glu Asn Ser Val Glu Leu Thr Met Ala Glu	
129 134 139 144	
gga ccc tac aag atc atc ttg aca gca cgg cca ttc cgc ctt gac cta	480
Gly Pro Tyr Lys Ile Ile Leu Thr Ala Arg Pro Phe Arg Leu Asp Leu	
145 150 155 160	
cta gag gac cga agt ctt ttg ctt agt gtc aat gcc cga gga ctc ttg	528
Leu Glu Asp Arg Ser Leu Leu Leu Ser Val Asn Ala Arg Gly Leu Leu	
161 166 171 176	
gag ttt gag cat cag agg gcc cct agg gtc tcg caa gga tca aaa gac	576
Glu Phe Glu His Gln Arg Ala Pro Arg Val Ser Gln Gly Ser Lys Asp	
177 182 187 192	
cca gct gag ggc gat ggg gcc cag cct gag gaa aca ccc agg gat ggc	624
Pro Ala Glu Gly Asp Gly Ala Gln Pro Glu Glu Thr Pro Arg Asp Gly	
193 198 203 208	
gac aag cca gag gag act cag ggg aag gca gag aaa gat gag cca gga	672
Asp Lys Pro Glu Glu Thr Gln Gly Lys Ala Glu Lys Asp Glu Pro Gly	
209 214 219 224	
gcc tgg gag gag aca ttc aaa act cac tct gac agc aag ccg tat ggc	720
Ala Trp Glu Glu Thr Phe Lys Thr His Ser Asp Ser Lys Pro Tyr Gly	
225 230 235 240	
ccc atg tct gtg ggt ttg gac ttc tct ctg cca ggc atg gag cat gtc	768
Pro Met Ser Val Gly Leu Asp Phe Ser Leu Pro Gly Met Glu His Val	
241 246 251 256	
tat ggg atc cct gag cat gca gac aac ctg agg ctg aag gtc act gag	816
Tyr Gly Ile Pro Glu His Ala Asp Asn Leu Arg Leu Lys Val Thr Glu	
257 262 267 272	
ggt ggg gag cca tat cgc ctc tac aat ttg gat gtg ttc cag tat gag	864
Gly Gly Glu Pro Tyr Arg Leu Tyr Asn Leu Asp Val Phe Gln Tyr Glu	
273 278 283 288	
ctg tac aac cca atg gcc ttg tat ggg tct gtg cct gtg ctc ctg gca	912

Leu 289	Tyr	Asn	Pro	Met	Ala 294	Leu	Tyr	Gly	Ser	Val 299	Pro	Val	Leu	Leu	Ala 304	
cac 305	aac	cct	cat	cgc	gac 310	ttg	ggc	atc	ttc	tgg 315	ctc	aat	gct	gca	gag 320	960
His	Asn	Pro	His	Arg	Asp	Leu	Gly	Ile	Phe	Trp	Leu	Asn	Ala	Ala	Glu	
acc 321	tgg	gtt	gat	ata	tct 326	tcc	aac	act	gcc	ggg 331	aag	acc	ctg	ttt	ggg 336	1008
Thr	Trp	Val	Asp	Ile	Ser	Ser	Asn	Thr	Ala	Gly	Lys	Thr	Leu	Phe	Gly	
aag 337	atg	atg	gac	tac	ctg 342	cag	ggc	tct	ggg	gag 347	acc	cca	cag	aca	gat 352	1056
Lys	Met	Met	Asp	Tyr	Leu	Gln	Gly	Ser	Gly	Glu	Thr	Pro	Gln	Thr	Asp	
gtt 353	cgc	tgg	atg	tca	gag 358	act	ggc	atc	att	gac 363	gtc	ttc	ctg	ctg	ctg 368	1104
Val	Arg	Trp	Met	Ser	Glu	Thr	Gly	Ile	Ile	Asp	Val	Phe	Leu	Leu	Leu	
ggg 369	ccc	tcc	atc	tct	gat 374	gtt	ttc	cgg	caa	tat 379	gct	agt	ctc	aca	gga 384	1152
Gly	Pro	Ser	Ile	Ser	Asp	Val	Phe	Arg	Gln	Tyr	Ala	Ser	Leu	Thr	Gly	
acc 385	cag	gcg	ttg	ccc	cca 390	ctc	ttc	tcc	ctc	ggc 395	tac	cac	cag	agc	cgt 400	1200
Thr	Gln	Ala	Leu	Pro	Pro	Leu	Phe	Ser	Leu	Gly	Tyr	His	Gln	Ser	Arg	
tgg 401	aac	tac	cgg	gac	gag 406	gct	gat	gtg	ctg	gaa 411	gtg	gat	cag	ggc	ttt 416	1248
Trp	Asn	Tyr	Arg	Asp	Glu	Ala	Asp	Val	Leu	Glu	Val	Asp	Gln	Gly	Phe	
gat 417	gat	cac	aac	ctg	ccc 422	tgt	gat	gtc	atc	tgg 427	cta	gac	att	gaa	cat 432	1296
Asp	Asp	His	Asn	Leu	Pro	Cys	Asp	Val	Ile	Trp	Leu	Asp	Ile	Glu	His	
gct 433	gat	ggc	aag	cgg	tat 438	ttc	acc	tgg	gac	ccc 443	agt	cgc	ttc	cct	cag 448	1344
Ala	Asp	Gly	Lys	Arg	Tyr	Phe	Thr	Trp	Asp	Pro	Ser	Arg	Phe	Pro	Gln	
ccc 449	cgc	acc	atg	ctt	gag 454	cgc	ttg	gct	tct	aag 459	agg	cgg	aag	ctg	gtg 464	1392
Pro	Arg	Thr	Met	Leu	Glu	Arg	Leu	Ala	Ser	Lys	Arg	Arg	Lys	Leu	Val	
gcc 465	atc	gta	gac	ccc	cac 470	atc	aag	gtg	gac	tcc 475	ggc	tac	cga	gtt	cac 480	1440
Ala	Ile	Val	Asp	Pro	His	Ile	Lys	Val	Asp	Ser	Gly	Tyr	Arg	Val	His	
gag 481	gag	ctg	cgg	aac	ctg 486	ggg	ctg	tat	gtt	aaa 491	acc	cgg	gat	ggc	tct 496	1488
Glu	Glu	Leu	Arg	Asn	Leu	Gly	Leu	Tyr	Val	Lys	Thr	Arg	Asp	Gly	Ser	
gac 497	tat	gag	ggc	tgg	tgc 502	tgg	cca	ggc	tca	gct 507	ggg	tac	cct	gac	ttc 512	1536
Asp	Tyr	Glu	Gly	Trp	Cys	Trp	Pro	Gly	Ser	Ala	Gly	Tyr	Pro	Asp	Phe	
act 1584	aat	ccc	acg	atg	agg	gcc	tgg	tgg	gct	aac	atg	ttc	agc	tat	gac	
Thr	Asn	Pro	Thr	Met	Arg	Ala	Trp	Trp	Ala	Asn	Met	Phe	Ser	Tyr	Asp	

513		518		523		528	
aat tat gag ggc tca gct ccc aac ctc ttt gtc tgg aat gac atg aac	1632						
Asn Tyr Glu Gly Ser Ala Pro Asn Leu Phe Val Trp Asn Asp Met Asn							
529		534		539		544	
gaa cca tct gtg ttc aat ggt cct gag gtc acc atg ctc aag gat gcc	1680						
Glu Pro Ser Val Phe Asn Gly Pro Glu Val Thr Met Leu Lys Asp Ala							
545		550		555		560	
cag cat tat ggg ggc tgg gag cac cgg gat gtg cat aac atc tat ggc	1728						
Gln His Tyr Gly Gly Trp Glu His Arg Asp Val His Asn Ile Tyr Gly							
561		566		571		576	
ctt tat gtg cac atg gcg act gct gat ggg ctg aga cag cgc tct ggg	1776						
Leu Tyr Val His Met Ala Thr Ala Asp Gly Leu Arg Gln Arg Ser Gly							
577		582		587		592	
ggc atg gaa cgc ccc ttt gtc ctg gcc agg gcc ttc ttc gct ggc tcc	1824						
Gly Met Glu Arg Pro Phe Val Leu Ala Arg Ala Phe Phe Ala Gly Ser							
593		598		603		608	
cag cgc ttt gga gcc gtg tgg aca ggg gac aac act gcc gag tgg gac	1872						
Gln Arg Phe Gly Ala Val Trp Thr Gly Asp Asn Thr Ala Glu Trp Asp							
609		614		619		624	
cat ttg aag atc tct att cct atg tgt ctc agc ttg ggg ctg gtg gga	1920						
His Leu Lys Ile Ser Ile Pro Met Cys Leu Ser Leu Gly Leu Val Gly							
625		630		635		640	
ctt tcc ttc tgt ggg gcg gat gtg ggt ggc ttc ttc aaa aac cca gag	1968						
Leu Ser Phe Cys Gly Ala Asp Val Gly Gly Phe Phe Lys Asn Pro Glu							
641		646		651		656	
cca gag ctg ctt gtg cgc tgg tac cag atg ggt gct tac cag cca ttc	2016						
Pro Glu Leu Leu Val Arg Trp Tyr Gln Met Gly Ala Tyr Gln Pro Phe							
657		662		667		672	
ttc cgg gca cat gcc cac ttg gac act ggg cga cga gag cca tgg ctg	2064						
Phe Arg Ala His Ala His Leu Asp Thr Gly Arg Arg Glu Pro Trp Leu							
673		678		683		688	
tta cca tct cag cac aat gat ata atc cga gat gcc ttg ggc cag cga	2112						
Leu Pro Ser Gln His Asn Asp Ile Ile Arg Asp Ala Leu Gly Gln Arg							
689		694		699		704	
tat tct ttg ctg ccc ttc tgg tac acc ctc tta tat cag gcc cat cgg	2160						
Tyr Ser Leu Leu Pro Phe Trp Tyr Thr Leu Leu Tyr Gln Ala His Arg							
705		710		715		720	
gaa ggc att cct gtc atg agg ccc ctg tgg gtg cag tac cct cag gat	2208						
Glu Gly Ile Pro Val Met Arg Pro Leu Trp Val Gln Tyr Pro Gln Asp							
721		726		731		736	
gtg act acc ttc aat ata gat gat cag tac ttg ctt ggg gat gcg ttg	2256						
Val Thr Thr Phe Asn Ile Asp Asp Gln Tyr Leu Leu Gly Asp Ala Leu							
737		742		747		752	

ctg gtt cac cct gta tca gac tct gga gcc cat ggt gtc cag gtc tat	2304
Leu Val His Pro Val Ser Asp Ser Gly Ala His Gly Val Gln Val Tyr	
753 758 763 768	
ctg cct ggc caa ggg gag gtg tgg tat gac att caa agc tac cag aag	2352
Leu Pro Gly Gln Gly Glu Val Trp Tyr Asp Ile Gln Ser Tyr Gln Lys	
769 774 779 784	
cat cat ggt ccc cag acc ctg tac ctg cct gta act cta agc agt atc	2400
His His Gly Pro Gln Thr Leu Tyr Leu Pro Val Thr Leu Ser Ser Ile	
785 790 795 800	
cct gtg ttc cag cgt gga ggg aca atc gtg cct cga tgg atg cga gtg	2448
Pro Val Phe Gln Arg Gly Gly Thr Ile Val Pro Arg Trp Met Arg Val	
801 806 811 816	
cgg cgg tct tca gaa tgt atg aag gat gac ccc atc act ctc ttt gtt	2496
Arg Arg Ser Ser Glu Cys Met Lys Asp Asp Pro Ile Thr Leu Phe Val	
817 822 827 832	
gca ctt agc cct cag ggt aca gct caa gga gag ctc ttt ctg gat gat	2544
Ala Leu Ser Pro Gln Gly Thr Ala Gln Gly Glu Leu Phe Leu Asp Asp	
833 838 843 848	
ggg cac acg ttc aac tat cag act cgc caa gag ttc ctg ctg cgt cga	2592
Gly His Thr Phe Asn Tyr Gln Thr Arg Gln Glu Phe Leu Leu Arg Arg	
849 854 859 864	
ttc tca ttc tct ggc aac acc ctt gtc tcc agc tca gca gac cct gaa	2640
Phe Ser Phe Ser Gly Asn Thr Leu Val Ser Ser Ser Ala Asp Pro Glu	
865 870 875 880	
gga cac ttt gag aca cca atc tgg att gag cgg gtg gtg ata ata ggg	2688
Gly His Phe Glu Thr Pro Ile Trp Ile Glu Arg Val Val Ile Ile Gly	
881 886 891 896	
gct gga aag cca gca gct gtg gta ctc cag aca aaa gga tct cca gaa	2736
Ala Gly Lys Pro Ala Ala Val Val Leu Gln Thr Lys Gly Ser Pro Glu	
897 902 907 912	
agc cgc ctg tcc ttc cag cat gac cct gag acc tct gtg ttg gtc ctg	2784
Ser Arg Leu Ser Phe Gln His Asp Pro Glu Thr Ser Val Leu Val Leu	
913 918 923 928	
cgc aag cct ggc atc aat gtg gca tct gat tgg agt att cac ctg cga	2832
Arg Lys Pro Gly Ile Asn Val Ala Ser Asp Trp Ser Ile His Leu Arg	
929 934 939 944	
taa ccca agggatgttc tgggttaggg ggaggggaagg ggagcattag tgctgagaga	2889
*	
945	
tattctttct tctgccttgg agttcggccc tccccagact tcaattatgc tagtctaaga	2949
cccagattct gccaacattt gggcaggatg agagggctga ccctgggctc caaattcctc	3009

```

ttgtgatctc ctcacctctc ccactccatt gataccaact ctttcccttc attcccccaa 3069
catcctgttg ctctaactgg agcacattca cttacgaaca ccaggaaacc acagggccct 3129
tgtcgcccoct tctctttccc ttatttagga gccctgaact cccccagagt ctatccattc 3189
atgcctcttg tatgttgatg ccacttcttg gaagaagatg agggcaatga gttagggctc 3249
cttttcccoct tccctcccac cagattgctc tcccaccttt catttcttcc tccaggcttt 3309
actccccctt ttatgcccc aagatacact gggaccaccc cttaccccg acaggatgaa 3369
tggatcaaag gagtgagggt gctaaagaac atccttttcc ctctcattct acccttttcc 3429
tctccccgat tccttgtaga gctgctgcaa ttcttagagg ggcagttcta cctcctctgt 3489
ccctcggcag aaagacgttt ccacacctct taggggatgc gcattaaact tcttttgccc 3549
ccttcttgct cccttgagg ggcacttaag atggagaaat cagttgtggt ttcagtgaat 3609
catggtcacc tgtatttatt gctaggagaa gcctgagggt ggggggagat gatcatgtgt 3669
gctcggggtt ggctggaagc cctgggtggg ggggtggggg aggactaatg gggagtcggg 3729
gaatatttgt gggatatttt tttacttcc tcttggttcc cagctgtgac acgttttgat 3789
caaaggagaa acaataaagg gataaaccat aaataaaaaa aaaaaaa 3836

```

```

<210> 131
<211> 2276
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (99)..(2276)

```

```

<400> 131
gggtggggatc tcgacgttga acgcctgcgg taccgggtccg gaattcccgg gtcgaccac 60

gcgtccgccc acgcgtccgc ccacgcgtcc gcttggac      atg aag acc gag ggg 113
                                   Met Lys Thr Glu Gly
                                   1

ggt aaa gtt ctt tac aaa gtt cgc tgg aaa ggc tat aca tcg gat gat 161
Gly Lys Val Leu Tyr Lys Val Arg Trp Lys Gly Tyr Thr Ser Asp Asp
  6                11                16                21

gat acc tgg gag ccc gag att cac ctg gag gac tgt aaa gaa gtg ctt 209
Asp Thr Trp Glu Pro Glu Ile His Leu Glu Asp Cys Lys Glu Val Leu
  22                27                32                37

ctt gaa ttt agg aag aga att gca gag aac ata gcc aaa gca gtc aag 257
Leu Glu Phe Arg Lys Arg Ile Ala Glu Asn Ile Ala Lys Ala Val Lys

```

38	43	48	53	
aag gat att cag aga cta tcc tta aat aac gac ata ttt gag gcg aac				305
Lys Asp Ile Gln Arg Leu Ser Leu Asn Asn Asp Ile Phe Glu Ala Asn				
54	59	64	69	
tct gat agc gat cag caa agt gag aca aaa gaa gat act tcc cca aag				353
Ser Asp Ser Asp Gln Gln Ser Glu Thr Lys Glu Asp Thr Ser Pro Lys				
70	75	80	85	
aag aaa aag aaa aaa ttg agg cag aga gaa gag aaa agc cca gat gat				401
Lys Lys Lys Lys Lys Leu Arg Gln Arg Glu Glu Lys Ser Pro Asp Asp				
86	91	96	101	
ctg aaa aag aaa aaa gca aag gcc ggg aag cta aaa gac aag tcc aaa				449
Leu Lys Lys Lys Lys Ala Lys Ala Gly Lys Leu Lys Asp Lys Ser Lys				
102	107	112	117	
cca gac ctg gag agc tcc ttg gaa agt tta gtt ttt gat tta agg aca				497
Pro Asp Leu Glu Ser Ser Leu Glu Ser Leu Val Phe Asp Leu Arg Thr				
118	123	128	133	
aag aaa aga att tct gaa gcc aaa gaa gaa cta aag gag tcc aaa aag				545
Lys Lys Arg Ile Ser Glu Ala Lys Glu Glu Leu Lys Glu Ser Lys Lys				
134	139	144	149	
ccc aaa aaa gat gaa gta aaa gaa aca aaa gaa tta aag aaa gtt aaa				593
Pro Lys Lys Asp Glu Val Lys Glu Thr Lys Glu Leu Lys Lys Val Lys				
150	155	160	165	
aag ggt gaa ata aga gat tta aag acg aaa aca aga gaa gat ccc aaa				641
Lys Gly Glu Ile Arg Asp Leu Lys Thr Lys Thr Arg Glu Asp Pro Lys				
166	171	176	181	
gaa aat aga aaa aca aaa aaa gaa aaa ttt gtc gaa tcc cag gtg gaa				689
Glu Asn Arg Lys Thr Lys Lys Glu Lys Phe Val Glu Ser Gln Val Glu				
182	187	192	197	
tct gaa tca agt gta ctt aat gat tct ccc ttt cca gag gat gac agt				737
Ser Glu Ser Ser Val Leu Asn Asp Ser Pro Phe Pro Glu Asp Asp Ser				
198	203	208	213	
gaa ggg cta cat tcc gac agc aga gaa gag aaa caa aac act aaa agt				785
Glu Gly Leu His Ser Asp Ser Arg Glu Glu Lys Gln Asn Thr Lys Ser				
214	219	224	229	
gca aga gag aga gca ggg cag gac atg ggg ctg gag cat ggc ttt gag				833
Ala Arg Glu Arg Ala Gly Gln Asp Met Gly Leu Glu His Gly Phe Glu				
230	235	240	245	
aag ccc cta gac agt gcc atg agt gct gag gag gat acc gat gtc aga				881
Lys Pro Leu Asp Ser Ala Met Ser Ala Glu Glu Asp Thr Asp Val Arg				
246	251	256	261	
ggc agg agg aaa aag aag acc ccg aga aag gct gag gac act aga gag				929
Gly Arg Arg Lys Lys Lys Thr Pro Arg Lys Ala Glu Asp Thr Arg Glu				
262	267	272	277	

aac agg aag cta gag aac aag aac gct ttc tta gag aag aaa act gtg	977
Asn Arg Lys Leu Glu Asn Lys Asn Ala Phe Leu Glu Lys Lys Thr Val	
278 283 288 293	
cct aaa aag cag agg aat caa gac aga agc aaa agt gct gca gag tta	1025
Pro Lys Lys Gln Arg Asn Gln Asp Arg Ser Lys Ser Ala Ala Glu Leu	
294 299 304 309	
gag aag ctg atg cct gta tct gcc caa acg cca aag ggc cgg agg ttg	1073
Glu Lys Leu Met Pro Val Ser Ala Gln Thr Pro Lys Gly Arg Arg Leu	
310 315 320 325	
agc ggg gaa gag aga ggc ctc tgg tcc acg gac tca gcc gag gag gac	1121
Ser Gly Glu Glu Arg Gly Leu Trp Ser Thr Asp Ser Ala Glu Glu Asp	
326 331 336 341	
aaa gaa acc aaa aga aat gaa tcc aaa gaa aaa tat cag aaa agg cat	1169
Lys Glu Thr Lys Arg Asn Glu Ser Lys Glu Lys Tyr Gln Lys Arg His	
342 347 352 357	
gat tct gac aag gaa gaa aaa ggc aga aaa gag cca aaa gga tta aag	1217
Asp Ser Asp Lys Glu Glu Lys Gly Arg Lys Glu Pro Lys Gly Leu Lys	
358 363 368 373	
aaa gcc att ttg gta caa gct tca aca tcc agc tat aga cag tct ggt	1265
Lys Ala Ile Leu Val Gln Ala Ser Thr Ser Ser Tyr Arg Gln Ser Gly	
374 379 384 389	
gtc ttt agc tgt ggg aaa ggt gct ggt gtg act tgg atc act ctg aga	1313
Val Phe Ser Cys Gly Lys Gly Ala Gly Val Thr Trp Ile Thr Leu Arg	
390 395 400 405	
ctc act gcc ttc agt agg cct ttg tca caa ctg cag gaa atc aga aat	1361
Leu Thr Ala Phe Ser Arg Pro Leu Ser Gln Leu Gln Glu Ile Arg Asn	
406 411 416 421	
gca ttt gat tta ttt aaa tta act cca gaa gaa aaa aat gat gtt tct	1409
Ala Phe Asp Leu Phe Lys Leu Thr Pro Glu Glu Lys Asn Asp Val Ser	
422 427 432 437	
gag aat aat cgg aaa agg gaa gaa ata cca ctg gat ttt aaa acc ata	1457
Glu Asn Asn Arg Lys Arg Glu Glu Ile Pro Leu Asp Phe Lys Thr Ile	
438 443 448 453	
gac gat cac aaa acc aag gaa aac aaa cag tca ctt aaa gaa agg aga	1505
Asp Asp His Lys Thr Lys Glu Asn Lys Gln Ser Leu Lys Glu Arg Arg	
454 459 464 469	
aac acc aga gac gaa acg gat act tgg gca tac att gct gca gaa ggt	1553
Asn Thr Arg Asp Glu Thr Asp Thr Trp Ala Tyr Ile Ala Ala Glu Gly	
470 475 480 485	
gat cag gag gtt tta gac agc gtg tgc caa gca gat gag aat tca ggg	1601
Asp Gln Glu Val Leu Asp Ser Val Cys Gln Ala Asp Glu Asn Ser Gly	
486 491 496 501	

gcc aac aga cgc ctc ata cag gag agc tcc ggc tgg cat ctg gcg ggt Ala Asn Arg Arg Leu Ile Gln Glu Ser Ser Gly Trp His Leu Ala Gly 502 507 512 517	1649
gcc cct ctg gga cga agc ttc cag agg aag gaa cag gca gca atc ttt Ala Pro Leu Gly Arg Ser Phe Gln Arg Lys Glu Gln Ala Ala Ile Phe 518 523 528 533	1697
gct gtt ctg cag ctt ccg ctg gtg ata ccc agg caa aca gag tct gga Ala Val Leu Gln Leu Pro Leu Val Ile Pro Arg Gln Thr Glu Ser Gly 534 539 544 549	1745
gat cac aac tcc tcg cca agg gaa caa aac tgg gcg gag aat gag ttt Asp His Asn Ser Ser Pro Arg Glu Gln Asn Trp Ala Glu Asn Glu Phe 550 555 560 565	1793
gac gaa ttg aca gaa gta ggc ttc aga agg tgg gta ata aac tcc tct Asp Glu Leu Thr Glu Val Gly Phe Arg Arg Trp Val Ile Asn Ser Ser 566 571 576 581	1841
gag cta aaa gag cat gtt cta acc caa tgc aag gaa gct aag aac ctt Glu Leu Lys Glu His Val Leu Thr Gln Cys Lys Glu Ala Lys Asn Leu 582 587 592 597	1889
gag aaa agg tta gag gaa ttg ctg act aga ata aca agt tta ggg aag Glu Lys Arg Leu Glu Glu Leu Leu Thr Arg Ile Thr Ser Leu Gly Lys 598 603 608 613	1937
aac aga aat gac ctg atg gag ctg aaa aca cag cac gag aac ttc atg Asn Arg Asn Asp Leu Met Glu Leu Lys Thr Gln His Glu Asn Phe Met 614 619 624 629	1985
aag cat aca caa gta tca ata acg aaa tcg gaa cgc agc tcc tca cca Lys His Thr Gln Val Ser Ile Thr Lys Ser Glu Arg Ser Ser Ser Pro 630 635 640 645	2033
gca acg gaa caa agc tgg atg gag aat gac ttt gac aag ttg aga gaa Ala Thr Glu Gln Ser Trp Met Glu Asn Asp Phe Asp Lys Leu Arg Glu 646 651 656 661	2081
ggc ttc aga cga tca aac tac tcc gag cta aag gag gaa gtt caa acc Gly Phe Arg Arg Ser Asn Tyr Ser Glu Leu Lys Glu Glu Val Gln Thr 662 667 672 677	2129
cat agc aaa gaa gtt aaa aac ctt gaa aaa aga tta gac gaa tgg cta His Ser Lys Glu Val Lys Asn Leu Glu Lys Arg Leu Asp Glu Trp Leu 678 683 688 693	2177
act aga ata acc aat gca gag aag tcc tta aag gac ctg atg gag ctg Thr Arg Ile Thr Asn Ala Glu Lys Ser Leu Lys Asp Leu Met Glu Leu 694 699 704 709	2225
aaa acc aag gca cga gaa cta cgt gac gaa cgc aca agc ctc agt agc Lys Thr Lys Ala Arg Glu Leu Arg Asp Glu Arg Thr Ser Leu Ser Ser 710 715 720 725	2273
tga	2276

*
726

<210> 132
<211> 3672
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (731)..(3451)

<400> 132

ctgatgctgg aattgatcat ggagatctcg tttctgttcc tgggcccgga tcatatccat	60
gaccttccgg ttttcaggga ggcaggtggg gcagtcagca tcactttccg agtaactctc	120
aaagcagtgt tgggtggaagg agtggccaca caggaagtgg actgagggca actccaaggc	180
actgttacag atgctgcact tgggtcttttg gaaaatctta ggatcccaa cccccgccc	240
ctcctttccc cgtttctcca gcagagggcg caggcccaa ggttccgccg accccgcccc	300
agcctggccc cgccccgccc cggcgtaggg gcggggaaga cgggcacaga aacctggccc	360
cggctttccg ggagctgtgg gcacgcgagc tgctcgaagc cgggtggccc gggatcgctg	420
ctgcccagtc cggccgcggc cggccgcttc cccgagctta ccagtaagcc ggtccgcctc	480
cgggacgcgc cccgcccgcc ccgggctcgc gcgctctgaa ggggcgcgtc ccgcgcactc	540
ccggcgccgc ccaactccct cccacgggcc gctcctccct ccgcccggat agccggcggc	600
ggcggcgggc gcggcgggcg cggcgggcggc ggcggccggg agaggcccct ccttcacgcc	660
ctgcttctct ccctcgctcg cagtcgagcc gagccggcgg acccgctgg gctccgacct	720
tgcccaggcc atg gcc ggc aac gtg aag aag agc tct ggg gcc ggg ggc	769
Met Ala Gly Asn Val Lys Lys Ser Ser Gly Ala Gly Gly	
1 5 10	
ggc agc ggc tcc ggg ggc tcg ggt tcg ggt ggc ctg att ggg ctc atg	817
Gly Ser Gly Ser Gly Gly Ser Gly Ser Gly Gly Leu Ile Gly Leu Met	
14 19 24 29	
aag gac gcc ttc cag ccg cac cac cac cac cac cac ctc agc ccc	865
Lys Asp Ala Phe Gln Pro His His His His His His His Leu Ser Pro	
30 35 40 45	
cac ccg ccg ggg acg gtg gac aag aag atg gtg gag aag tgc tgg aag	913
His Pro Pro Gly Thr Val Asp Lys Lys Met Val Glu Lys Cys Trp Lys	
46 51 56 61	

ctc atg gac aag gtg gtg cgg ttg tgt cag aac cca aag ctg gcg cta Leu Met Asp Lys Val Val Arg Leu Cys Gln Asn Pro Lys Leu Ala Leu 62 67 72 77	961
aag aat agc cca cct tat atc tta gac ctg cta cca gat acc tac cag Lys Asn Ser Pro Pro Tyr Ile Leu Asp Leu Leu Pro Asp Thr Tyr Gln 78 83 88 93	1009
cat ctc cgt act atc ttg tca aga tat gag ggg aag atg gag aca ctt His Leu Arg Thr Ile Leu Ser Arg Tyr Glu Gly Lys Met Glu Thr Leu 94 99 104 109	1057
gga gaa aat gag tat ttt agg gtg ttt atg gag aat ttg atg aag aaa Gly Glu Asn Glu Tyr Phe Arg Val Phe Met Glu Asn Leu Met Lys Lys 110 115 120 125	1105
act aag caa acc ata agc ctc ttc aag gag gga aaa gaa aga atg tat Thr Lys Gln Thr Ile Ser Leu Phe Lys Glu Gly Lys Glu Arg Met Tyr 126 131 136 141	1153
gag gag aat tct cag cct agg cga aac cta acc aaa ctg tcc ctc atc Glu Glu Asn Ser Gln Pro Arg Arg Asn Leu Thr Lys Leu Ser Leu Ile 142 147 152 157	1201
ttc agc cac atg ctg gca gaa cta aaa gga atc ttt cca agt gga ctc Phe Ser His Met Leu Ala Glu Leu Lys Gly Ile Phe Pro Ser Gly Leu 158 163 168 173	1249
ttt cag gga gac aca ttt cgg att act aaa gca gat gct gcg gaa ttt Phe Gln Gly Asp Thr Phe Arg Ile Thr Lys Ala Asp Ala Ala Glu Phe 174 179 184 189	1297
tgg aga aaa gct ttt ggg gaa aag aca ata gtc cct tgg aag agc ttt Trp Arg Lys Ala Phe Gly Glu Lys Thr Ile Val Pro Trp Lys Ser Phe 190 195 200 205	1345
cga cag gct cta cat gaa gtg cat ccc atc agt tct ggg ctg gag gcc Arg Gln Ala Leu His Glu Val His Pro Ile Ser Ser Gly Leu Glu Ala 206 211 216 221	1393
atg gct ctg aaa tcc act att gat ctg acc tgc aat gat tat att tcg Met Ala Leu Lys Ser Thr Ile Asp Leu Thr Cys Asn Asp Tyr Ile Ser 222 227 232 237	1441
gtt ttt gaa ttt gac atc ttt acc cga ctc ttt cag ccc tgg tcc tct Val Phe Glu Phe Asp Ile Phe Thr Arg Leu Phe Gln Pro Trp Ser Ser 238 243 248 253	1489
ttg ctc agg aat tgg aac agc ctt gct gta act cat cct ggc tac atg Leu Leu Arg Asn Trp Asn Ser Leu Ala Val Thr His Pro Gly Tyr Met 254 259 264 269	1537
gct ttt ttg acg tat gac gaa gtg aaa gct cgg ctc cag aaa ttc att Ala Phe Leu Thr Tyr Asp Glu Val Lys Ala Arg Leu Gln Lys Phe Ile 270 275 280 285	1585
cac aaa cct ggc agt tat atc ttc cgg ctg agc tgt act cgt ctg ggt	1633

His Lys Pro Gly Ser Tyr Ile Phe Arg Leu Ser Cys Thr Arg Leu Gly	
286 291 296 301	
cag tgg gct att ggg tat gtt act gct gat ggg aac att ctc cag aca	1681
Gln Trp Ala Ile Gly Tyr Val Thr Ala Asp Gly Asn Ile Leu Gln Thr	
302 307 312 317	
atc cct cac aat aaa cct ctc ttc caa gca ctg att gat ggc ttc agg	1729
Ile Pro His Asn Lys Pro Leu Phe Gln Ala Leu Ile Asp Gly Phe Arg	
318 323 328 333	
gaa ggc ttc tat ttg ttt cct gat gga cga aat cag aat cct gat ctg	1777
Glu Gly Phe Tyr Leu Phe Pro Asp Gly Arg Asn Gln Asn Pro Asp Leu	
334 339 344 349	
act ggc tta tgt gaa cca act ccc caa gac cat atc aaa gtg acc cag	1825
Thr Gly Leu Cys Glu Pro Thr Pro Gln Asp His Ile Lys Val Thr Gln	
350 355 360 365	
gaa caa tat gaa tta tac tgt gag atg ggc tcc aca ttc caa cta tgt	1873
Glu Gln Tyr Glu Leu Tyr Cys Glu Met Gly Ser Thr Phe Gln Leu Cys	
366 371 376 381	
aaa ata tgt gct gaa aat gat aag gat gta aag att gag ccc tgt gga	1921
Lys Ile Cys Ala Glu Asn Asp Lys Asp Val Lys Ile Glu Pro Cys Gly	
382 387 392 397	
cac ctc atg tgc aca tcc tgt ctt aca tcc tgg cag gaa tca gaa ggt	1969
His Leu Met Cys Thr Ser Cys Leu Thr Ser Trp Gln Glu Ser Glu Gly	
398 403 408 413	
cag ggc tgt cct ttc tgc cga tgt gaa att aaa ggt act gaa ccc atc	2017
Gln Gly Cys Pro Phe Cys Arg Cys Glu Ile Lys Gly Thr Glu Pro Ile	
414 419 424 429	
gtg gta gat ccg ttt gat cct aga ggg agt ggc agc ctg ttg agg caa	2065
Val Val Asp Pro Phe Asp Pro Arg Gly Ser Gly Ser Leu Leu Arg Gln	
430 435 440 445	
gga gca gag gga gct ccc tcc cca aat tat gat gat gat gat gat gaa	2113
Gly Ala Glu Gly Ala Pro Ser Pro Asn Tyr Asp Asp Asp Asp Asp Glu	
446 451 456 461	
cga gct gat gat act ctc ttc atg atg aag gaa ttg gct ggt gcc aag	2161
Arg Ala Asp Asp Thr Leu Phe Met Met Lys Glu Leu Ala Gly Ala Lys	
462 467 472 477	
gtg gaa cgg ccg cct tct cca ttc tcc atg gcc cca caa gct tcc ctt	2209
Val Glu Arg Pro Pro Ser Pro Phe Ser Met Ala Pro Gln Ala Ser Leu	
478 483 488 493	
ccc ccg gtg cca cca cga ctt gac ctt ctg ccg cag cga gta tgt gtt	2257
Pro Pro Val Pro Pro Arg Leu Asp Leu Leu Pro Gln Arg Val Cys Val	
494 499 504 509	
ccc tca agt gct tct gct ctt gga act gct tct aag gct gct tct ggc	2305
Pro Ser Ser Ala Ser Ala Leu Gly Thr Ala Ser Lys Ala Ala Ser Gly	

510	515										520					525					
tcc ctt cat aaa gac	aaa cca ttg cca gta	cct ccc aca ctt cga	gat	2353																	
Ser Leu His Lys Asp	Lys Pro Leu Pro Val	Pro Pro Thr Leu Arg	Asp																		
526	531										536					541					
ctt cca cca cca ccg	cct cca gac cgg cca	tat tct gtt gga gca	gaa	2401																	
Leu Pro Pro Pro Pro	Pro Pro Asp Arg Pro	Tyr Ser Val Gly Ala	Glu																		
542	547										552					557					
tcc cga cct caa aga	cgc ccc ttg cct tgt	aca cca ggc gac tgt	ccc	2449																	
Ser Arg Pro Gln Arg	Arg Pro Leu Pro Cys	Thr Pro Gly Asp Cys	Pro																		
558	563										568					573					
tcc aga gac aaa ctg	ccc cct gtc ccc tct	agc cgc ctt gga gac	tca	2497																	
Ser Arg Asp Lys Leu	Pro Pro Val Pro Ser	Ser Ser Arg Leu Gly	Asp																		
574	579										584					589					
tgg ctg ccc cgg cca	atc ccc aaa gta cca	gta tct gcc cca agt	tcc	2545																	
Trp Leu Pro Arg Pro	Ile Pro Lys Val Pro	Val Ser Ala Pro Ser	Ser																		
590	595										600					605					
agt gat ccc tgg aca	gga aga gaa tta acc	aac cgg cac tca ctt	cca	2593																	
Ser Asp Pro Trp Thr	Gly Arg Glu Leu Thr	Asn Arg His Ser Leu	Pro																		
606	611										616					621					
ttt tca ttg ccc tca	caa atg gag ccc aga	cca gat gtg cct agg	ctc	2641																	
Phe Ser Leu Pro Ser	Gln Met Glu Pro Arg	Pro Asp Val Pro Arg	Leu																		
622	627										632					637					
gga agc acg ttc agt	ctg gat acc tcc atg	agt atg aat agc agc	cca	2689																	
Gly Ser Thr Phe Ser	Leu Asp Thr Ser Met	Ser Met Asn Ser Ser	Pro																		
638	643										648					653					
tta gta ggt cca gag	tgt gac cac ccc aaa	atc aaa cct tcc tca	tct	2737																	
Leu Val Gly Pro Glu	Cys Asp His Pro Lys	Ile Lys Pro Ser Ser	Ser																		
654	659										664					669					
gcc aat gcc att tat	tct ctg gct gcc aga	cct ctt cct gtg cca	aaa	2785																	
Ala Asn Ala Ile Tyr	Ser Leu Ala Ala Arg	Pro Leu Pro Val Pro	Lys																		
670	675										680					685					
ctg cca cct ggg gag	caa tgt gag ggt gaa	gag gac aca gag tac	atg	2833																	
Leu Pro Pro Gly Glu	Gln Cys Glu Gly Glu	Glu Asp Thr Glu Tyr	Met																		
686	691										696					701					
act ccc tct tcc agg	cct cta cgg cct ttg	gat aca tcc cag agt	tca	2881																	
Thr Pro Ser Ser Arg	Pro Leu Arg Pro Leu	Asp Thr Ser Gln Ser	Ser																		
702	707										712					717					
cga gca tgt gat tgc	gac cag cag att gat	agc tgt acg tat gaa	gca	2929																	
Arg Ala Cys Asp Cys	Asp Gln Gln Ile Asp	Ser Cys Thr Tyr Glu	Ala																		
718	723										728					733					
atg tat aat att cag	tcc cag gcg cca tct	atc acc gag agc agc	acc	2977																	
Met Tyr Asn Ile Gln	Ser Gln Ala Pro Ser	Ile Thr Glu Ser Ser	Thr																		
734	739										744					749					

ttt ggt gaa ggg aat ttg gcc gca gcc cat gcc aac act ggt ccc gag Phe Gly Glu Gly Asn Leu Ala Ala Ala His Ala Asn Thr Gly Pro Glu 750 755 760 765	3025
gag tca gaa aat gag gat gat ggg tat gat gtc cca aag cca cct gtg Glu Ser Glu Asn Glu Asp Asp Gly Tyr Asp Val Pro Lys Pro Pro Val 766 771 776 781	3073
ccg gcc gtg ctg gcc cgc cga act ctc tca gat atc tct aat gcc agc Pro Ala Val Leu Ala Arg Arg Thr Leu Ser Asp Ile Ser Asn Ala Ser 782 787 792 797	3121
tcc tcc ttt ggc tgg ttg tct ctg gat ggt gat cct aca aca aat gtc Ser Ser Phe Gly Trp Leu Ser Leu Asp Gly Asp Pro Thr Thr Asn Val 798 803 808 813	3169
act gaa ggt tcc caa gtt ccc gag agg cct cca aaa cca ttc ccg cgg Thr Glu Gly Ser Gln Val Pro Glu Arg Pro Pro Lys Pro Phe Pro Arg 814 819 824 829	3217
aga atc aac tct gaa cgg aaa gct ggc agc tgt cag caa ggt agt ggt Arg Ile Asn Ser Glu Arg Lys Ala Gly Ser Cys Gln Gln Gly Ser Gly 830 835 840 845	3265
cct gcc gcc tct gct gcc acc gcc tca cct cag ctc tcc agt gag atc Pro Ala Ala Ser Ala Thr Ala Ser Pro Gln Leu Ser Ser Glu Ile 846 851 856 861	3313
gag aac ctc atg agt cag ggg tac tcc tac cag gac atc cag aaa gct Glu Asn Leu Met Ser Gln Gly Tyr Ser Tyr Gln Asp Ile Gln Lys Ala 862 867 872 877	3361
ttg gtc att gcc cag aac aac atc gag atg gcc aaa aac atc ctc cgg Leu Val Ile Ala Gln Asn Asn Ile Glu Met Ala Lys Asn Ile Leu Arg 878 883 888 893	3409
gaa ttt gtt tcc att tct tct cct gcc cat gta gct acc tag cacacca Glu Phe Val Ser Ile Ser Ser Pro Ala His Val Ala Thr *	3458
894 899 904	
tctccctgct gcaggtttag aggaccagtg agttgggagt tattactcaa gtggcaccta	3518
gaagggcagg agttcctttg gtgacttcac agtgaagtct tgccctctct gtgggatatc	3578
acatcagtggt ttccaagatt tcaaagtggg gaaatgaaaa tggagcagct agtatgtttt	3638
attatttttat gggctcttgag tgcatttgaa ggtg	3672

<210> 133
<211> 2865
<212> DNA
<213> Homo sapiens

Regression Statistics	
R	0.999
R Square	0.998
Adjusted R Square	0.997
Standard Error	0.000
Observations	1

ANOVA					
	Sum of Squares	df	Mean Square	F	Sig.
Regression	0.998	1	0.998	1000.000	.000
Residual	0.002	0			
Total	1.000	1			

Coefficients				
	Unstandardized Coefficients	Standardized Coefficients	t	Sig.
(Constant)	0.000			
Dependent Variable	0.999	1.000	1000.000	.000

466

188	193	198	203	
aag ctg gat gcc cag	gcc tct ttc ctg ccg	aag gaa ctg gca gcc caa		734
Lys Leu Asp Ala Gln	Ala Ser Phe Leu Pro	Lys Glu Leu Ala Ala Gln		
204	209	214	219	
act atc aag aag tcc	ttc tca gga aaa aag	ggt cat gtg ctg ttc cgt		782
Thr Ile Lys Lys Ser	Phe Ser Gly Lys Lys	Gly His Val Leu Phe Arg		
220	225	230	235	
ccc acc gtg agc cag	cag cag tcc tgc ccc	aca tgc tct aca tcc tta		830
Pro Thr Val Ser Gln	Gln Gln Ser Cys Pro	Thr Cys Ser Thr Ser Leu		
236	241	246	251	
ctg aac ggg cac ttc	aag gtg acc tac gat	gtc agt cga gac aag atc		878
Leu Asn Gly His Phe	Lys Val Thr Tyr Asp	Val Ser Arg Asp Lys Ile		
252	257	262	267	
tgc gac ctc ctg gtg	gcc aat aac cac ttt	gcc cac ttc ttt gcc ccc		926
Cys Asp Leu Leu Val	Ala Asn Asn His Phe	Ala His Phe Phe Ala Pro		
268	273	278	283	
caa aac ctg aca aac	atg aac aag aac gtg	gtt ttt gtg att gac atc		974
Gln Asn Leu Thr Asn	Met Asn Lys Asn Val	Val Phe Val Ile Asp Ile		
284	289	294	299	
agt ggc tcc atg aga	ggc cag aaa gtg aag	cag acc aag gag gca ctc		1022
Ser Gly Ser Met Arg	Gly Gln Lys Val Lys	Gln Thr Lys Glu Ala Leu		
300	305	310	315	
ctt aaa att ctg ggg	gac atc cac cca ggg	gac tac ttt gac ctg gtt		1070
Leu Lys Ile Leu Gly	Asp Ile His Pro Gly	Asp Tyr Phe Asp Leu Val		
316	321	326	331	
ctt ttt ggg act cga	gta caa tcg tgg aag	ggc tcg ctg gtg caa gca		1118
Leu Phe Gly Thr Arg	Val Gln Ser Trp Lys	Gly Ser Leu Val Gln Ala		
332	337	342	347	
tct gag gcc aac cta	caa gca gct caa gac	ttt gtg cgg ggc ttt tcc		1166
Ser Glu Ala Asn Leu	Gln Ala Ala Gln Asp	Phe Val Arg Gly Phe Ser		
348	353	358	363	
ctg gat gag gcc aca	aac ctg aat gga ggt	ttg ctc cgg gga att gag		1214
Leu Asp Glu Ala Thr	Asn Leu Asn Gly Gly	Leu Leu Arg Gly Ile Glu		
364	369	374	379	
atc ttg aac caa gtt	cag gaa agc ctc cca	gaa ctc agc aac cat gcc		1262
Ile Leu Asn Gln Val	Gln Glu Ser Leu Pro	Glu Leu Ser Asn His Ala		
380	385	390	395	
tca ata ctc atc atg	ttg aca gat ggc gat	ccc aca gag ggg gtg acg		1310
Ser Ile Leu Ile Met	Leu Thr Asp Gly Asp	Pro Thr Glu Gly Val Thr		
396	401	406	411	
gac cgt tcc caa atc	ctc aag aac gtc cgc	aac gcc atc cgg ggc agg		1358
Asp Arg Ser Gln Ile	Leu Lys Asn Val Arg	Asn Ala Ile Arg Gly Arg		
412	417	422	427	

ttc ccg ctc tac aac ctg ggt ttc ggc cac aat gtg gac ttt aac ttt	1406
Phe Pro Leu Tyr Asn Leu Gly Phe Gly His Asn Val Asp Phe Asn Phe	
428 433 438 443	
ctg gag gtc atg tcc atg gag aac aac gga cgg gcc cag aga atc tac	1454
Leu Glu Val Met Ser Met Glu Asn Asn Gly Arg Ala Gln Arg Ile Tyr	
444 449 454 459	
gag gac cat gat gcc acc cag cag ctg cag ggt ttc tac agc cag gta	1502
Glu Asp His Asp Ala Thr Gln Gln Leu Gln Gly Phe Tyr Ser Gln Val	
460 465 470 475	
gcc aaa ccc ctg ctg gtg gat gtg gat ttg cag tac ccc cag gat gct	1550
Ala Lys Pro Leu Leu Val Asp Val Asp Leu Gln Tyr Pro Gln Asp Ala	
476 481 486 491	
gtc ttg gcc ctg acc cag aac cac cat aaa cag tac tac gaa ggc tca	1598
Val Leu Ala Leu Thr Gln Asn His His Lys Gln Tyr Tyr Glu Gly Ser	
492 497 502 507	
gag att gtg gtg gcc ggg cgc att gct gac aac aaa cag agc agc ttc	1646
Glu Ile Val Val Ala Gly Arg Ile Ala Asp Asn Lys Gln Ser Ser Phe	
508 513 518 523	
aag gct gat gtg cag gcc cat ggg gag gga caa gaa ttc agt ata acc	1694
Lys Ala Asp Val Gln Ala His Gly Glu Gly Gln Glu Phe Ser Ile Thr	
524 529 534 539	
tgc cta gtg gat gag gag gag atg aag aaa ctg ctc cga gag cgt ggc	1742
Cys Leu Val Asp Glu Glu Glu Met Lys Lys Leu Leu Arg Glu Arg Gly	
540 545 550 555	
cac atg ctg gag aac cac gtc gag cgc ctc tgg gcc tac ctc acc atc	1790
His Met Leu Glu Asn His Val Glu Arg Leu Trp Ala Tyr Leu Thr Ile	
556 561 566 571	
cag gag ctg ctg gcc aag cgg atg aag gtg gac agg gag gtg agg gcc	1838
Gln Glu Leu Leu Ala Lys Arg Met Lys Val Asp Arg Glu Val Arg Ala	
572 577 582 587	
aac ctg tca tcc cag gcc ctg cgg atg tcg ctg gac tat ggg ttt gtg	1886
Asn Leu Ser Ser Gln Ala Leu Arg Met Ser Leu Asp Tyr Gly Phe Val	
588 593 598 603	
acc cca ctg acc tcc atg agc atc agg ggc atg gcg gac cag gac ggc	1934
Thr Pro Leu Thr Ser Met Ser Ile Arg Gly Met Ala Asp Gln Asp Gly	
604 609 614 619	
ctg aag ccc acc atc gac aag ccc tca gag gat tct ccg cct ttg gag	1982
Leu Lys Pro Thr Ile Asp Lys Pro Ser Glu Asp Ser Pro Pro Leu Glu	
620 625 630 635	
atg ctg gga ccc aga agg acg ttc gtg ctg tca gcc ttg cag cct tct	2030
Met Leu Gly Pro Arg Arg Thr Phe Val Leu Ser Ala Leu Gln Pro Ser	
636 641 646 651	

cct act cat tcc agc tcc aat acc cag cgg ctg cca gac cga gtg acc	2078
Pro Thr His Ser Ser Ser Asn Thr Gln Arg Leu Pro Asp Arg Val Thr	
652 657 662 667	
ggc ggc ttc tca gtg aat gga cag ctc att ggc aac aag gcc agg agc	2126
Gly Gly Phe Ser Val Asn Gly Gln Leu Ile Gly Asn Lys Ala Arg Ser	
668 673 678 683	
cct ggg cag cat gac ggc acg tac ttc ggg cgg ctg gga atc gca aac	2174
Pro Gly Gln His Asp Gly Thr Tyr Phe Gly Arg Leu Gly Ile Ala Asn	
684 689 694 699	
cct gcc acg gac ttt cag ttg gaa gtg act cct cag aac att acg ctg	2222
Pro Ala Thr Asp Phe Gln Leu Glu Val Thr Pro Gln Asn Ile Thr Leu	
700 705 710 715	
aac ccc ggc ttt ggt ggg cct gtg ttt tcc tgg agg gac caa gct gtg	2270
Asn Pro Gly Phe Gly Gly Pro Val Phe Ser Trp Arg Asp Gln Ala Val	
716 721 726 731	
ctg cgg cag gac ggg gtg gtg gtg acc atc aac aag aag agg aac ctg	2318
Leu Arg Gln Asp Gly Val Val Val Thr Ile Asn Lys Lys Arg Asn Leu	
732 737 742 747	
gtg gtg tct gtg gac gac ggt ggc acc ttt gag gtt gtt ttg cac cga	2366
Val Val Ser Val Asp Asp Gly Gly Thr Phe Glu Val Val Leu His Arg	
748 753 758 763	
gtg tgg aag ggg agc tcg gtc cac cag gac ttc ctg ggc ttc tat gtg	2414
Val Trp Lys Gly Ser Ser Val His Gln Asp Phe Leu Gly Phe Tyr Val	
764 769 774 779	
ctg gac agt cat cgg atg tca gcc cgg acg cac ggg ctg ctg ggg caa	2462
Leu Asp Ser His Arg Met Ser Ala Arg Thr His Gly Leu Leu Gly Gln	
780 785 790 795	
ttt ttc cac ccc atc ggt ttt gaa gtg tct gac atc cac cca ggc tct	2510
Phe Phe His Pro Ile Gly Phe Glu Val Ser Asp Ile His Pro Gly Ser	
796 801 806 811	
gac ccc aca aag cca gat gcc acg atg gtg gtg agg aac cgc cgg ctc	2558
Asp Pro Thr Lys Pro Asp Ala Thr Met Val Val Arg Asn Arg Arg Leu	
812 817 822 827	
acg gtc acc agg ggt ttg caa aaa gac tac agc aag gac ccg tgg cat	2606
Thr Val Thr Arg Gly Leu Gln Lys Asp Tyr Ser Lys Asp Pro Trp His	
828 833 838 843	
ggg gcc gag gtg tcc tgc tgg ttc att cac aac aat ggg gct gga ctc	2654
Gly Ala Glu Val Ser Cys Trp Phe Ile His Asn Asn Gly Ala Gly Leu	
844 849 854 859	
atc gat ggt gcc tac act gat tat atc gtc ccc gac atc ttc tga gcc	2702
Ile Asp Gly Ala Tyr Thr Asp Tyr Ile Val Pro Asp Ile Phe *	
860 865 870	
ctctggccag cagcctgtc ctccccggg gccaaaggcag aggaggagga cgacatcctg	2762

acctgctgct gaggtgttac ctccttgact aagctgggtc cttgtgtcaa agcacctcat 2822
gccttccatt aaagagaggc cgtgtccacc caaaaaaaaaaaa aaa 2865

<210> 134
<211> 3336
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (132) .. (1751)

<400> 134
atcgaccac gcgtccggga gcttgcgcca gtctcttcgc ggcgtccacc acttagacgc 60
aagttgctga agccggccgg ggagaagggtg ttgttgccgg agctgagacc gggcggccac 120
agtccgcagg g atg aac ctc gag ttg ctg gag tcc ttt ggg cag aac tat 170
Met Asn Leu Glu Leu Leu Glu Ser Phe Gly Gln Asn Tyr
1 5 10
cca gag gaa gct gat gga act ttg gat tgt atc agc atg gct ttg act 218
Pro Glu Glu Ala Asp Gly Thr Leu Asp Cys Ile Ser Met Ala Leu Thr
14 19 24 29
tgc acc ttt aac agg tgg ggc aca ctg ctt gca gtt ggc tgt aat gat 266
Cys Thr Phe Asn Arg Trp Gly Thr Leu Leu Ala Val Gly Cys Asn Asp
30 35 40 45
ggc cga att gtc atc tgg gat ttc ttg aca aga ggc att gct aaa att 314
Gly Arg Ile Val Ile Trp Asp Phe Leu Thr Arg Gly Ile Ala Lys Ile
46 51 56 61
aaa ttt agt gca cac atc cat cca gtg tgt tct tta tgc tgg agc cga 362
Lys Phe Ser Ala His Ile His Pro Val Cys Ser Leu Cys Trp Ser Arg
62 67 72 77
gat ggt cat aaa ctc gtg agt gct tcc act gat aac ata gtg tca cag 410
Asp Gly His Lys Leu Val Ser Ala Ser Thr Asp Asn Ile Val Ser Gln
78 83 88 93
tgg gat gtt ctt tca ggc gac tgt gac cag agg ttt cga ttc cct tca 458
Trp Asp Val Leu Ser Gly Asp Cys Asp Gln Arg Phe Arg Phe Pro Ser
94 99 104 109
ccc atc tta aaa gtc caa tat cat cca cga gat cag aac aag gtt ctc 506
Pro Ile Leu Lys Val Gln Tyr His Pro Arg Asp Gln Asn Lys Val Leu
110 115 120 125
gtg tgt ccc atg aaa tct gct cct gtc atg ttg acc ctt tca gat tcc 554
Val Cys Pro Met Lys Ser Ala Pro Val Met Leu Thr Leu Ser Asp Ser
126 131 136 141

aaa cat gtt gtt ctg ccg gtg gac gat gac tcc gat ttg aac gtt gtg	602
Lys His Val Val Leu Pro Val Asp Asp Asp Ser Asp Leu Asn Val Val	
142 147 152 157	
gca tct ttt gat agg cga ggg gaa tat att tat acg gga aac gca aaa	650
Ala Ser Phe Asp Arg Arg Gly Glu Tyr Ile Tyr Thr Gly Asn Ala Lys	
158 163 168 173	
ggc aag att ttg gtc cta aaa aca gat tct cag gat ctt gtt gct tcc	698
Gly Lys Ile Leu Val Leu Lys Thr Asp Ser Gln Asp Leu Val Ala Ser	
174 179 184 189	
ttc aga gtg aca act gga aca agc aat acc aca gcc att aag tca att	746
Phe Arg Val Thr Thr Gly Thr Ser Asn Thr Thr Ala Ile Lys Ser Ile	
190 195 200 205	
gag ttt gcc cgg aag ggg agt tgc ttt tta att aac acg gca gat cga	794
Glu Phe Ala Arg Lys Gly Ser Cys Phe Leu Ile Asn Thr Ala Asp Arg	
206 211 216 221	
ata atc aga gtt tat gat ggc aga gaa atc tta aca tgt gga aga gat	842
Ile Ile Arg Val Tyr Asp Gly Arg Glu Ile Leu Thr Cys Gly Arg Asp	
222 227 232 237	
gga gag cct gaa cct atg cag gaa ttg cag gat ttg gtg aat agg acc	890
Gly Glu Pro Glu Pro Met Gln Glu Leu Gln Asp Leu Val Asn Arg Thr	
238 243 248 253	
cca tgg aag aaa tgt tgt ttc tct ggg gat ggg gaa tac atc gtg gca	938
Pro Trp Lys Lys Cys Cys Phe Ser Gly Asp Gly Glu Tyr Ile Val Ala	
254 259 264 269	
ggt tct gcc cgg cag cat gcc ctg tac atc tgg gag aag agc att ggc	986
Gly Ser Ala Arg Gln His Ala Leu Tyr Ile Trp Glu Lys Ser Ile Gly	
270 275 280 285	
aac ctg gtg aag att ctc cat ggg acg aga gga gaa ctc ctc ttg gat	1034
Asn Leu Val Lys Ile Leu His Gly Thr Arg Gly Glu Leu Leu Leu Asp	
286 291 296 301	
gta gct tgg cat cct gtt cga ccc atc ata gca tcc att tcc agt gga	1082
Val Ala Trp His Pro Val Arg Pro Ile Ile Ala Ser Ile Ser Ser Gly	
302 307 312 317	
gtg gta tct atc tgg gca cag aat caa gta gaa aac tgg agt gca ttt	1130
Val Val Ser Ile Trp Ala Gln Asn Gln Val Glu Asn Trp Ser Ala Phe	
318 323 328 333	
gca cca gac ttc aaa gaa ttg gat gaa aat gta gaa tac gaa gaa agg	1178
Ala Pro Asp Phe Lys Glu Leu Asp Glu Asn Val Glu Tyr Glu Glu Arg	
334 339 344 349	
gaa tca ggg ttt gat att gaa gat gaa gat aag agt gag cct gag cag	1226
Glu Ser Gly Phe Asp Ile Glu Asp Glu Asp Lys Ser Glu Pro Glu Gln	
350 355 360 365	

aca ggg gct gat gct gca gaa gat gag gaa gtg gat gtc acc agc gtg Thr Gly Ala Asp Ala Ala Glu Asp Glu Glu Val Asp Val Thr Ser Val 366 371 376 381	1274
gac cct att gct gcc ttc tgt agc agt gat gaa gag ctg gaa gat tca Asp Pro Ile Ala Ala Phe Cys Ser Ser Asp Glu Glu Leu Glu Asp Ser 382 387 392 397	1322
aag gct cta ttg tat tta ccc att gcc cct gag gta gaa gac cca gaa Lys Ala Leu Leu Tyr Leu Pro Ile Ala Pro Glu Val Glu Asp Pro Glu 398 403 408 413	1370
gaa aat cct tac ggc ccc cca ccg gat gca gtc caa acc tcc ttg atg Glu Asn Pro Tyr Gly Pro Pro Pro Asp Ala Val Gln Thr Ser Leu Met 414 419 424 429	1418
gat gaa ggg gct agt tca gag aag aag agg cag tcc tca gca gat ggg Asp Glu Gly Ala Ser Ser Glu Lys Lys Arg Gln Ser Ser Ala Asp Gly 430 435 440 445	1466
tcc cag cca cct aag aag aaa ccc aaa aca acc aat ata gaa ctt caa Ser Gln Pro Pro Lys Lys Lys Pro Lys Thr Thr Asn Ile Glu Leu Gln 446 451 456 461	1514
gga gta cca aat gat gaa gtc cat cca cta ctg ggt gtg aag ggg gat Gly Val Pro Asn Asp Glu Val His Pro Leu Leu Gly Val Lys Gly Asp 462 467 472 477	1562
ggc aaa tcc aag aag aag caa gca ggc cgg cct aaa gga tca aaa ggt Gly Lys Ser Lys Lys Lys Gln Ala Gly Arg Pro Lys Gly Ser Lys Gly 478 483 488 493	1610
aaa gag aaa gat tct cca ttt aaa ccg aaa ctc tac aaa ggg gac aga Lys Glu Lys Asp Ser Pro Phe Lys Pro Lys Leu Tyr Lys Gly Asp Arg 494 499 504 509	1658
ggt tta cct ctg gaa gga tca gcg aag ggt aaa gtg cag gcg gaa ctc Gly Leu Pro Leu Glu Gly Ser Ala Lys Gly Lys Val Gln Ala Glu Leu 510 515 520 525	1706
agc cag ccc ttg aca gca gga gga gca atc tca gaa ctg tta tga aga Ser Gln Pro Leu Thr Ala Gly Gly Ala Ile Ser Glu Leu Leu * 526 531 536	1754
ccttcgaagt tcttcattct ttctcacttt gccatcatgt ggcctctgga cactgtggtc	1814
agtcatttga aaattgactt taatttaaaa caaaggcctg tgccctccac ccaggaggtg	1874
ggaggggtgaa ttttatgttt aaatgaagaa gtgaattatg gaagaagagt atacgacctt	1934
cccttccctt tcaagcataa gtccaaatag actctcagga atgaagattt gtgaagacat	1994
cagataggaa ttttgactca tttaaacttt gatgcttagt tatgttgctg gagaaaagat	2054
acttatgttt tgctcatcta acttcattgt acccagcgtc attttgacat gtcatttcct	2114
atctccatt tgccctcggt cctcaatgca tgtctttgag tgacttctta tctgaaattt	2174

Table 1. Demographic characteristics of the study population	
Age (years)	65.0 ± 10.0
Gender	
Male	100 (50.0%)
Female	100 (50.0%)
Education (years)	12.0 ± 3.0
Marital status	
Married	100 (50.0%)
Single	100 (50.0%)
Occupation	
Retired	100 (50.0%)
Unemployed	100 (50.0%)
Income (USD/month)	1,000.0 ± 500.0
Health status	
Good	100 (50.0%)
Poor	100 (50.0%)
Smoking status	
Smoker	100 (50.0%)
Non-smoker	100 (50.0%)
Alcohol consumption	
Drinker	100 (50.0%)
Non-drinker	100 (50.0%)
Comorbidities	
Hypertension	100 (50.0%)
Diabetes	100 (50.0%)
Cholesterol	100 (50.0%)
Heart disease	100 (50.0%)
Stroke	100 (50.0%)
Arthritis	100 (50.0%)
Depression	100 (50.0%)
Medication use	
Yes	100 (50.0%)
No	100 (50.0%)
Health insurance	
Yes	100 (50.0%)
No	100 (50.0%)
Healthcare access	
Yes	100 (50.0%)
No	100 (50.0%)
Healthcare utilization	
Yes	100 (50.0%)
No	100 (50.0%)
Healthcare satisfaction	
Yes	100 (50.0%)
No	100 (50.0%)
Healthcare access barriers	
Yes	100 (50.0%)
No	100 (50.0%)
Healthcare utilization barriers	
Yes	100 (50.0%)
No	100 (50.0%)
Healthcare satisfaction barriers	
Yes	100 (50.0%)
No	100 (50.0%)
Healthcare access barriers	
Yes	100 (50.0%)
No	100 (50.0%)
Healthcare utilization barriers	
Yes	100 (50.0%)
No	100 (50.0%)
Healthcare satisfaction barriers	
Yes	100 (50.0%)
No	100 (50.0%)
Healthcare access barriers	
Yes	100 (50.0%)
No	100 (50.0%)
Healthcare utilization barriers	
Yes	100 (50.0%)
No	100 (50.0%)
Healthcare satisfaction barriers	
Yes	100 (50.0%)
No	100 (50.0%)
Healthcare access barriers	
Yes	100 (50.0%)
No	100 (50.0%)
Healthcare utilization barriers	
Yes	100 (50.0%)
No	100 (50.0%)
Healthcare satisfaction barriers	
Yes	100 (50.0%)
No	100 (50.0%)
Healthcare access barriers	
Yes	100 (50.0%)
No	100 (50.0%)
Healthcare utilization barriers	
Yes	100 (50.0%)
No	100 (50.0%)
Healthcare satisfaction barriers	
Yes	100 (50.0%)
No	100 (50.0%)
Healthcare access barriers	
Yes	100 (50.0%)
No	100 (50.0%)
Healthcare utilization barriers	
Yes	100 (50.0%)
No	100 (50.0%)
Healthcare satisfaction barriers	
Yes	100 (50.0%)
No	100 (50.0%)
Healthcare access barriers	
Yes	100 (50.0%)
No	100 (50.0%)
Healthcare utilization barriers	
Yes	100 (50.0%)
No	100 (50.0%)
Healthcare satisfaction barriers	
Yes	100 (50.0%)
No	100 (50.0%)
Healthcare access barriers	
Yes	100 (50.0%)
No	100 (50.0%)
Healthcare utilization barriers	
Yes	100 (50.0%)
No	100 (50.0%)
Healthcare satisfaction barriers	
Yes	100 (50.0%)
No	100 (50.0%)
Healthcare access barriers	
Yes	100 (50.0%)
No	100 (50.0%)
Healthcare utilization barriers	
Yes	100 (50.0%)
No	100 (50.0%)
Healthcare satisfaction barriers	
Yes	100 (50.0%)
No	100 (50.0%)
Healthcare access barriers	
Yes	100 (50.0%)
No	100 (50.0%)
Healthcare utilization barriers	
Yes	100 (50.0%)
No	100 (50.0%)
Healthcare satisfaction barriers	
Yes	100 (50.0%)
No	100 (50.0%)
Healthcare access barriers	
Yes	100 (50.0%)
No	100 (50.0%)
Healthcare utilization barriers	
Yes	100 (50.0%)
No	100 (50.0%)
Healthcare satisfaction barriers	
Yes	100 (50.0%)
No	100 (50.0%)
Healthcare access barriers	
Yes	100 (50.0%)
No	100 (50.0%)
Healthcare utilization barriers	
Yes	100 (50.0%)
No	100 (50.0%)
Healthcare satisfaction barriers	
Yes	100 (50.0%)
No	100 (50.0%)
Healthcare access barriers	

Table 1. Demographic characteristics of the study population	
Age (years)	65.0 ± 10.0
Gender	
Male	50%
Female	50%
Education (years)	12.0 ± 2.0
Marital status	
Married	70%
Single	30%
Occupation	
Retired	80%
Unemployed	20%
Health status	
Good	60%
Fair	40%
Poor	10%
Medical history	
Hypertension	45%
Diabetes	35%
Cholesterol	55%
Smoking status	
Smoker	25%
Non-smoker	75%
Alcohol consumption	
Regular	15%
Occasional	35%
Never	50%
Family size	3.5 ± 1.0
Income (USD/month)	1,200 ± 300
Living alone	10%
Living with family	90%
Access to healthcare	
Regular	65%
Irregular	35%
Health insurance	
Yes	85%
No	15%
Medication adherence	
High	70%
Low	30%
Physical activity	
Regular	40%
Irregular	60%
Stress level	
High	30%
Low	70%
Social support	
Strong	60%
Weak	40%
Loneliness	
Yes	20%
No	80%
Depression	
Yes	15%
No	85%
Anxiety	
Yes	25%
No	75%
Quality of life	
High	55%
Low	45%
Life satisfaction	
High	60%
Low	40%
Overall health	
Good	50%
Fair	40%
Poor	10%

act caa cac tac aga att cat act ggt gag aaa ccc tac ata tgt aac	1574
Thr Gln His Tyr Arg Ile His Thr Gly Glu Lys Pro Tyr Ile Cys Asn	
443 448 453 458	
gaa tgt gga aaa gcc ttt cgt ctt caa gga gaa ctt acc cga cat cac	1622
Glu Cys Gly Lys Ala Phe Arg Leu Gln Gly Glu Leu Thr Arg His His	
459 464 469 474	
aga att cat aca tgt gag aaa ccc tat gaa tgt aag gaa tgt ggg aag	1670
Arg Ile His Thr Cys Glu Lys Pro Tyr Glu Cys Lys Glu Cys Gly Lys	
475 480 485 490	
gct ttt att cat agc aat caa ttt att tca cac cag cga att cac acc	1718
Ala Phe Ile His Ser Asn Gln Phe Ile Ser His Gln Arg Ile His Thr	
491 496 501 506	
agt gag agc acc tac ata tgt aaa gaa tgt ggg aag att ttt agt cgt	1766
Ser Glu Ser Thr Tyr Ile Cys Lys Glu Cys Gly Lys Ile Phe Ser Arg	
507 512 517 522	
cgc tat aat ctt act caa cat ttt aaa att cat act ggt gaa aaa ccc	1814
Arg Tyr Asn Leu Thr Gln His Phe Lys Ile His Thr Gly Glu Lys Pro	
523 528 533 538	
tac ata tgt aat gaa tgt ggg aaa gcc ttt cga ttt caa aca gaa ctt	1862
Tyr Ile Cys Asn Glu Cys Gly Lys Ala Phe Arg Phe Gln Thr Glu Leu	
539 544 549 554	
act cag cat cac aga att cat act ggt gaa aaa ccc tat aaa tgt aca	1910
Thr Gln His His Arg Ile His Thr Gly Glu Lys Pro Tyr Lys Cys Thr	
555 560 565 570	
gaa tgt ggg aag gcc ttt att cgt agc act cat ctc acg caa cat cac	1958
Glu Cys Gly Lys Ala Phe Ile Arg Ser Thr His Leu Thr Gln His His	
571 576 581 586	
aga att cat act ggt gag aaa ccc tac gaa tgt acg gaa tgt ggg aag	2006
Arg Ile His Thr Gly Glu Lys Pro Tyr Glu Cys Thr Glu Cys Gly Lys	
587 592 597 602	
acg ttt agt cgg cac tat cat ctt act caa cat cac aga ggc cat act	2054
Thr Phe Ser Arg His Tyr His Leu Thr Gln His His Arg Gly His Thr	
603 608 613 618	
ggt gag aag ccc tac ata tgt aat gaa tgt ggg aat gct ttt att tgc	2102
Gly Glu Lys Pro Tyr Ile Cys Asn Glu Cys Gly Asn Ala Phe Ile Cys	
619 624 629 634	
agt tat cga ctt aca tta cat caa aga att cac act ggt gag ctt cca	2150
Ser Tyr Arg Leu Thr Leu His Gln Arg Ile His Thr Gly Glu Leu Pro	
635 640 645 650	
tat gaa tgt aag gaa tgt gga aag acc ttt agt cgt cgg tat cat ctt	2198
Tyr Glu Cys Lys Glu Cys Gly Lys Thr Phe Ser Arg Arg Tyr His Leu	
651 656 661 666	

act caa cat ttt aga ctt cat act ggt gag aaa cct tat agc tgt aaa	2246
Thr Gln His Phe Arg Leu His Thr Gly Glu Lys Pro Tyr Ser Cys Lys	
667 672 677 682	
 gaa tgt ggg aat gcc ttt cgt ctt caa gca gaa ctt act cga cat cac	 2294
Glu Cys Gly Asn Ala Phe Arg Leu Gln Ala Glu Leu Thr Arg His His	
683 688 693 698	
 ata gtt cac acg ggt gag aaa ccc tat aaa tgt aaa gaa tgt ggg aaa	 2342
Ile Val His Thr Gly Glu Lys Pro Tyr Lys Cys Lys Glu Cys Gly Lys	
699 704 709 714	
 gcc ttc agt gtt aat tca gaa ctt act cga cat cac aga att cat act	 2390
Ala Phe Ser Val Asn Ser Glu Leu Thr Arg His His Arg Ile His Thr	
715 720 725 730	
 ggt gaa aaa ccc tat caa tgt aaa gaa tgt gga aaa gcc ttt att cgt	 2438
Gly Glu Lys Pro Tyr Gln Cys Lys Glu Cys Gly Lys Ala Phe Ile Arg	
731 736 741 746	
 agt gat caa ctt act tta cat cag aga aat cat att agt gag gaa gtc	 2486
Ser Asp Gln Leu Thr Leu His Gln Arg Asn His Ile Ser Glu Glu Val	
747 752 757 762	
 cta tgc ata atg taa agagaatacg atggccttta gaaaatgccc tttagcagag	 2541
Leu Cys Ile Met *	
763	
 aatttgtaat ttaagaaatt ttctgtttgt tacggaacat gtgggaatcc cttttacttc	 2601
atgctcacaa tttatcagaa attatttcgt atgttaaaga gtcgaaaga	2650
 <210> 136	
<211> 791	
<212> DNA	
<213> Homo sapiens	
 <220>	
<221> CDS	
<222> (208) .. (738)	
 <400> 136	
tgcttatttt tcccttaact actccagtgt tttggcattt ttgccttttg agtgaggggc	60
ttcccagcct gggactgggg aaggactaat tcagagagtc tctgtccaca gactgatgct	120
gagaagcact cacaggtgga gaggaattcc ctgtggtctg gtgatgatgt caagaaatca	180
gacggaggct cagacagcgg cataaaa atg gag cca ggt tcc aag tgg agg	231
Met Glu Pro Gly Ser Lys Trp Arg	
1 5	
 cgg aat cct tct gat gtg tct gac gag tcc gac aaa agc acg tcg ggc	 279
Arg Asn Pro Ser Asp Val Ser Asp Glu Ser Asp Lys Ser Thr Ser Gly	

9	14	19	24	
aag aag aat cct gtc atc tcc cag aca ggc tca tgg cgg cga ggc atg				327
Lys Lys Asn Pro Val Ile Ser Gln Thr Gly Ser Trp Arg Arg Gly Met				
25	30	35	40	
aca gct cag gtg ggc atc acc atg cca agg acg aag gct tca gcc ccg				375
Thr Ala Gln Val Gly Ile Thr Met Pro Arg Thr Lys Ala Ser Ala Pro				
41	46	51	56	
gca ggc gca ctg aag acc cca gga act ggt aag agg ccg ggg ctg tct				423
Ala Gly Ala Leu Lys Thr Pro Gly Thr Gly Lys Arg Pro Gly Leu Ser				
57	62	67	72	
tgg ccc tgg ggc acc aac gcc agc agc tcc tcc gca gtt agc aag gat				471
Trp Pro Trp Gly Thr Asn Ala Ser Ser Ser Ser Ala Val Ser Lys Asp				
73	78	83	88	
ggc ctg ggc ttt cag tct gtc agc agc ctc cac acc agc tgt gag tcc				519
Gly Leu Gly Phe Gln Ser Val Ser Ser Leu His Thr Ser Cys Glu Ser				
89	94	99	104	
atc gac atc tcc ctc agc agt gga ggg gtc ccc agc cac aat tct tcc				567
Ile Asp Ile Ser Leu Ser Ser Gly Gly Val Pro Ser His Asn Ser Ser				
105	110	115	120	
act ggc ctc atc gcc tcc tcc aag gac gac tcc ttg act ccc ttt gtc				615
Thr Gly Leu Ile Ala Ser Ser Lys Asp Asp Ser Leu Thr Pro Phe Val				
121	126	131	136	
aga act aac agt gtg aag acc aca ctg tca gaa agg ttg gtg ctg tgc				663
Arg Thr Asn Ser Val Lys Thr Thr Leu Ser Glu Arg Leu Val Leu Cys				
137	142	147	152	
ctc tgg ctg cct ttc tca gaa aga cac cct tcc aaa aat aaa aag att				711
Leu Trp Leu Pro Phe Ser Glu Arg His Pro Ser Lys Asn Lys Lys Ile				
153	158	163	168	
agc tta gga atc cca aat gtc gaa tag ccttt gcctgtaaga tttctcctcg				763
Ser Leu Gly Ile Pro Asn Val Glu *				
169	174			
tgccgaatct cttgctcgag ggccaaat				791

<210> 137
 <211> 3277
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (145) .. (792)

 <400> 137

cacctttcgg aattcccggg tcgacgattt cgtgggggag acggagcccc aggagtgttg	60
aagcctggaa atccccctccc ctttcccctc ccccctttac agtatcccccc tccctccacc	120
ctttcccatt ctgataatct ggcc atg act agc aga agc aca gct agg ccc	171
Met Thr Ser Arg Ser Thr Ala Arg Pro	
1 5	
aat ggg caa ccc cag gcc agc aaa att tgc cag ttc aaa ttg gtc ctg	219
Asn Gly Gln Pro Gln Ala Ser Lys Ile Cys Gln Phe Lys Leu Val Leu	
10 15 20 25	
ctg gga gaa tct gca gtg gga aag tca agc ctg gta tta cgt ttt gtc	267
Leu Gly Glu Ser Ala Val Gly Lys Ser Ser Leu Val Leu Arg Phe Val	
26 31 36 41	
aaa ggg cag ttc cat gag tac cag gag agc acc att gga gcg gcc ttc	315
Lys Gly Gln Phe His Glu Tyr Gln Glu Ser Thr Ile Gly Ala Ala Phe	
42 47 52 57	
ctc acc cag tcc gtt tgt cta gat gac aca aca gtg aag ttt gag atc	363
Leu Thr Gln Ser Val Cys Leu Asp Asp Thr Thr Val Lys Phe Glu Ile	
58 63 68 73	
tgg gac aca gct ggg cag gag cga tat cac agc tta gcc ccc atg tac	411
Trp Asp Thr Ala Gly Gln Glu Arg Tyr His Ser Leu Ala Pro Met Tyr	
74 79 84 89	
tac agg ggt gcc caa gct gca atc gtg gtt tac gac att act aat cag	459
Tyr Arg Gly Ala Gln Ala Ala Ile Val Val Tyr Asp Ile Thr Asn Gln	
90 95 100 105	
gaa acc ttt gcc cga gca aag aca tgg gtg aag gaa cta cag cga cag	507
Glu Thr Phe Ala Arg Ala Lys Thr Trp Val Lys Glu Leu Gln Arg Gln	
106 111 116 121	
gcc agt cct agc atc gtt att gcc ctg gca ggg aac aaa gct gac ctg	555
Ala Ser Pro Ser Ile Val Ile Ala Leu Ala Gly Asn Lys Ala Asp Leu	
122 127 132 137	
gcc aac aaa cgt atg gtg gag tat gaa gag gcc cag gca tat gca gat	603
Ala Asn Lys Arg Met Val Glu Tyr Glu Glu Ala Gln Ala Tyr Ala Asp	
138 143 148 153	
gac aac agc tta ttg ttc atg gag act tca gcc aag aca gct atg aac	651
Asp Asn Ser Leu Leu Phe Met Glu Thr Ser Ala Lys Thr Ala Met Asn	
154 159 164 169	
gtg aat gat ctc ttc ctg gca ata gct aag aag ttg cca aag agt gaa	699
Val Asn Asp Leu Phe Leu Ala Ile Ala Lys Lys Leu Pro Lys Ser Glu	
170 175 180 185	
ccc cag aat ctg gga ggt gca gca ggc cga agc cgg ggt gtg gat ctc	747
Pro Gln Asn Leu Gly Gly Ala Ala Gly Arg Ser Arg Gly Val Asp Leu	
186 191 196 201	
cat gaa cag tcc cag cag aac aag agc cag tgt tgt agc aac tga ggg	795

His Glu Gln Ser Gln Gln Asn Lys Ser Gln Cys Cys Ser Asn *
 202 207 212

ggtggctagc	agcaaacaag	tatggagcta	gcacaagagc	taagaaataa	cctccatccc	855
taccctcag	cacacaaccc	ctacggtaac	agcacactga	gccctggctc	ccaagggctg	915
cctcctgaca	gctccgtcat	ggcacttttt	aacgcttcag	caacaaacac	caggcagctg	975
ttgccactgg	cctcctaccc	cctactctgg	ggcttggggg	tcaactcccc	ccaggactta	1035
ccttccaaaa	caaactttct	tcactttgta	ttataggtac	aagacagcga	cttacgtatc	1095
ttttctctct	ctccctagt	ttcctcccca	ttttttcaga	aaacacttct	gactcctgtc	1155
ccttccccct	ctgcttttgg	tcagtcctct	ttcttgagcc	tctttttctc	tctccccagg	1215
atgcagaaa	tggtgaaccc	aggaactgag	gaaggaggtt	tccagttcat	ttacattaag	1275
ggccctgggg	gagaataaag	ctcagagcag	gagggagtaa	ggaaacattt	cctttttggt	1335
tttatttggt	tggagtttct	catatttgaa	aacattgcgg	tatccatgat	ttggccttgt	1395
ggaggggtgt	cctaggtaga	ggtgagaatg	gggaggcaag	atctcaggca	ccaggcagga	1455
ggtgccttgt	aagctaactg	ggcggaggtg	gaggtgcagt	gtcaactgtg	gctctgtaac	1515
tcttcaaagg	cccagtttcc	cctcacgcag	cctcttaggt	agcgtttccc	ctaatacgtg	1575
gggttggacc	ccagagtctt	ccaaagaatt	ttactgggtt	gcctgcatct	ttggctctgc	1635
tgtgatctga	ttggaggagg	gacagtttct	ggtacccatc	ctctgattta	tacatatgca	1695
ttttttcccc	tctggccttt	agatggcctc	agccccagcc	accatatacc	cctgcagttt	1755
gcactttaat	tgatggtagt	tcagttgggg	tacttgtttt	atggaagttt	tgattgattt	1815
acttgccctc	ccaccttctt	tttaattcaa	tgaaatctga	ggttaatgcg	aggttcgagg	1875
agaggttata	gataaaacta	ccagtggcag	ctactcaagt	cctatctoca	ctgttagctt	1935
cctccaactc	taattattaa	cctatattct	tgccaagcta	actattgact	ataggtttgc	1995
ctttcctgga	gaattaattg	agcaattgag	gagtgtctca	ggatagcaca	ggccaaggta	2055
ggggagtaaa	aaggagggtca	ggcaaaagg	aggagttttc	tgtcctttcc	caggtttcac	2115
actcaatttg	atatccatta	ccatgtcttt	tctacttctt	tgtaaataagg	tatgatcttt	2175
attcccactg	tacagtctgt	tctatcctct	gcctcccatc	aggccctggt	tctttgttcc	2235
tttgtaata	tcttgaattt	agtccctcca	tccttaatcc	ccccatccct	ccccatcatg	2295
caaccagtgg	tttaatccat	gtaccaatag	gggctagtag	cacagaggcc	tcctgtgggtg	2355
ccctcgtatc	ataccacctg	ttcctgtgga	gaggggaatga	ccggcactga	aggtacctta	2415

```

caactggctc atattatcag aggaccttgg tcctttctaa atctctagtc tctcttcata 2475
tccttcatca ggtgttttaa gatgtctctg agaagccatc aaggcaaaag agaactttaa 2535
gttccttggt ccagcccga gttttgggaa agaaagaaag gaaagggtcac agtgacctag 2595
gattggaacc ttctgtccct tttggcttgc agactgcctt ctatcccaga acagctgaga 2655
aatctatgaa gctgagattc tgaaggacc agcttagggt cttccactta ggccctcaatt 2715
cccttccttt tccaggggca gccttagttc ccatggccct gaaacacaca catttcccc 2775
ttcctttccc agaagccact ggccccccat agcaccaggt gcatcctttt tacaagtgga 2835
agaactagga tggctttcca aagtcttcta gaaatgaagt tctttctctg tgcagctttc 2895
ccccttgag caggagtga gatgtttcat tatcttgggc ctgggaaacc acttccccag 2955
gcttctccct cccccaccc ccataggaac aggatttggc cttagcttct gggcctatcg 3015
gctgccttcc ctctacttcc taccacctct tctgccttcc tttgagctct gttgggcttg 3075
gggatcttag ttttcttttg tttatttccc agctcatttt tttcttctgg tcagtttttt 3135
taaggggggg tgttggtggt ttttgttttt gttttgcttc tgagaaagca tttgcctttc 3195
ttcctctccc aacataacaa tcgtggtaac agaatgcgac tgctgattta ccgatgtatt 3255
taatgtaagt aaaaaaaaaa aa 3277

```

```

<210> 138
<211> 2818
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (75)..(2468)

```

```

<400> 138
gaattccgga caggacgtga agatagttgg gtttggaggc ggccgccagg ccagggcccg 60

gtggacctgc cgcc atg cag gac ggt aac ttc ctg ctg tcg gcc ctg cag 110
Met Gln Asp Gly Asn Phe Leu Leu Ser Ala Leu Gln
1 5 10

cct gag gcc ggc gtg tgc tcc ctg gcg ctg ccc tct gac ctg cag ctg 158
Pro Glu Ala Gly Val Cys Ser Leu Ala Leu Pro Ser Asp Leu Gln Leu
13 18 23 28

gac cgc cgg ggc gcc gag ggg ccg gag gcc gag cgg ctg cgg gca gcc 206
Asp Arg Arg Gly Ala Glu Gly Pro Glu Ala Glu Arg Leu Arg Ala Ala
29 34 39 44

```

cgc gtc cag gag cag gtc cgc gcc cgc ctc ttg cag ctg gga cag cag	254
Arg Val Gln Glu Gln Val Arg Ala Arg Leu Leu Gln Leu Gly Gln Gln	
45 50 55 60	
ccg cgg cac aac ggg gcc gct gag ccc gag cct gag gcc gag act gcc	302
Pro Arg His Asn Gly Ala Ala Glu Pro Glu Pro Glu Ala Glu Thr Ala	
61 66 71 76	
aga ggc aca tcc agg ggg cag tac cac acc ctg cag gct ggc ttc agc	350
Arg Gly Thr Ser Arg Gly Gln Tyr His Thr Leu Gln Ala Gly Phe Ser	
77 82 87 92	
tct cgc tct cag ggc ctg agt ggg gac aag acc tcg ggc ttc cgg ccc	398
Ser Arg Ser Gln Gly Leu Ser Gly Asp Lys Thr Ser Gly Phe Arg Pro	
93 98 103 108	
atc gcc aag ccg gcc tac agc cca gcc tcc tgg tcc tcc cgc tcc gcc	446
Ile Ala Lys Pro Ala Tyr Ser Pro Ala Ser Trp Ser Ser Arg Ser Ala	
109 114 119 124	
gtg gat ctg agc tgc agt cgg agg ctg agt tca gcc cac aac ggg ggc	494
Val Asp Leu Ser Cys Ser Arg Arg Leu Ser Ser Ala His Asn Gly Gly	
125 130 135 140	
agc gcc ttt ggg gcc gct ggg tac ggg ggt gcc cag ccc acc cct ccc	542
Ser Ala Phe Gly Ala Ala Gly Tyr Gly Gly Ala Gln Pro Thr Pro Pro	
141 146 151 156	
atg ccc acc agg ccc gtg tcc ttc cat gag cgc ggt ggg gtt ggg agc	590
Met Pro Thr Arg Pro Val Ser Phe His Glu Arg Gly Gly Val Gly Ser	
157 162 167 172	
cgg gcc gac tat gac aca ctc tcc ctg cgc tcg ctg cgg ctg ggg ccc	638
Arg Ala Asp Tyr Asp Thr Leu Ser Leu Arg Ser Leu Arg Leu Gly Pro	
173 178 183 188	
ggg ggc ctg gac gac cgc tac agc ctg gtg tct gag cag ctg gag ccc	686
Gly Gly Leu Asp Asp Arg Tyr Ser Leu Val Ser Glu Gln Leu Glu Pro	
189 194 199 204	
gcg gcc acc tcc acc tac agg gcc ttt gcg tac gag cgc cag gcc agc	734
Ala Ala Thr Ser Thr Tyr Arg Ala Phe Ala Tyr Glu Arg Gln Ala Ser	
205 210 215 220	
tcc agc tcc agc cgg gca ggg ggg ctg gac tgg ccc gag gcc act gag	782
Ser Ser Ser Ser Arg Ala Gly Gly Leu Asp Trp Pro Glu Ala Thr Glu	
221 226 231 236	
gtt tcc ccg agc cgg acc atc cgt gcc cct gcc gtg cgg acc ctg cag	830
Val Ser Pro Ser Arg Thr Ile Arg Ala Pro Ala Val Arg Thr Leu Gln	
237 242 247 252	
cga ttc cag agc agc cac cgg agc cgc ggg gta ggc ggg gca gtg ccg	878
Arg Phe Gln Ser Ser His Arg Ser Arg Gly Val Gly Gly Ala Val Pro	
253 258 263 268	
ggg gcc gtc ctg gag cca gtg gct cga gcg cca tct gtg cgc agc ctc	926

Gly	Ala	Val	Leu	Glu	Pro	Val	Ala	Arg	Ala	Pro	Ser	Val	Arg	Ser	Leu	
269					274					279					284	
agc	ctc	agc	ctg	gct	gac	tcg	ggc	cac	ctg	ccg	gac	gtg	cat	ggg	ttc	974
Ser	Leu	Ser	Leu	Ala	Asp	Ser	Gly	His	Leu	Pro	Asp	Val	His	Gly	Phe	
285					290					295					300	
aac	agc	tac	ggg	agc	cac	cga	acc	ctg	cag	aga	ctc	agc	agc	ggg	ttt	1022
Asn	Ser	Tyr	Gly	Ser	His	Arg	Thr	Leu	Gln	Arg	Leu	Ser	Ser	Gly	Phe	
301					306					311					316	
gat	gac	att	gac	ctg	ccc	tca	gca	gtc	aag	tac	ctc	atg	gct	tca	gac	1070
Asp	Asp	Ile	Asp	Leu	Pro	Ser	Ala	Val	Lys	Tyr	Leu	Met	Ala	Ser	Asp	
317					322					327					332	
ccc	aac	ctg	cag	gtg	ctg	gga	gcg	gcc	tac	atc	cag	cac	aag	tgc	tac	1118
Pro	Asn	Leu	Gln	Val	Leu	Gly	Ala	Ala	Tyr	Ile	Gln	His	Lys	Cys	Tyr	
333					338					343					348	
agc	gat	gca	gcc	gcc	aag	aag	cag	gcc	cgc	agc	ctt	cag	gcc	gtg	cct	1166
Ser	Asp	Ala	Ala	Ala	Lys	Lys	Gln	Ala	Arg	Ser	Leu	Gln	Ala	Val	Pro	
349					354					359					364	
agg	ctg	gtg	aag	ctc	ttc	aac	cac	gcc	aac	cag	gaa	gtg	cag	cgc	cat	1214
Arg	Leu	Val	Lys	Leu	Phe	Asn	His	Ala	Asn	Gln	Glu	Val	Gln	Arg	His	
365					370					375					380	
gcc	aca	ggg	gcc	atg	cgc	aac	ctc	atc	tac	gac	aac	gct	gac	aac	aag	1262
Ala	Thr	Gly	Ala	Met	Arg	Asn	Leu	Ile	Tyr	Asp	Asn	Ala	Asp	Asn	Lys	
381					386					391					396	
ctg	gcc	ctg	gtg	gag	gag	aac	ggg	atc	ttc	gag	ctg	ctg	cgg	aca	ctg	1310
Leu	Ala	Leu	Val	Glu	Glu	Asn	Gly	Ile	Phe	Glu	Leu	Leu	Arg	Thr	Leu	
397					402					407					412	
cgg	gag	cag	gat	gat	gag	ctt	cgc	aaa	aat	gtc	aca	ggg	atc	ctg	tgg	1358
Arg	Glu	Gln	Asp	Asp	Glu	Leu	Arg	Lys	Asn	Val	Thr	Gly	Ile	Leu	Trp	
413					418					423					428	
aac	ctt	tca	tcc	agc	gac	cac	ctg	aag	gac	cgc	ctg	gcc	aga	gac	acg	1406
Asn	Leu	Ser	Ser	Ser	Asp	His	Leu	Lys	Asp	Arg	Leu	Ala	Arg	Asp	Thr	
429					434					439					444	
ctg	gag	cag	ctc	aca	gac	ctg	gtg	ttg	agc	ccc	ctg	tcg	ggg	gct	ggg	1454
Leu	Glu	Gln	Leu	Thr	Asp	Leu	Val	Leu	Ser	Pro	Leu	Ser	Gly	Ala	Gly	
445					450					455					460	
ggg	ccc	ccc	ctc	atc	cag	cag	aac	gcc	tcg	gag	gcg	gag	atc	ttc	tac	1502
Gly	Pro	Pro	Leu	Ile	Gln	Gln	Asn	Ala	Ser	Glu	Ala	Glu	Ile	Phe	Tyr	
461					466					471					476	
aac	gcc	acc	ggc	ttc	ctc	agg	aac	ctc	agc	tca	gcc	tct	cag	gcc	act	1550
Asn	Ala	Thr	Gly	Phe	Leu	Arg	Asn	Leu	Ser	Ser	Ala	Ser	Gln	Ala	Thr	
477					482					487					492	
cgc	cag	aag	atg	cgg	gag	tgc	cac	ggg	ctg	gtg	gac	gcc	ctg	gtc	acc	1598
Arg	Gln	Lys	Met	Arg	Glu	Cys	His	Gly	Leu	Val	Asp	Ala	Leu	Val	Thr	

493		498		503		508	
tct atc aac cac gcc ctg gac gcg ggc aaa tgc gag gac aag agc gtg	1646						
Ser Ile Asn His Ala Leu Asp Ala Gly Lys Cys Glu Asp Lys Ser Val							
509		514		519		524	
gag aac gcg gtg tgc gtc ctg cgg aac ctg tcc tac cgc ctc tac gac	1694						
Glu Asn Ala Val Cys Val Leu Arg Asn Leu Ser Tyr Arg Leu Tyr Asp							
525		530		535		540	
gag atg ccg ccg tcc gcg ctg cag cgg ctg gag ggt cgc ggc cgc agg	1742						
Glu Met Pro Pro Ser Ala Leu Gln Arg Leu Glu Gly Arg Gly Arg Arg							
541		546		551		556	
gac ctg gcg ggg gcg ccg ccg gga gag gtc gtg ggc tgc ttc acg ccg	1790						
Asp Leu Ala Gly Ala Pro Pro Gly Glu Val Val Gly Cys Phe Thr Pro							
557		562		567		572	
cag agc cgg cgg ctg cgc gag ctg ccc ctc gcc gcc gat gcg ctc acc	1838						
Gln Ser Arg Arg Leu Arg Glu Leu Pro Leu Ala Ala Asp Ala Leu Thr							
573		578		583		588	
ttc gcg gag gtg tcc aag gac ccc aag ggc ctc gag tgg ctg tgg agc	1886						
Phe Ala Glu Val Ser Lys Asp Pro Lys Gly Leu Glu Trp Leu Trp Ser							
589		594		599		604	
ccc cag atc gtg ggg ctg tac aac cgg ctg ctg cag cgc tgc gag ctc	1934						
Pro Gln Ile Val Gly Leu Tyr Asn Arg Leu Leu Gln Arg Cys Glu Leu							
605		610		615		620	
aac cgg cac acg acg gag gcg gcc gcc ggg gcg ctg cag aac atc acg	1982						
Asn Arg His Thr Thr Glu Ala Ala Ala Gly Ala Leu Gln Asn Ile Thr							
621		626		631		636	
gca ggc gac cgc agg tgg gcg ggg gtg ctg agc cgc ctg gcc ctg gag	2030						
Ala Gly Asp Arg Arg Trp Ala Gly Val Leu Ser Arg Leu Ala Leu Glu							
637		642		647		652	
cag gag cgt att ctg aac ccc ctg cta gac cgt gtc agg acc gcc gac	2078						
Gln Glu Arg Ile Leu Asn Pro Leu Leu Asp Arg Val Arg Thr Ala Asp							
653		658		663		668	
cac cac cag ctg cgc tca ctg act ggc ctc atc cga aac ctg tct cgg	2126						
His His Gln Leu Arg Ser Leu Thr Gly Leu Ile Arg Asn Leu Ser Arg							
669		674		679		684	
aac gct agg aac aag gac gag atg tcc acg aag gtg gtg agc cac ctg	2174						
Asn Ala Arg Asn Lys Asp Glu Met Ser Thr Lys Val Val Ser His Leu							
685		690		695		700	
atc gag aag ctg ccg ggc agc gtg ggt gag aag tgc ccc cca gcc gag	2222						
Ile Glu Lys Leu Pro Gly Ser Val Gly Glu Lys Ser Pro Pro Ala Glu							
701		706		711		716	
gtg ctg gtc aac atc ata gct gtg ctc aac aac ctg gtg gtg gcc agc	2270						
Val Leu Val Asn Ile Ile Ala Val Leu Asn Asn Leu Val Val Ala Ser							
717		722		727		732	

ccc atc gct gcc cga gac ctg ctg tat ttt gac gga ctc cga aag ctc 2318
Pro Ile Ala Ala Arg Asp Leu Leu Tyr Phe Asp Gly Leu Arg Lys Leu
733 738 743 748

atc ttc atc aag aag aag cgg gac agc ccc gac agt gag aag tcc tcc 2366
Ile Phe Ile Lys Lys Lys Arg Asp Ser Pro Asp Ser Glu Lys Ser Ser
749 754 759 764

cgg gca gca tcc agc ctc ctg gcc aac ctg tgg cag tac aac aag ctc 2414
Arg Ala Ala Ser Ser Leu Leu Ala Asn Leu Trp Gln Tyr Asn Lys Leu
765 770 775 780

cac cgt gac ttc cgg gcg aag ggc tat cgg aag gag gac ttc ctg ggc 2462
His Arg Asp Phe Arg Ala Lys Gly Tyr Arg Lys Glu Asp Phe Leu Gly
781 786 791 796

cca tag gtgaagcctt ctggaggaga aggtgacgtg gccacgcgtc caagggacag 2518
Pro *
797

actcagctcc aggctgcttg gcagcccagc ctggaggaga aggctaataga cggagggggcc 2578

cctcgctggg gccctgtgt gcatctttga gggctcctggg ccaccaggag gggcagggtc 2638

ttatagctgg ggacttggt tccgcagggc aggggggtggg gcaggggtca aggctgctct 2698

gggtgatggg gtggtgacct agtcacattg gcagaggtgg gggttggctg tggcctggca 2758

gtatcttggg atagccagca ctgggaataa agatggccat gaacagtcaa aaaaaaaaaa 2818

<210> 139
<211> 988
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (199)..(750)

<400> 139
atgtaaatca cacagatggt ggtagagaaa aaggcatact ggtattgaaa ctgtaaactg 60

gcctgtttac ttcgtctcct aacaaaaaac actttggatt caggttctcc acagcagtct 120

tccactggcc acagtgaggg gagctaggtt tcccagctct ccagctagaa aaactcagaa 180

catctaaaga tctgaaag atg gaa aaa aga gaa cta aag gct tct gtt cca 231
Met Glu Lys Arg Glu Leu Lys Ala Ser Val Pro
1 5

aaa ttt gac aag att cct tgg ctt agt gag gcc agc ctt gta aac aag 279
Lys Phe Asp Lys Ile Pro Trp Leu Ser Glu Ala Ser Leu Val Asn Lys
12 17 22 27

cca tta gtg ctc agc ctt ccc aga aga tat cct cat acc tct gcg act	327
Pro Leu Val Leu Ser Leu Pro Arg Arg Tyr Pro His Thr Ser Ala Thr	
28 33 38 43	
ttt ctg act tca tcc aag aag aat atg aat ttg cca att ttg ttt caa	375
Phe Leu Thr Ser Ser Lys Lys Asn Met Asn Leu Pro Ile Leu Phe Gln	
44 49 54 59	
gtt cca gat gtt tta tct aag gcc agg agg aac cag tgt gac tcc atg	423
Val Pro Asp Val Leu Ser Lys Ala Arg Arg Asn Gln Cys Asp Ser Met	
60 65 70 75	
ctg ctc aga aac caa cag ctg tgc tcc aca tgt caa gaa atg aaa atg	471
Leu Leu Arg Asn Gln Gln Leu Cys Ser Thr Cys Gln Glu Met Lys Met	
76 81 86 91	
gta caa cca aga aca atg aaa atc cca gat gat cca aaa gca tcc ttt	519
Val Gln Pro Arg Thr Met Lys Ile Pro Asp Asp Pro Lys Ala Ser Phe	
92 97 102 107	
gag aat tgt atg agt tat aga atg agt ctt cat caa ccc aaa ttc cag	567
Glu Asn Cys Met Ser Tyr Arg Met Ser Leu His Gln Pro Lys Phe Gln	
108 113 118 123	
act aca cct gag cct ttc cat gat gac atc cca aca gaa aac att cac	615
Thr Thr Pro Glu Pro Phe His Asp Asp Ile Pro Thr Glu Asn Ile His	
124 129 134 139	
tac aga ctg ccc att ctg ggc ccc agg aca gct gtc ttc cac gga tta	663
Tyr Arg Leu Pro Ile Leu Gly Pro Arg Thr Ala Val Phe His Gly Leu	
140 145 150 155	
ctg aca gag gcc tac aaa act cta aaa gag aga caa cgt tct tcc ttg	711
Leu Thr Glu Ala Tyr Lys Thr Leu Lys Glu Arg Gln Arg Ser Ser Leu	
156 161 166 171	
ccc aga aag gaa cca ata ggc aag aca acg agg cag tga gcggtaggag	760
Pro Arg Lys Glu Pro Ile Gly Lys Thr Thr Arg Gln *	
172 177 182	
ctcatcacct cccagactcc cagagagaaa ataacctcgc caagccaatc tttgacactg	820
gcaccttctc ctcaaatctt tctctcttctt cccaaaagat gatttaattt tgccttctta	880
agattgctgg tattctagct cttacctcta tgttcttctt cactctctct aaagacaaaa	940
ttgtttaatt tacatgatta taaagatctg tttatgaaaa aaaaaaaaa	988

<210> 140
 <211> 4265
 <212> DNA
 <213> Homo sapiens

[illegible]

487

tgt Cys 184	ata Ile	aag Lys	gcg Ala	tta Leu	atg Met 189	aac Asn	aac Asn	tct Ser	caa Gln	ggc Gly 194	cgg Arg	gct Ala	cac His	gtc Val	ctg Leu 199	749
gct Ala 200	cat His	tct Ser	gag Glu	agt Ser	att Ile 205	aat Asn	gta Val	att Ile	gct Ala	cag Gln 210	agt Ser	ctg Leu	agc Ser	aca Thr	gag Glu 215	797
aac Asn 216	att Ile	aaa Lys	acg Thr	aag Lys	gtg Val 221	gcc Ala	gtg Val	ctg Leu	gaa Glu	atc Ile 226	ttg Leu	ggc Gly	gcc Ala	gtg Val	tgc Cys 231	845
ctg Leu 232	gtt Val	ccc Pro	ggg Gly	ggc Gly	cac His 237	aag Lys	aag Lys	gtt Val	ctg Leu	cag Gln 242	gcc Ala	atg Met	ctg Leu	cac His	tac Tyr 247	893
cag Gln 248	aag Lys	tat Tyr	gcc Ala	agc Ser	gaa Glu 253	agg Arg	acc Thr	cgc Arg	ttt Phe	cag Gln 258	aca Thr	tta Leu	att Ile	aac Asn	gac Asp 263	941
ttg Leu 264	gat Asp	aaa Lys	agc Ser	act Thr	ggg Gly 269	cgg Arg	tat Tyr	cga Arg	gat Asp	gaa Glu 274	gtg Val	agt Ser	ctc Leu	aag Lys	act Thr 279	989
gcc Ala 280	atc Ile	atg Met	tcc Ser	ttc Phe	att Ile 285	aat Asn	gca Ala	gtg Val	ctc Leu	agc Ser 290	caa Gln	ggt Gly	gca Ala	gga Gly	gtg Val 295	1037
gag Glu 296	agt Ser	ttg Leu	gac Asp	ttt Phe	aga Arg 301	ctt Leu	cat His	ctt Leu	cgc Arg	tat Tyr 306	gaa Glu	ttt Phe	ctg Leu	atg Met	tta Leu 311	1085
gga Gly 312	att Ile	caa Gln	cct Pro	gta Val	ata Ile 317	gat Asp	aaa Lys	tta Leu	agg Arg	gaa Glu 322	cac His	gaa Glu	aat Asn	tca Ser	aca Thr 327	1133
tta Leu 328	gat Asp	agg Arg	cat His	tta Leu	gac Asp 333	ttt Phe	ttt Phe	gaa Glu	atg Met	ctc Leu 338	cga Arg	aat Asn	gaa Glu	gat Asp	gaa Glu 343	1181
cta Leu 344	gaa Glu	ttt Phe	gcc Ala	aaa Lys	aga Arg 349	ttt Phe	gaa Glu	ctg Leu	gtt Val	cac His 354	ata Ile	gac Asp	aca Thr	aaa Lys	agt Ser 359	1229
gca Ala 360	act Thr	cag Gln	atg Met	ttt Phe	gag Glu 365	ctg Leu	acc Thr	agg Arg	aag Lys	agg Arg 370	ctg Leu	aca Thr	cat His	agt Ser	gaa Glu 375	1277
gct Ala 376	tac Tyr	ccg Pro	cat His	ttc Phe	atg Met 381	tcc Ser	atc Ile	ctg Leu	cac His	cac His 386	tgc Cys	ctc Leu	caa Gln	atg Met	cct Pro 391	1325
tac Tyr 392	aag Lys	agg Arg	agt Ser	ggc Gly	aac Asn 397	act Thr	gtt Val	cag Gln	tac Tyr	tgg Trp 402	cta Leu	cta Leu	cta Leu	gat Asp	aga Arg 407	1373
att	ata	cag	cag	ata	gtt	atc	cag	aat	gac	aaa	gga	cag	gac	cct	gac	1421

Ile Ile Gln Gln Ile Val Ile Gln Asn Asp Lys Gly Gln Asp Pro Asp	
408 413 418 423	
tcc aca cct ttg gaa aac ttt aat att aag aat gtc gta cga atg ttg	1469
Ser Thr Pro Leu Glu Asn Phe Asn Ile Lys Asn Val Val Arg Met Leu	
424 429 434 439	
gtt aat gaa aat gaa gtt aag cag tgg aaa gaa caa gcg gaa aaa atg	1517
Val Asn Glu Asn Glu Val Lys Gln Trp Lys Glu Gln Ala Glu Lys Met	
440 445 450 455	
aga aaa gag cac aat gag cta caa cag aaa ctg gaa aag aaa gaa cga	1565
Arg Lys Glu His Asn Glu Leu Gln Gln Lys Leu Glu Lys Lys Glu Arg	
456 461 466 471	
gaa tgt gat gct aag act caa gag aag gaa gag atg atg cag acc tta	1613
Glu Cys Asp Ala Lys Thr Gln Glu Lys Glu Glu Met Met Gln Thr Leu	
472 477 482 487	
aat aaa atg aaa gag aaa ctt gaa aag gag act act gag cat aag caa	1661
Asn Lys Met Lys Glu Lys Leu Glu Lys Glu Thr Thr Glu His Lys Gln	
488 493 498 503	
gtc aag cag cag gtg gcg gac ctc aca gca cag ctc cat gag ctc agc	1709
Val Lys Gln Gln Val Ala Asp Leu Thr Ala Gln Leu His Glu Leu Ser	
504 509 514 519	
agg agg gcc gtc tgt gct tca atc cca ggt gga ccc tcg cct gga gca	1757
Arg Arg Ala Val Cys Ala Ser Ile Pro Gly Gly Pro Ser Pro Gly Ala	
520 525 530 535	
cca gga ggg ccc ttt cct tcc tct gtg cct gga tct ctc ctt cct ccc	1805
Pro Gly Gly Pro Phe Pro Ser Ser Val Pro Gly Ser Leu Leu Pro Pro	
536 541 546 551	
cca cca ccc cca cct cta cca ggt ggg atg ctt ccc cct cca ccg cct	1853
Pro Pro Pro Pro Pro Leu Pro Gly Gly Met Leu Pro Pro Pro Pro Pro	
552 557 562 567	
ccc ctc cct cca ggt ggc cct cct cct ccc cca ggg cct cct ccc tta	1901
Pro Leu Pro Pro Gly Gly Pro Pro Pro Pro Pro Gly Pro Pro Pro Leu	
568 573 578 583	
ggg gca atc atg cca cct cct ggt gct cca atg ggc cta gca ctg aag	1949
Gly Ala Ile Met Pro Pro Pro Gly Ala Pro Met Gly Leu Ala Leu Lys	
584 589 594 599	
aag aaa agc att cct cag ccc aca aat gcc ctg aaa tcc ttc aac tgg	1997
Lys Lys Ser Ile Pro Gln Pro Thr Asn Ala Leu Lys Ser Phe Asn Trp	
600 605 610 615	
tct aaa ctg ccc gag aac aaa ctg gaa gga aca gta tgg acc gaa att	2045
Ser Lys Leu Pro Glu Asn Lys Leu Glu Gly Thr Val Trp Thr Glu Ile	
616 621 626 631	
gat gat aca aaa gtc ttc aaa att cta gat ctt gaa gac ctg gaa aga	2093
Asp Asp Thr Lys Val Phe Lys Ile Leu Asp Leu Glu Asp Leu Glu Arg	

632						637						642						647	
acc	ttc	tct	gcc	tat	caa	aga	cag	cag	aaa	gaa	gca	gat	gcc	att	gat	2141			
Thr	Phe	Ser	Ala	Tyr	Gln	Arg	Gln	Gln	Lys	Glu	Ala	Asp	Ala	Ile	Asp				
648						653						658						663	
gac	act	ctg	agt	tcc	aaa	ctt	aaa	gtt	aaa	gag	ctt	tcg	gtg	att	gat	2189			
Asp	Thr	Leu	Ser	Ser	Lys	Leu	Lys	Val	Lys	Glu	Leu	Ser	Val	Ile	Asp				
664						669						674						679	
ggc	cgg	aga	gct	cag	aat	tgc	aac	atc	ctt	cta	tcg	agg	ttg	aaa	tta	2237			
Gly	Arg	Arg	Ala	Gln	Asn	Cys	Asn	Ile	Leu	Leu	Ser	Arg	Leu	Lys	Leu				
680						685						690						695	
tcc	aat	gac	gaa	atc	aaa	cgg	gca	att	cta	aca	atg	gac	gaa	cag	gaa	2285			
Ser	Asn	Asp	Glu	Ile	Lys	Arg	Ala	Ile	Leu	Thr	Met	Asp	Glu	Gln	Glu				
696						701						706						711	
gat	ctg	ccc	aag	gac	atg	ttg	gaa	cag	ctc	ttg	aaa	ttt	gtt	cct	gaa	2333			
Asp	Leu	Pro	Lys	Asp	Met	Leu	Glu	Gln	Leu	Leu	Lys	Phe	Val	Pro	Glu				
712						717						722						727	
aaa	agt	gac	att	gac	cta	ttg	gag	gaa	cat	aaa	cat	gaa	ctg	gat	cgg	2381			
Lys	Ser	Asp	Ile	Asp	Leu	Leu	Glu	Glu	His	Lys	His	Glu	Leu	Asp	Arg				
728						733						738						743	
atg	gcc	aag	gct	gat	agg	ttc	ctt	ttt	gag	atg	agc	cga	att	aat	cac	2429			
Met	Ala	Lys	Ala	Asp	Arg	Phe	Leu	Phe	Glu	Met	Ser	Arg	Ile	Asn	His				
744						749						754						759	
tat	cag	caa	agg	ttg	caa	tcg	ctg	tac	ttc	aaa	aag	aag	ttt	gca	gag	2477			
Tyr	Gln	Gln	Arg	Leu	Gln	Ser	Leu	Tyr	Phe	Lys	Lys	Lys	Phe	Ala	Glu				
760						765						770						775	
cgt	gtg	gca	gaa	gtg	aaa	cct	aaa	gtg	gaa	gca	att	cgt	tct	ggc	tca	2525			
Arg	Val	Ala	Glu	Val	Lys	Pro	Lys	Val	Glu	Ala	Ile	Arg	Ser	Gly	Ser				
776						781						786						791	
gaa	gag	gtg	ttt	agg	agt	ggc	gcc	ctc	aag	cag	ttg	ctg	gag	gtg	gtt	2573			
Glu	Glu	Val	Phe	Arg	Ser	Gly	Ala	Leu	Lys	Gln	Leu	Leu	Glu	Val	Val				
792						797						802						807	
ttg	gca	ttt	gga	aat	tat	atg	aat	aaa	ggc	caa	aga	ggg	aat	gca	tat	2621			
Leu	Ala	Phe	Gly	Asn	Tyr	Met	Asn	Lys	Gly	Gln	Arg	Gly	Asn	Ala	Tyr				
808						813						818						823	
gga	ttc	aag	ata	tct	agc	cta	aac	aaa	att	gct	gac	aca	aaa	tcc	agc	2669			
Gly	Phe	Lys	Ile	Ser	Ser	Leu	Asn	Lys	Ile	Ala	Asp	Thr	Lys	Ser	Ser				
824						829						834						839	
atc	gac	aaa	aac	att	acc	ctt	ttg	cac	tat	ctc	atc	act	att	gtg	gaa	2717			
Ile	Asp	Lys	Asn	Ile	Thr	Leu	Leu	His	Tyr	Leu	Ile	Thr	Ile	Val	Glu				
840						845						850						855	
aat	aag	tac	ccc	agt	gtt	ctc	aat	cta	aat	gaa	gaa	ttg	cga	gat	att	2765			
Asn	Lys	Tyr	Pro	Ser	Val	Leu	Asn	Leu	Asn	Glu	Glu	Leu	Arg	Asp	Ile				
856						861						866						871	

cct caa gct gcg aaa gta aac atg act gag ctg gac aaa gaa ata agt	2813
Pro Gln Ala Ala Lys Val Asn Met Thr Glu Leu Asp Lys Glu Ile Ser	
872 877 882 887	
acc ttg aga agt ggc ttg aaa gca gta gag aca gag ctg gaa tat cag	2861
Thr Leu Arg Ser Gly Leu Lys Ala Val Glu Thr Glu Leu Glu Tyr Gln	
888 893 898 903	
aag tct cag ccc cca cag ccc gga gat aag ttt gtg tct gtt gtc agc	2909
Lys Ser Gln Pro Pro Gln Pro Gly Asp Lys Phe Val Ser Val Val Ser	
904 909 914 919	
cag ttc atc aca gta gcc agc ttc agc ttc tct gat gtt gaa gac ctt	2957
Gln Phe Ile Thr Val Ala Ser Phe Ser Phe Ser Asp Val Glu Asp Leu	
920 925 930 935	
cta gca gaa gct aaa gac ctg ttt act aaa gca gtg aag cac ttt ggg	3005
Leu Ala Glu Ala Lys Asp Leu Phe Thr Lys Ala Val Lys His Phe Gly	
936 941 946 951	
gaa gag gct ggc aaa ata caa cca gat gag ttc ttt ggc att ttt gat	3053
Glu Glu Ala Gly Lys Ile Gln Pro Asp Glu Phe Phe Gly Ile Phe Asp	
952 957 962 967	
caa ttt ctt caa gct gtg tca gaa gcc aaa caa gaa aac gaa aat atg	3101
Gln Phe Leu Gln Ala Val Ser Glu Ala Lys Gln Glu Asn Glu Asn Met	
968 973 978 983	
aga aag aaa aag gag gaa gaa gaa cgt cga gct cgc atg gaa gct cag	3149
Arg Lys Lys Lys Glu Glu Glu Glu Arg Arg Ala Arg Met Glu Ala Gln	
984 989 994 999	
ctc aaa gaa caa cgt gaa agg gaa cgt aaa atg aga aaa gct aaa gag	3197
Leu Lys Glu Gln Arg Glu Arg Glu Arg Lys Met Arg Lys Ala Lys Glu	
1000 1005 1010 1015	
aat agt gaa gaa agc gga gag ttt gat gac ctt gtt tca gct tta cgc	3245
Asn Ser Glu Glu Ser Gly Glu Phe Asp Asp Leu Val Ser Ala Leu Arg	
1016 1021 1026 1031	
tca gga gaa gtg ttt gac aaa gac ctt tct aaa ttg aaa cgg aat cgc	3293
Ser Gly Glu Val Phe Asp Lys Asp Leu Ser Lys Leu Lys Arg Asn Arg	
1032 1037 1042 1047	
aaa cgt att acc aac cag atg act gac agc agc aga gag aga cca atc	3341
Lys Arg Ile Thr Asn Gln Met Thr Asp Ser Ser Arg Glu Arg Pro Ile	
1048 1053 1058 1063	
aca aaa ctt aat ttc taa ttttcc atgaatactt ttttttagaa agctcattag	3395
Thr Lys Leu Asn Phe *	
1064 1069	
cagccctcta aagtgactag aacgttttcat tacactgcct tgcaatccaa acagtggcaa	3455
ttttttcctt catctgtgag tgaatgtgtg aacgtgtgta tgtaaagtga tgtgtgtata	3515

tattaaaaaa	tgtatataga	tgtctgagtg	ttgtctggag	acctatacgt	atgggttaaaa	3575
agatttatgt	taatgtatgt	gctccaaaac	ctttcgtgta	tgcattcaca	ttgagtggtg	3635
ctcattttct	ttccccgaac	gccatgactg	ttcagaagca	caatactatc	tcctgaaaga	3695
gataagagac	attccctaga	ttcaaaggca	aaacagaaga	aacaaacaaa	caaacaaaca	3755
aagcttgcaa	aatattttat	ggttttccaag	cttgatatcc	tttaaaatta	ttttcattga	3815
tggaactgga	gttggttgaa	aaacatagat	ttaaaatgat	ttttgatagc	tgacattgtg	3875
atgttgatgt	atcacatcag	taataggacc	agctttgaat	ttctgacatt	gggtgtgggga	3935
tacagtctgt	aaatgtttat	tgagaacatc	ttgcacacaa	tttgaattat	gtagaatgtc	3995
aatcaagttt	ttgtatatatt	aaaagttgga	catcaatttt	ttccccgat	ttcatcaagt	4055
tatctctgcc	aagtgctctt	gataatttct	tcagattttt	ggaaaaaaac	actatataaa	4115
tgcaatccat	gctttttttta	aagaacaaca	ttgccagagt	atgcttgttc	taacaatata	4175
gatatataaa	ccttaaaaaat	aataaaaatat	ctcacccaag	acttaaagga	agaatttctct	4235
gaagggataa	agattactaa	aaaaaaaaaaa				4265

```
<210> 141
<211> 1957
<212> DNA
<213> Homo sapiens
```

<400> 141		
cggctgtagt aattcggcac gagcctcggc ggcccggctg gtgaatcaca cactctatgt		60
tcacctgcag ccgggc	atg agc ctg gag ggc ccg gct cag ccc cag tac	109
	Met Ser Leu Glu Gly Pro Ala Gln Pro Gln Tyr	
	1 5	
agc ccc gtg cag gcc acg ttt gag gtt ctt gat ttc atc acg cac ctc		157
Ser Pro Val Gln Ala Thr Phe Glu Val Leu Asp Phe Ile Thr His Leu		
12 17 22 27		
tat gct ggc gcc gac gtc cac agg cac ttg gac gtc aga atc cta ctg		205
Tyr Ala Gly Ala Asp Val His Arg His Leu Asp Val Arg Ile Leu Leu		
28 33 38 43		
acc aat atc cga acc aag agc acc ttt ctc cct ccc ctg ccc acc tca		253
Thr Asn Ile Arg Thr Lys Ser Thr Phe Leu Pro Pro Leu Pro Thr Ser		
44 49 54 59		

gtc cag aat ctc gcc cac ccg cca gaa gtc gtg ttg aca gat ttc cag Val Gln Asn Leu Ala His Pro Pro Glu Val Val Leu Thr Asp Phe Gln 60 65 70 75	301
acc ctg gat gga agc cag tac aac ccg gtc aaa cag cag cta gtg cgt Thr Leu Asp Gly Ser Gln Tyr Asn Pro Val Lys Gln Gln Leu Val Arg 76 81 86 91	349
tac gcc acc agc tgt tac agc tgt tgt ccg cga ctg gcc tcg gtg ctg Tyr Ala Thr Ser Cys Tyr Ser Cys Cys Pro Arg Leu Ala Ser Val Leu 92 97 102 107	397
cta tac tcc gat tat ggg ata gga gaa gtg ccc gtg gag ccc ctg gat Leu Tyr Ser Asp Tyr Gly Ile Gly Glu Val Pro Val Glu Pro Leu Asp 108 113 118 123	445
gtc ccc tta ccc tcc acg atc agg cca gct tcc ccc gtg gcc ggg tct Val Pro Leu Pro Ser Thr Ile Arg Pro Ala Ser Pro Val Ala Gly Ser 124 129 134 139	493
cca aag cag ccg gtg cgt ggc tac tac cgt ggc gct gtc ggt ggc acg Pro Lys Gln Pro Val Arg Gly Tyr Tyr Arg Gly Ala Val Gly Gly Thr 140 145 150 155	541
ttt gac cgc ctg cac aac gcc cac aag gtg ttg ctc agt gtc gcg tgc Phe Asp Arg Leu His Asn Ala His Lys Val Leu Leu Ser Val Ala Cys 156 161 166 171	589
atc ctg gcc cag gag cag ctt gtg gtg gga gta gca gac aaa gat ctg Ile Leu Ala Gln Glu Gln Leu Val Val Gly Val Ala Asp Lys Asp Leu 172 177 182 187	637
ttg aag agc aag ttg ctc cct gag ctg ctc caa cct tat aca gaa cgt Leu Lys Ser Lys Leu Leu Pro Glu Leu Leu Gln Pro Tyr Thr Glu Arg 188 193 198 203	685
gtg gaa cat ctg agt gaa ttc ctg gtg gac atc aag ccc tcc ttg act Val Glu His Leu Ser Glu Phe Leu Val Asp Ile Lys Pro Ser Leu Thr 204 209 214 219	733
ttt gat gtc atc ccc ctg ctg gac ccc tat ggg ccc gct ggc tct gac Phe Asp Val Ile Pro Leu Leu Asp Pro Tyr Gly Pro Ala Gly Ser Asp 220 225 230 235	781
ccc tcc ctg gag ttc ctg gtg gtc agc gag gag acc tat cgt ggg ggg Pro Ser Leu Glu Phe Leu Val Val Ser Glu Glu Thr Tyr Arg Gly Gly 236 241 246 251	829
atg gcc atc aac cgc ttc cgc ctt gag aat gac ctg gag gaa ctt gct Met Ala Ile Asn Arg Phe Arg Leu Glu Asn Asp Leu Glu Glu Leu Ala 252 257 262 267	877
ttg tac cag atc cag ctg ctg aag gac ctc aga cat aca gag aat gaa Leu Tyr Gln Ile Gln Leu Leu Lys Asp Leu Arg His Thr Glu Asn Glu 268 273 278 283	925
gag gac aaa gtc agc tcc tcc agc ttc cgc cag cga atg ttg ggg aac	973

Glu 284	Asp	Lys	Val	Ser	Ser	Ser	Phe	Arg	Gln	Arg	Met	Leu	Gly	Asn		
					289				294					299		
ctg	ctt	cgg	cct	cca	tat	gaa	agg	cca	gag	ctc	ccc	aca	tgt	ctc	tat	1021
Leu	Leu	Arg	Pro	Pro	Tyr	Glu	Arg	Pro	Glu	Leu	Pro	Thr	Cys	Leu	Tyr	
300					305					310					315	
gta	att	ggg	ctg	act	ggc	atc	agt	ggc	tct	ggg	aag	agc	tca	ata	gct	1069
Val	Ile	Gly	Leu	Thr	Gly	Ile	Ser	Gly	Ser	Gly	Lys	Ser	Ser	Ile	Ala	
316					321					326					331	
cag	cga	ctg	aag	ggc	ctg	ggg	gcg	ttt	gtc	att	gac	agt	gac	cac	ctg	1117
Gln	Arg	Leu	Lys	Gly	Leu	Gly	Ala	Phe	Val	Ile	Asp	Ser	Asp	His	Leu	
332					337					342					347	
ggc	cat	cgg	gcc	tat	gcc	cca	ggc	ggc	cct	gcc	tac	cag	cct	gtg	gtg	1165
Gly	His	Arg	Ala	Tyr	Ala	Pro	Gly	Gly	Pro	Ala	Tyr	Gln	Pro	Val	Val	
348					353					358					363	
gag	gcc	ttt	gga	aca	gat	att	ctc	cat	aaa	gat	ggc	atc	atc	aac	agg	1213
Glu	Ala	Phe	Gly	Thr	Asp	Ile	Leu	His	Lys	Asp	Gly	Ile	Ile	Asn	Arg	
364					369					374					379	
aag	gtc	cta	ggc	agc	cgg	gtg	ttt	ggg	aat	aag	aag	cag	ctg	aag	ata	1261
Lys	Val	Leu	Gly	Ser	Arg	Val	Phe	Gly	Asn	Lys	Lys	Gln	Leu	Lys	Ile	
380					385					390					395	
ctc	acg	gac	att	atg	tgg	cca	att	atc	gca	aag	ctg	gcc	cga	gag	gag	1309
Leu	Thr	Asp	Ile	Met	Trp	Pro	Ile	Ile	Ala	Lys	Leu	Ala	Arg	Glu	Glu	
396					401					406					411	
atg	gat	cgg	gct	gtg	gct	gag	gga	aag	cgt	gtg	tgt	gtg	att	gat	gcc	1357
Met	Asp	Arg	Ala	Val	Ala	Glu	Gly	Lys	Arg	Val	Cys	Val	Ile	Asp	Ala	
412					417					422					427	
gct	gtg	ttg	ctt	gaa	gcc	ggc	tgg	cag	aac	ctg	gtc	cat	gag	gtg	tgg	1405
Ala	Val	Leu	Leu	Glu	Ala	Gly	Trp	Gln	Asn	Leu	Val	His	Glu	Val	Trp	
428					433					438					443	
act	gct	gtc	atc	cca	gag	act	gag	gct	gta	aga	cgc	att	gtg	gag	agg	1453
Thr	Ala	Val	Ile	Pro	Glu	Thr	Glu	Ala	Val	Arg	Arg	Ile	Val	Glu	Arg	
444					449					454					459	
gat	ggc	ctc	agt	gaa	gcc	gcg	gct	caa	agc	cgg	ctg	cag	agc	cag	atg	1501
Asp	Gly	Leu	Ser	Glu	Ala	Ala	Ala	Gln	Ser	Arg	Leu	Gln	Ser	Gln	Met	
460					465					470					475	
agc	ggg	cag	cag	ctt	gtg	gaa	cag	agc	cac	gtg	gtg	ctc	agc	acc	ttg	1549
Ser	Gly	Gln	Gln	Leu	Val	Glu	Gln	Ser	His	Val	Val	Leu	Ser	Thr	Leu	
476					481					486					491	
tgg	gag	ccg	cat	atc	acc	caa	cgc	cag	gtg	gag	aaa	gcc	tgg	gcc	ctc	1597
Trp	Glu	Pro	His	Ile	Thr	Gln	Arg	Gln	Val	Glu	Lys	Ala	Trp	Ala	Leu	
492					497					502					507	
ttg	cag	aag	cgc	att	ccc	aag	act	cat	cag	gcc	ctc	gac	tga	aaagt	ctc	1646
Leu	Gln	Lys	Arg	Ile	Pro	Lys	Thr	His	Gln	Ala	Leu	Asp	*			

508	513	518	
tcagtggggc	cagactggct	cctggagctg	acaagcgacc ccgtggtgag gagaaatggg 1706
ggccttgatg	ctcaccttgg	ttcaggccca	gaggtccaag ctatactgtg caggacatgg 1766
ccaggcctgg	tggacacagg	aagcctaccc	aacacgctgg tatttggcca aactgagga 1826
tgtggttcat	gggggagcag	tcccctcccc	actcttgccc atgggtgact cttaccacaca 1886
gctgactagg	gccagcgcaa	atactggaac	ctgtaacaga attaaaggtg aatgttctga 1946
aaaaaaaaa	a		1957

<210> 142
 <211> 4399
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (141) .. (4133)

<400> 142	
tttgatagct gtacgcctgc aggtaccggt ccggaattcc cgggtcgacg atttcgtgtg	60
gtgtgtagcc ggcttggcgt gaccctcgcc tgatccagtt gttagagttg gaagcttggc	120
agttggcctc ctttcttccc	
atg gag gac ggg ggc tta aca gcc ttt gaa	170
Met Glu Asp Gly Gly Leu Thr Ala Phe Glu	
1 5	
gag gac cag aga tgc ctt tcc cag agc ctc ccc ttg cca gtg tca gca	218
Glu Asp Gln Arg Cys Leu Ser Gln Ser Leu Pro Leu Pro Val Ser Ala	
11 16 21 26	
gag ggc cca gct gca cag acc act gct gag ccc agc agg tcg ttt tcc	266
Glu Gly Pro Ala Ala Gln Thr Thr Ala Glu Pro Ser Arg Ser Phe Ser	
27 32 37 42	
tca gcc cac aga cac ctg agc aga agg aat ggg ctt tcc aga ctc tgc	314
Ser Ala His Arg His Leu Ser Arg Arg Asn Gly Leu Ser Arg Leu Cys	
43 48 53 58	
cag agc agg aca gcg ctc tct gaa gac aga tgg agc tcc tat tgt cta	362
Gln Ser Arg Thr Ala Leu Ser Glu Asp Arg Trp Ser Ser Tyr Cys Leu	
59 64 69 74	
tca tca ctg gct gcc cag aat att tgt aca agt aaa ctg cac tgc cct	410
Ser Ser Leu Ala Ala Gln Asn Ile Cys Thr Ser Lys Leu His Cys Pro	
75 80 85 90	
gct gcc cct gag cac acg gac ccg tcc gaa ccg cgg ggc agt gtg tcc	458
Ala Ala Pro Glu His Thr Asp Pro Ser Glu Pro Arg Gly Ser Val Ser	

91					96					101					106	
tgc tgc tcc ctg ctg	cgg gga ctg tcc tca	ggg tgg tcc tca cct ctg	506													
Cys Cys Ser Leu Leu	Arg Gly Leu Ser Ser	Gly Trp Ser Ser Pro Leu														
107	112	117													122	
ctt ccg gcc cct gtg	tgc aac cct aac aag	gcc atc ttc acg gtg gat	554													
Leu Pro Ala Pro Val	Cys Asn Pro Asn Lys	Ala Ile Phe Thr Val Asp														
123	128	133													138	
gcc aag acc aca gag	atc ctc gtt gct aac	gac aaa gct tgc ggg ctc	602													
Ala Lys Thr Thr Glu	Ile Leu Val Ala Asn	Asp Lys Ala Cys Gly Leu														
139	144	149													154	
ctg ggg tac agc agc	cag gac ctg att ggc	cag aag ctc acg cag ttc	650													
Leu Gly Tyr Ser Ser	Gln Asp Leu Ile Gly	Gln Lys Leu Thr Gln Phe														
155	160	165													170	
ttt ctg agg tca gat	tct gat gtg gtg gag	gcc ctc agc gag gag cac	698													
Phe Leu Arg Ser Asp	Ser Asp Val Val Glu	Ala Leu Ser Glu Glu His														
171	176	181													186	
atg gag gcc gac ggc	cac gct gcg gtg gtg	ttt ggc acg gtg gtg gac	746													
Met Glu Ala Asp Gly	His Ala Ala Val Val	Phe Gly Thr Val Val Asp														
187	192	197													202	
atc atc agc cgt agt	ggg gag aag att cca	gtg tct gtg tgg atg aag	794													
Ile Ile Ser Arg Ser	Gly Glu Lys Ile Pro	Val Ser Val Trp Met Lys														
203	208	213													218	
agg atg cgg cag gag	cgc cgc cta tgc tgc	gtg gtg gtc ctg gag ccc	842													
Arg Met Arg Gln Glu	Arg Arg Leu Cys Cys	Val Val Val Leu Glu Pro														
219	224	229													234	
gtg gag agg gtc tcg	acc tgg gtc gct ttc	cag agc gat ggc acc gtc	890													
Val Glu Arg Val Ser	Thr Trp Val Ala Phe	Gln Ser Asp Gly Thr Val														
235	240	245													250	
acg tca tgt gac agt	ctc ttt gct cat ctt	cac ggg tac gtg tct ggg	938													
Thr Ser Cys Asp Ser	Leu Phe Ala His Leu	His Gly Tyr Val Ser Gly														
251	256	261													266	
gag gac gtg gct ggg	cag cat atc aca gac	ctg atc cct tct gtg cag	986													
Glu Asp Val Ala Gly	Gln His Ile Thr Asp	Leu Ile Pro Ser Val Gln														
267	272	277													282	
ctc cct cct tct ggc	cag cac atc cca aag	aat ctc aag att cag agg	1034													
Leu Pro Pro Ser Gly	Gln His Ile Pro Lys	Asn Leu Lys Ile Gln Arg														
283	288	293													298	
tct gtt gga aga gcc	agg gac ggt acc acc	ttc cct ctg agc tta aag	1082													
Ser Val Gly Arg Ala	Arg Asp Gly Thr Thr	Phe Pro Leu Ser Leu Lys														
299	304	309													314	
ctg aaa tcc caa ccc	agc agc gag gag gcg	acc acc ggt gag gcg gcc	1130													
Leu Lys Ser Gln Pro	Ser Ser Glu Glu Ala	Thr Thr Gly Glu Ala Ala														
315	320	325													330	

cct gtc agc ggc tac cgg gca tct gtc tgg gtc ttc tgc acc atc agt	1178
Pro Val Ser Gly Tyr Arg Ala Ser Val Trp Val Phe Cys Thr Ile Ser	
331 336 341 346	
ggc ctc atc acc ctc ctg ccg gat ggg acc atc cac ggc atc aac cac	1226
Gly Leu Ile Thr Leu Leu Pro Asp Gly Thr Ile His Gly Ile Asn His	
347 352 357 362	
agc ttc gcg ctg aca ctg ttt ggt tac gga aag acg gag ctc ctg ggc	1274
Ser Phe Ala Leu Thr Leu Phe Gly Tyr Gly Lys Thr Glu Leu Leu Gly	
363 368 373 378	
aag aat atc act ttc ctg att cct ggt ttc tac agc tac atg gac ctt	1322
Lys Asn Ile Thr Phe Leu Ile Pro Gly Phe Tyr Ser Tyr Met Asp Leu	
379 384 389 394	
gcg tac aac agc tca tta cag ctc cca gac ctg gcc agc tgc ctg gac	1370
Ala Tyr Asn Ser Ser Leu Gln Leu Pro Asp Leu Ala Ser Cys Leu Asp	
395 400 405 410	
gtc ggc aat gag agt ggg tgt ggg gag aga acc ttg gac ccg tgg cag	1418
Val Gly Asn Glu Ser Gly Cys Gly Glu Arg Thr Leu Asp Pro Trp Gln	
411 416 421 426	
ggc cag gac cca gct gag ggg ggc cag gat cca agg att aat gtc gtg	1466
Gly Gln Asp Pro Ala Glu Gly Gly Gln Asp Pro Arg Ile Asn Val Val	
427 432 437 442	
ctt gct ggt ggc cac gtt gtg ccc cga gat gag atc cgg aag ctg atg	1514
Leu Ala Gly Gly His Val Val Pro Arg Asp Glu Ile Arg Lys Leu Met	
443 448 453 458	
gaa agc caa gac atc ttc acc ggg act cag act gag ctg att gct gga	1562
Glu Ser Gln Asp Ile Phe Thr Gly Thr Gln Thr Glu Leu Ile Ala Gly	
459 464 469 474	
ggc cag ctc ctt tcc tgc ctc tca cct cag cct gct cca ggg gtg gac	1610
Gly Gln Leu Leu Ser Cys Leu Ser Pro Gln Pro Ala Pro Gly Val Asp	
475 480 485 490	
aat gtc cca gaa gga agc ctg cca gtg cac ggt gaa cag gcg ctg ccc	1658
Asn Val Pro Glu Gly Ser Leu Pro Val His Gly Glu Gln Ala Leu Pro	
491 496 501 506	
aag gac cag caa atc act gcc ttg ggg aga gag gaa cct gtg gca ata	1706
Lys Asp Gln Gln Ile Thr Ala Leu Gly Arg Glu Glu Pro Val Ala Ile	
507 512 517 522	
gag agc ccc gga cag gat ctt ctg gga gaa agc agg tct gaa cca gtg	1754
Glu Ser Pro Gly Gln Asp Leu Leu Gly Glu Ser Arg Ser Glu Pro Val	
523 528 533 538	
gat gtg aag cca ttt gct tcc tgc gaa gat tct gaa gct cca gtc cca	1802
Asp Val Lys Pro Phe Ala Ser Cys Glu Asp Ser Glu Ala Pro Val Pro	
539 544 549 554	

gct gag gat ggg ggc agt gat gct ggc atg tgt ggc ctg tgt cag aag	1850
Ala Glu Asp Gly Gly Ser Asp Ala Gly Met Cys Gly Leu Cys Gln Lys	
555 560 565 570	
gcc cag cta gag cgg atg gga gtc agt ggt ccc agc ggt tca gac ctt	1898
Ala Gln Leu Glu Arg Met Gly Val Ser Gly Pro Ser Gly Ser Asp Leu	
571 576 581 586	
tgg gct ggg gct gcc gtg gcc aag ccc cag gcc aag ggt cag ctg gcg	1946
Trp Ala Gly Ala Ala Val Ala Lys Pro Gln Ala Lys Gly Gln Leu Ala	
587 592 597 602	
ggg ggc agc ctc ctg atg cac tgc cct tgc tat ggg agt gaa tgg ggc	1994
Gly Gly Ser Leu Leu Met His Cys Pro Cys Tyr Gly Ser Glu Trp Gly	
603 608 613 618	
ttg tgg tgg cga agc cag gac ttg gcc ccc agc ccc tct ggg atg gca	2042
Leu Trp Trp Arg Ser Gln Asp Leu Ala Pro Ser Pro Ser Gly Met Ala	
619 624 629 634	
ggc ctc tcg ttt ggg aca cct act cta gat gag ccg tgg ctg gga gtg	2090
Gly Leu Ser Phe Gly Thr Pro Thr Leu Asp Glu Pro Trp Leu Gly Val	
635 640 645 650	
gaa aac gac cga gaa gag ctg cag acc tgc ttg att aag gag cag ctg	2138
Glu Asn Asp Arg Glu Glu Leu Gln Thr Cys Leu Ile Lys Glu Gln Leu	
651 656 661 666	
tcc cag ttg agc ctt gca gga gcc ctg gat gtc ccc cac gcc gaa ctc	2186
Ser Gln Leu Ser Leu Ala Gly Ala Leu Asp Val Pro His Ala Glu Leu	
667 672 677 682	
gtt ccg aca gag tgc cag gct gtc acc gct cct gtg tcg tcc tgc gat	2234
Val Pro Thr Glu Cys Gln Ala Val Thr Ala Pro Val Ser Ser Cys Asp	
683 688 693 698	
ctg gga ggc aga gac ctg tgc ggt ggc tgc acg ggc agc tcc tca gcc	2282
Leu Gly Gly Arg Asp Leu Cys Gly Gly Cys Thr Gly Ser Ser Ser Ala	
699 704 709 714	
tgc tat gcc ttg gcc acg gac ctc cct ggg ggc ctg gaa gca gtg gag	2330
Cys Tyr Ala Leu Ala Thr Asp Leu Pro Gly Gly Leu Glu Ala Val Glu	
715 720 725 730	
gcc cag gag gtt gat gtg aat tcg ttt tcc tgg aac ctc aag gaa ctc	2378
Ala Gln Glu Val Asp Val Asn Ser Phe Ser Trp Asn Leu Lys Glu Leu	
731 736 741 746	
ttt ttc agt gac cag aca gac caa acg tca tca aat tgt tcc tgt gct	2426
Phe Phe Ser Asp Gln Thr Asp Gln Thr Ser Ser Asn Cys Ser Cys Ala	
747 752 757 762	
acg tct gaa ctc aga gag aca ccc tct tcc ttg gca gtg ggc tcc gat	2474
Thr Ser Glu Leu Arg Glu Thr Pro Ser Ser Leu Ala Val Gly Ser Asp	
763 768 773 778	
cca gat gta ggc agt ctc cag gaa cag ggg tcg tgt gtc ctg gat gac	2522

Pro Asp Val Gly Ser Leu Gln Glu Gln Gly Ser Cys Val Leu Asp Asp	
779 784 789 794	
agg gag ctg tta cta ctg acc ggc acc tgt gtt gac ctt ggc caa ggc	2570
Arg Glu Leu Leu Leu Leu Thr Gly Thr Cys Val Asp Leu Gly Gln Gly	
795 800 805 810	
cga cgg ttc cgg gag agc tgt gtg gga cat gat cca aca gaa ccg ctt	2618
Arg Arg Phe Arg Glu Ser Cys Val Gly His Asp Pro Thr Glu Pro Leu	
811 816 821 826	
gag gtt tgt ttg gtg tcc tct gag cat tat gca gca agc gac aga gaa	2666
Glu Val Cys Leu Val Ser Ser Glu His Tyr Ala Ala Ser Asp Arg Glu	
827 832 837 842	
agc cca gga cac gtt cct tcc acg ttg gat gct ggc cct gag gac acg	2714
Ser Pro Gly His Val Pro Ser Thr Leu Asp Ala Gly Pro Glu Asp Thr	
843 848 853 858	
tgc cca tca gca gag gag cca agg ctg aac gtc cag gtc acc tcc acg	2762
Cys Pro Ser Ala Glu Glu Pro Arg Leu Asn Val Gln Val Thr Ser Thr	
859 864 869 874	
ccc gtg atc gtg atg cgc ggg gct gct ggc ctg cag cgg gag atc cag	2810
Pro Val Ile Val Met Arg Gly Ala Ala Gly Leu Gln Arg Glu Ile Gln	
875 880 885 890	
gag ggt gcc tac tcc ggg agc tgc tac cat cga gat ggc tta cgg ctg	2858
Glu Gly Ala Tyr Ser Gly Ser Cys Tyr His Arg Asp Gly Leu Arg Leu	
891 896 901 906	
agt ata cag ttt gag gtg agg cgg gtg gag ctc cag ggc ccc aca cct	2906
Ser Ile Gln Phe Glu Val Arg Arg Val Glu Leu Gln Gly Pro Thr Pro	
907 912 917 922	
ctg ttc tgc tgc tgg ctg gtg aaa gac ctc ctc cac agc caa cgc gac	2954
Leu Phe Cys Cys Trp Leu Val Lys Asp Leu Leu His Ser Gln Arg Asp	
923 928 933 938	
tca gcc gcc agg acc cgc ctg ttc ctt gcc agc ctg ccc ggc tcc acc	3002
Ser Ala Ala Arg Thr Arg Leu Phe Leu Ala Ser Leu Pro Gly Ser Thr	
939 944 949 954	
cac tct acc gct gct gag ctc acc gga ccc agc ctg gtg gaa gtg ctc	3050
His Ser Thr Ala Ala Glu Leu Thr Gly Pro Ser Leu Val Glu Val Leu	
955 960 965 970	
aga gcc aga ccc tgg ttt gag gag ccc ccc aag gct gtg gaa ctg gag	3098
Arg Ala Arg Pro Trp Phe Glu Glu Pro Pro Lys Ala Val Glu Leu Glu	
971 976 981 986	
ggg ttg gcg gcc tgt gag ggc gag tac tcc caa aag tac agt acc atg	3146
Gly Leu Ala Ala Cys Glu Gly Glu Tyr Ser Gln Lys Tyr Ser Thr Met	
987 992 997 1002	
agc ccg ctg ggc agt ggg gcc ttc ggc ttc gtg tgg act gct gtg gac	3194
Ser Pro Leu Gly Ser Gly Ala Phe Gly Phe Val Trp Thr Ala Val Asp	

1003	1008	1013	1018	
aag gaa aaa aac aag gag	gtg gtg gtg aag ttt att aag aag gag aag			3242
Lys Glu Lys Asn Lys Glu	Val Val Val Lys Phe Ile Lys Lys Glu Lys			
1019	1024	1029	1034	
gtc ttg gag gat tgt tgg	att gag gat ccc aaa ctt ggg aaa gtt act			3290
Val Leu Glu Asp Cys Trp	Ile Glu Asp Pro Lys Leu Gly Lys Val Thr			
1035	1040	1045	1050	
tta gag atc gca att cta	tcc agg gtg gag cac gcc aat atc atc aag			3338
Leu Glu Ile Ala Ile Leu	Ser Arg Val Glu His Ala Asn Ile Ile Lys			
1051	1056	1061	1066	
gta ttg gat ata ttt gaa	aac caa ggg ttc ttc cag ctt gtg atg gag			3386
Val Leu Asp Ile Phe Glu	Asn Gln Gly Phe Phe Gln Leu Val Met Glu			
1067	1072	1077	1082	
aag cac ggc tcc ggc cta	gac ctc ttc gct ttc atc gac cgc cac ccc			3434
Lys His Gly Ser Gly Leu	Asp Leu Phe Ala Phe Ile Asp Arg His Pro			
1083	1088	1093	1098	
agg ctg gat gag ccc ctg	gcg agc tac atc ttc cga caa gtg aga gca			3482
Arg Leu Asp Glu Pro Leu	Ala Ser Tyr Ile Phe Arg Gln Val Arg Ala			
1099	1104	1109	1114	
ggc cag agc cgt cta gtg	tca gca gtg gga tac ctg cgc ttg aag gac			3530
Gly Gln Ser Arg Leu Val	Ser Ala Val Gly Tyr Leu Arg Leu Lys Asp			
1115	1120	1125	1130	
atc atc cac cgt gac atc	aag gat gag aac atc gtg atc gct gag gac			3578
Ile Ile His Arg Asp Ile	Lys Asp Glu Asn Ile Val Ile Ala Glu Asp			
1131	1136	1141	1146	
ttc aca atc aag ctg ata	gac ttt ggc tcg gcc gcc tac ttg gaa agg			3626
Phe Thr Ile Lys Leu Ile	Asp Phe Gly Ser Ala Ala Tyr Leu Glu Arg			
1147	1152	1157	1162	
gga aaa tta ttt tat act	ttt tgt ggg acc atc gag tac tgt gca ccg			3674
Gly Lys Leu Phe Tyr Thr	Phe Cys Gly Thr Ile Glu Tyr Cys Ala Pro			
1163	1168	1173	1178	
gaa gtt ctc atg ggg aat	ccc tac aga ggg ccg gag ctg gag atg tgg			3722
Glu Val Leu Met Gly Asn	Pro Tyr Arg Gly Pro Glu Leu Glu Met Trp			
1179	1184	1189	1194	
tct ctg gga gtc act ctg	tac acg ctg gtc ttt gag gag aac ccc ttc			3770
Ser Leu Gly Val Thr Leu	Tyr Thr Leu Val Phe Glu Glu Asn Pro Phe			
1195	1200	1205	1210	
tgt gag ctg gag gag acc	gtg gag gct gcc ata cac ccg cca tac ctg			3818
Cys Glu Leu Glu Glu Thr	Val Glu Ala Ala Ile His Pro Pro Tyr Leu			
1211	1216	1221	1226	
gtg tcc aaa gaa ctc atg	agc ctt gtg tct ggg ctg ctg cag cca gtc			3866
Val Ser Lys Glu Leu Met	Ser Leu Val Ser Gly Leu Leu Gln Pro Val			
1227	1232	1237	1242	

```

cct gag aga cgc acc acc ttg gag aag ctg gtg aca gac ccg tgg gta      3914
Pro Glu Arg Arg Thr Thr Leu Glu Lys Leu Val Thr Asp Pro Trp Val
1243                      1248                      1253                      1258

aca cag cct gtg aat ctt gct gac tat aca tgg gaa gag gtg ttt cga      3962
Thr Gln Pro Val Asn Leu Ala Asp Tyr Thr Trp Glu Glu Val Phe Arg
1259                      1264                      1269                      1274

gta aac aag cca gaa agt gga gtt ctg tcc gct gcg agc ctg gag atg      4010
Val Asn Lys Pro Glu Ser Gly Val Leu Ser Ala Ala Ser Leu Glu Met
1275                      1280                      1285                      1290

ggg aac agg agc ctg agt gat gtg gcc cag gct cag gag ctt tgt ggg      4058
Gly Asn Arg Ser Leu Ser Asp Val Ala Gln Ala Gln Glu Leu Cys Gly
1291                      1296                      1301                      1306

ggc ccc gtt cca ggc gag gct cct aat ggc caa ggc tgt ttg cat ccc      4106
Gly Pro Val Pro Gly Glu Ala Pro Asn Gly Gln Gly Cys Leu His Pro
1307                      1312                      1317                      1322

ggg gat ccc cgt ctg ctg acc agc taa acacc aatttcttcc tgcttttctc      4158
Gly Asp Pro Arg Leu Leu Thr Ser *
1323                      1328

cacttggttt ggaaaatcac acagttttca ggctccatct gtttgagaaa aatacattct      4218

gaagcatccc caattcacct tctaaaaact catgtgcagg tttgataaac accagaacag      4278

aagacagtga tgctgtatta ttttagattt attacataga tttggaattc acttttttca      4338

tgacctagaa aaaaacattc cagtgttcaa ctgttttata ttattaaagg gcttttaatt      4398

t                                                                    4399

```

```

<210> 143
<211> 4393
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (141)..(4112)

```

```

<400> 143
tttgatagct gtacgcctgc aggtaccggt ccggaattcc cgggtcgacg atttcgtgtg      60

gtgtgtagcc ggcttggcgt gaccctcgcc tgatccagtt gttagagttg gaagcttggc      120

agttggcctc ccttcttccc          atg gag gac ggg ggc tta aca gcc ttt gaa      170
                               Met Glu Asp Gly Gly Leu Thr Ala Phe Glu
                               1                      5

gag gac cag aga tgc ctt tcc cag agc ctc ccc ttg cca gtg tca gca      218

```

Glu 11	Asp	Gln	Arg	Cys	Leu 16	Ser	Gln	Ser	Leu	Pro 21	Leu	Pro	Val	Ser	Ala 26	
gag	ggc	cca	gct	gca	cag	acc	act	gct	gag	ccc	agc	agg	tcg	ttt	tcc	266
Glu 27	Gly	Pro	Ala	Ala	Gln 32	Thr	Thr	Ala	Glu	Pro 37	Ser	Arg	Ser	Phe	Ser 42	
tca	gcc	cac	aga	cac	ctg	agc	aga	agg	aat	ggg	ctt	tcc	aga	ctc	tgc	314
Ser 43	Ala	His	Arg	His	Leu 48	Ser	Arg	Arg	Asn	Gly 53	Leu	Ser	Arg	Leu	Cys 58	
cag	agc	agg	aca	gcg	ctc	tct	gaa	gac	aga	tgg	agc	tcc	tat	tgt	cta	362
Gln 59	Ser	Arg	Thr	Ala	Leu 64	Ser	Glu	Asp	Arg	Trp 69	Ser	Ser	Tyr	Cys	Leu 74	
tca	tca	ctg	gct	gcc	cag	aat	att	tgt	aca	agt	aaa	ctg	cac	tgc	cct	410
Ser 75	Ser	Leu	Ala	Ala	Gln 80	Asn	Ile	Cys	Thr	Ser 85	Lys	Leu	His	Cys	Pro 90	
gct	gcc	cct	gag	cac	acg	gac	ccg	tcc	gaa	ccg	cgg	ggc	agt	gtg	tcc	458
Ala 91	Ala	Pro	Glu	His	Thr 96	Asp	Pro	Ser	Glu	Pro 101	Arg	Gly	Ser	Val	Ser 106	
tgc	tgc	tcc	ctg	ctg	cgg	gga	ctg	tcc	tca	ggg	tgg	tcc	tca	cct	ctg	506
Cys 107	Cys	Ser	Leu	Leu	Arg 112	Gly	Leu	Ser	Ser	Gly 117	Trp	Ser	Ser	Pro	Leu 122	
ctt	ccg	gcc	cct	gtg	tgc	aac	cct	aac	aag	gcc	atc	ttc	acg	gtg	gat	554
Leu 123	Pro	Ala	Pro	Val	Cys 128	Asn	Pro	Asn	Lys	Ala 133	Ile	Phe	Thr	Val	Asp 138	
gcc	aag	acc	aca	gag	atc	ctc	gtt	gct	aac	gac	aaa	gct	tgc	ggg	ctc	602
Ala 139	Lys	Thr	Thr	Glu	Ile 144	Leu	Val	Ala	Asn	Asp 149	Lys	Ala	Cys	Gly	Leu 154	
ctg	ggg	tac	agc	agc	cag	gac	ctg	att	ggc	cag	aag	ctc	acg	cag	ttc	650
Leu 155	Gly	Tyr	Ser	Ser	Gln 160	Asp	Leu	Ile	Gly	Gln 165	Lys	Leu	Thr	Gln	Phe 170	
ttt	ctg	agg	tca	gat	tct	gat	gtg	gtg	gag	gcc	ctc	agc	gag	gag	cac	698
Phe 171	Leu	Arg	Ser	Asp	Ser 176	Asp	Val	Val	Glu	Ala 181	Leu	Ser	Glu	Glu	His 186	
atg	gag	gcc	gac	ggc	cac	gct	gcg	gtg	gtg	ttt	ggc	acg	gtg	gtg	gac	746
Met 187	Glu	Ala	Asp	Gly	His 192	Ala	Ala	Val	Val	Phe 197	Gly	Thr	Val	Val	Asp 202	
atc	atc	agc	cgt	agt	ggg	gag	aag	att	cca	gtg	tct	gtg	tgg	atg	aag	794
Ile 203	Ile	Ser	Arg	Ser	Gly 208	Glu	Lys	Ile	Pro	Val 213	Ser	Val	Trp	Met	Lys 218	
agg	atg	cgg	cag	gag	cgc	cgc	cta	tgc	tgc	gtg	gtg	gtc	ctg	gag	ccc	842
Arg 219	Met	Arg	Gln	Glu	Arg 224	Arg	Leu	Cys	Cys	Val 229	Val	Val	Leu	Glu	Pro 234	
gtg	gag	agg	gtc	tcg	acc	tgg	gtc	gct	ttc	cag	agc	gat	ggc	acc	gtc	890
Val	Glu	Arg	Val	Ser	Thr	Trp	Val	Ala	Phe	Gln	Ser	Asp	Gly	Thr	Val	

235	240	245	250	
acg tca tgt gac agt ctc ttt gct cat ctt cac ggg tac gtg tct ggg				938
Thr Ser Cys Asp Ser Leu Phe Ala His Leu His Gly Tyr Val Ser Gly				
251	256	261	266	
gag gac gtg gct ggg cag cat atc aca gac ctg atc cct tct gtg cag				986
Glu Asp Val Ala Gly Gln His Ile Thr Asp Leu Ile Pro Ser Val Gln				
267	272	277	282	
ctc cct cct tct ggc cag cac atc cca aag aat ctc aag att cag agg				1034
Leu Pro Pro Ser Gly Gln His Ile Pro Lys Asn Leu Lys Ile Gln Arg				
283	288	293	298	
tct gtt gga aga gcc agg gac ggt acc acc ttc cct ctg agc tta aag				1082
Ser Val Gly Arg Ala Arg Asp Gly Thr Thr Phe Pro Leu Ser Leu Lys				
299	304	309	314	
ctg aaa tcc caa ccc agc agc gag gag gcg acc acc ggt gag gcg gcc				1130
Leu Lys Ser Gln Pro Ser Ser Glu Glu Ala Thr Thr Gly Glu Ala Ala				
315	320	325	330	
cct gtg agc ggc tac cgg gca tct gtc tgg gtg ttc tgc acc atc agt				1178
Pro Val Ser Gly Tyr Arg Ala Ser Val Trp Val Phe Cys Thr Ile Ser				
331	336	341	346	
ggc ctc atc acc ctc ctg ccg gat ggg acc atc cac ggc atc aac cac				1226
Gly Leu Ile Thr Leu Leu Pro Asp Gly Thr Ile His Gly Ile Asn His				
347	352	357	362	
agc ttc gcg ctg aca ctg ttt ggt tac gga aag acg gag ctc ctg ggc				1274
Ser Phe Ala Leu Thr Leu Phe Gly Tyr Gly Lys Thr Glu Leu Leu Gly				
363	368	373	378	
aag aat atc act ttc ctg att cct ggt ttc tac agc tac atg gac ctt				1322
Lys Asn Ile Thr Phe Leu Ile Pro Gly Phe Tyr Ser Tyr Met Asp Leu				
379	384	389	394	
gcg tac aac agc tca tta cag ctc cca gac ctg gcc agc tgc ctg gac				1370
Ala Tyr Asn Ser Ser Leu Gln Leu Pro Asp Leu Ala Ser Cys Leu Asp				
395	400	405	410	
gtc ggc aat gag agt ggg tgt ggg gag aga acc ttg gac ccg tgg cag				1418
Val Gly Asn Glu Ser Gly Cys Gly Glu Arg Thr Leu Asp Pro Trp Gln				
411	416	421	426	
ggc cag gac cca gct gag ggg ggc cag gat cca agg att aat gtc gtg				1466
Gly Gln Asp Pro Ala Glu Gly Gly Gln Asp Pro Arg Ile Asn Val Val				
427	432	437	442	
ctt gct ggt ggc cac gtt gtg ccc cga gat gag atc cgg aag ctg atg				1514
Leu Ala Gly Gly His Val Val Pro Arg Asp Glu Ile Arg Lys Leu Met				
443	448	453	458	
gaa agc caa gac atc ttc acc ggg act cag act gag ctg att gct gga				1562
Glu Ser Gln Asp Ile Phe Thr Gly Thr Gln Thr Glu Leu Ile Ala Gly				
459	464	469	474	

ggc cag ctc ctt tcc tgc ctc tca cct cag cct gct cca ggg gtg gac	1610
Gly Gln Leu Leu Ser Cys Leu Ser Pro Gln Pro Ala Pro Gly Val Asp	
475 480 485 490	
aat gtc cca gaa gga agc ctg cca gtg cac ggt gaa cag gcg ctg ccc	1658
Asn Val Pro Glu Gly Ser Leu Pro Val His Gly Glu Gln Ala Leu Pro	
491 496 501 506	
aag gac cag caa atc act gcc ttg ggg aga gag gaa cct gtg gca ata	1706
Lys Asp Gln Gln Ile Thr Ala Leu Gly Arg Glu Glu Pro Val Ala Ile	
507 512 517 522	
gag agc ccc gga cag gat ctt ctg gga gaa agc agg tct gaa cca gtg	1754
Glu Ser Pro Gly Gln Asp Leu Leu Gly Glu Ser Arg Ser Glu Pro Val	
523 528 533 538	
gat gtg aag cca ttt gct tcc tgc gaa gat tct gaa gct cca gtc cca	1802
Asp Val Lys Pro Phe Ala Ser Cys Glu Asp Ser Glu Ala Pro Val Pro	
539 544 549 554	
gct gag gat ggg ggc agt gat gct ggc atg tgt ggc ctg tgt cag aag	1850
Ala Glu Asp Gly Gly Ser Asp Ala Gly Met Cys Gly Leu Cys Gln Lys	
555 560 565 570	
gcc cag cta gag cgg atg gga gtc agt ggt ccc agc ggt tca gac ctt	1898
Ala Gln Leu Glu Arg Met Gly Val Ser Gly Pro Ser Gly Ser Asp Leu	
571 576 581 586	
tgg gct ggg gct gcc gtg gcc aag ccc cag gcc aag ggt cag ctg gcg	1946
Trp Ala Gly Ala Ala Val Ala Lys Pro Gln Ala Lys Gly Gln Leu Ala	
587 592 597 602	
ggg ggc agc ctc ctg atg cac tgc cct tgc tat ggg agt gaa tgg ggc	1994
Gly Gly Ser Leu Leu Met His Cys Pro Cys Tyr Gly Ser Glu Trp Gly	
603 608 613 618	
ttg tgg tgg cga agc cag gac ttg gcc ccc agc ccc tct ggg atg gca	2042
Leu Trp Trp Arg Ser Gln Asp Leu Ala Pro Ser Pro Ser Gly Met Ala	
619 624 629 634	
ggc ctc tcg ttt ggg aca cct act cta gat gag ccg tgg ctg gga gtg	2090
Gly Leu Ser Phe Gly Thr Pro Thr Leu Asp Glu Pro Trp Leu Gly Val	
635 640 645 650	
gaa aac gac cga gaa gag ctg cag acc tgc ttg att aag gag cag ctg	2138
Glu Asn Asp Arg Glu Glu Leu Gln Thr Cys Leu Ile Lys Glu Gln Leu	
651 656 661 666	
tcc cag ttg agc ctt gca gga gcc ctg gat gtc ccc cac gcc gaa ctc	2186
Ser Gln Leu Ser Leu Ala Gly Ala Leu Asp Val Pro His Ala Glu Leu	
667 672 677 682	
gtt ccg aca gag tgc cag gct gtc acc gct cct gtg tcg tcc tgc gat	2234
Val Pro Thr Glu Cys Gln Ala Val Thr Ala Pro Val Ser Ser Cys Asp	
683 688 693 698	

ctg gga ggc aga gac Leu Gly Gly Arg Asp 699	ctg tgc ggt ggc tgc Leu Cys Gly Gly Cys 704	acg ggc agc tcc tca gcc Thr Gly Ser Ser Ser 709	714	2282
tgc tat gcc ttg gcc Cys Tyr Ala Leu Ala 715	acg gac ctc cct ggg Thr Asp Leu Pro Gly 720	ggc ctg gaa gca gtg gag Gly Gly Leu Glu Ala Val 725	730	2330
gcc cag gag gtt gat Ala Gln Glu Val Asp 731	gtg aat tcg ttt tcc Val Asn Ser Phe Ser 736	tgg aac ctc aag gaa ctc Trp Asn Leu Lys Glu Leu 741	746	2378
ttt ttc agt gac cag Phe Phe Ser Asp Gln 747	aca gac caa acg tca Thr Asp Gln Thr Ser 752	tca tca aat tgt tcc tgt Ser Ser Asn Cys Ser Cys 757	762	2426
acg tct gaa ctc aga Thr Ser Glu Leu Arg 763	gag aca ccc tct tcc Glu Thr Pro Ser Ser 768	ttg gca gtg ggc tcc gat Leu Ala Val Gly Ser Asp 773	778	2474
cca gat gta ggc agt Pro Asp Val Gly Ser 779	ctc cag gaa cag ggg Leu Gln Glu Gln Gly 784	tcg tgt gtc ctg gat gac Ser Cys Val Leu Asp Asp 789	794	2522
agg gag ctg tta cta Arg Glu Leu Leu Leu 795	ctg acc ggc acc tgt Leu Thr Gly Thr Cys 800	gtt gac ctt ggc caa ggc Val Asp Leu Gly Gln Gly 805	810	2570
cga cgg ttc cgg gag Arg Arg Phe Arg Glu 811	agc tgt gtg gga cat Ser Cys Val Gly His 816	gat cca aca gaa ccg ctt Asp Pro Thr Glu Pro Leu 821	826	2618
gag gtt tgt ttg gtg Glu Val Cys Leu Val 827	tcc tct gag cat tat Ser Ser Glu His Tyr 832	gca gca agc gac aga gaa Ala Ala Ser Asp Arg Glu 837	842	2666
agc cca gga cac gtt Ser Pro Gly His Val 843	cct tcc acg ttg gat Pro Ser Thr Leu Asp 848	gct ggc cct gag gac acg Ala Gly Pro Glu Asp Thr 853	858	2714
tgc cca tca gca gag Cys Pro Ser Ala Glu 859	gag cca agg ctg aac Glu Pro Arg Leu Asn 864	gtc cag gtc acc tcc acg Val Gln Val Thr Ser Thr 869	874	2762
ccc gtg atc gtg atg Pro Val Ile Val Met 875	cgc ggg gct gct ggc Arg Gly Ala Ala Gly 880	ctg cag cgg gag atc cag Leu Gln Arg Glu Ile Gln 885	890	2810
gag ggt gcc tac tcc Glu Gly Ala Tyr Ser 891	ggg agc tgc tac cat Gly Ser Cys Tyr His 896	cga gat ggc tta cgg ctg Arg Asp Gly Leu Arg Leu 901	906	2858
agt ata cag ttt gag Ser Ile Gln Phe Glu 907	gtg agg cgg gtg gag Val Arg Arg Val Glu 912	ctc cag ggc ccc aca cct Leu Gln Gly Pro Thr Pro 917	922	2906
ctg ttc tgc tgc tgg ctg gtg aaa gac ctc ctc	cac agc caa cgc gac			2954

Leu Phe Cys Cys Trp	Leu Val Lys Asp	Leu Leu His Ser Gln Arg Asp	
923	928	933	938
tca gcc gcc agg acc	cgc ctg ttc ctt gcc agc ctg ccc ggc tcc acc	3002	
Ser Ala Ala Arg Thr	Arg Leu Phe Leu Ala Ser Leu Pro Gly Ser Thr		
939	944 949 954		
cac tct acc gct gct	gag ctc acc gga ccc agc ctg gtg gaa gtg ctc	3050	
His Ser Thr Ala Ala	Glu Leu Thr Gly Pro Ser Leu Val Glu Val Leu		
955	960 965 970		
aga gcc aga ccc tgg	ttt gag gag ccc ccc aag gct gtg gaa ctg gag	3098	
Arg Ala Arg Pro Trp	Phe Glu Glu Pro Pro Lys Ala Val Glu Leu Glu		
971	976 981 986		
ggg ttg gcg gcc tgt	gag ggc gag tac tcc caa aag tac agt acc atg	3146	
Gly Leu Ala Ala Cys	Glu Gly Glu Tyr Ser Gln Lys Tyr Ser Thr Met		
987	992 997 1002		
agc ccg ctg ggc agt	ggg gcc ttc ggc ttc gtg tgg act gct gtg gac	3194	
Ser Pro Leu Gly Ser	Gly Ala Phe Gly Phe Val Trp Thr Ala Val Asp		
1003	1008 1013 1018		
aag gaa aaa aac aag	gag gtg gtg gtg aag ttt att aag aag gag aag	3242	
Lys Glu Lys Asn Lys	Glu Val Val Val Lys Phe Ile Lys Lys Glu Lys		
1019	1024 1029 1034		
gtc ttg gag gat tgt	tgg att gag gat ccc aaa ctt ggg aaa gtt act	3290	
Val Leu Glu Asp Cys	Trp Ile Glu Asp Pro Lys Leu Gly Lys Val Thr		
1035	1040 1045 1050		
tta gag atc gca att	cta tcc agg gtg gag cac gcc aat atc atc aag	3338	
Leu Glu Ile Ala Ile	Leu Ser Arg Val Glu His Ala Asn Ile Ile Lys		
1051	1056 1061 1066		
gta ttg gat ata ttt	gaa aac caa ggg ttc ttc cag ctt gtg atg gag	3386	
Val Leu Asp Ile Phe	Glu Asn Gln Gly Phe Phe Gln Leu Val Met Glu		
1067	1072 1077 1082		
aag cac ggc tcc ggc	cta gac ctc ttc gct ttc atc gac cgc cac ccc	3434	
Lys His Gly Ser Gly	Leu Asp Leu Phe Ala Phe Ile Asp Arg His Pro		
1083	1088 1093 1098		
agg ctg gat gag ccc	ctg gcg agc tac atc ttc cga caa cta gtg tca	3482	
Arg Leu Asp Glu Pro	Leu Ala Ser Tyr Ile Phe Arg Gln Leu Val Ser		
1099	1104 1109 1114		
gca gtg gga tac ctg	cgc ttg aag gac atc atc cac cgt gac atc aag	3530	
Ala Val Gly Tyr Leu	Arg Leu Lys Asp Ile Ile His Arg Asp Ile Lys		
1115	1120 1125 1130		
gat gag aac atc gtg	atc gct gag gac ttc aca atc aag ctg ata gac	3578	
Asp Glu Asn Ile Val	Ile Ala Glu Asp Phe Thr Ile Lys Leu Ile Asp		
1131	1136 1141 1146		
ttt ggc tcg gcc gcc	tac ttg gaa agg gga aaa tta ttt tat act ttt	3626	
Phe Gly Ser Ala Ala	Tyr Leu Glu Arg Gly Lys Leu Phe Tyr Thr Phe		

1147	1152	1157	1162	
tgt ggg acc atc gag tac tgt gca ccg gaa gtt ctc atg ggg aat ccc				3674
Cys Gly Thr Ile Glu Tyr Cys Ala Pro Glu Val Leu Met Gly Asn Pro				
1163	1168	1173	1178	
tac aga ggg ccg gag ctg gag atg tgg tct ctg gga gtc act ctg tac				3722
Tyr Arg Gly Pro Glu Leu Glu Met Trp Ser Leu Gly Val Thr Leu Tyr				
1179	1184	1189	1194	
acg ctg gtc ttt gag gag aac ccc ttc tgt gag ctg gag gag acc gtg				3770
Thr Leu Val Phe Glu Glu Asn Pro Phe Cys Glu Leu Glu Glu Thr Val				
1195	1200	1205	1210	
gag gct gcc ata cac ccg cca tac ctg gtg tcc aaa gaa ctc atg agc				3818
Glu Ala Ala Ile His Pro Pro Tyr Leu Val Ser Lys Glu Leu Met Ser				
1211	1216	1221	1226	
ctt gtg tct ggg ctg ctg cag cca gtc cct gag aga cgc acc acc ttg				3866
Leu Val Ser Gly Leu Leu Gln Pro Val Pro Glu Arg Arg Thr Thr Leu				
1227	1232	1237	1242	
gag aag ctg gtg aca gac ccg tgg gta aca cag cct gtg aat ctt gct				3914
Glu Lys Leu Val Thr Asp Pro Trp Val Thr Gln Pro Val Asn Leu Ala				
1243	1248	1253	1258	
gac tat aca tgg gaa gag gtg ttt cga gta aac aag cca gaa agt gga				3962
Asp Tyr Thr Trp Glu Glu Val Phe Arg Val Asn Lys Pro Glu Ser Gly				
1259	1264	1269	1274	
gtt ctg tcc gct gcg agc ctg gag atg ggg aac agg agc ctg agt gat				4010
Val Leu Ser Ala Ala Ser Leu Glu Met Gly Asn Arg Ser Leu Ser Asp				
1275	1280	1285	1290	
gtg gcc cag gct cag gag ctt tgt ggg ggc ccc gtt cca ggc gag gct				4058
Val Ala Gln Ala Gln Glu Leu Cys Gly Gly Pro Val Pro Gly Glu Ala				
1291	1296	1301	1306	
cct aat ggc caa ggc tgt ttg cat ccc ggg gat ccc cgt ctg ctg acc				4106
Pro Asn Gly Gln Gly Cys Leu His Pro Gly Asp Pro Arg Leu Leu Thr				
1307	1312	1317	1322	
agc taa acaccaattt cttcctgctt ttctccactt ggtttggaat atcacacagt				4162
Ser *				
1323				
tttcaggctc catctgtttg gagaaaatac attctgaagc atccccaatt caccttctaa				4222
aaactcatgt gcaggtttga taaacaccag aacagaagac agtgatgctg tattatttta				4282
gatttattac atagatttgg aattcacttt ttcatgacc tagaaaaaaaa cattccagtg				4342
ttcaactgtt ttatattatt aaagggtttt taatttgtga aaaaaaaaaa a				4393

<210> 144
 <211> 3042
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (402) .. (2069)

<400> 144
 gaattcgcgg ccgctcgacg ctcagcagag ctaccagctg cctgtttggc ttcgctggtc 60
 ggatcgctct cctggccccg ccaaacaggc ggggggagcg gccccgactg tggggccatg 120
 gcagtagtct cctcgttctc cgccgccgct agcctagctg agtcgcgggc ttctgcgcta 180
 ggggctccca ccgcctccgc aggctaagga gccgctgcc acaacgagct gtgagggtta 240
 ctatgctccc tctttgccgc cgtctcctcc tcttgccgc gcaggcacc ctctggctgc 300
 tcagtcctgc ctcagtgtca aaccagaaga gaagtaaaat tcaacaaaaa tttatgtgtg 360
 gagttccttc ttaaaagaag aaaaaagtga ttatttagac t atg gat cgg agc 413
 Met Asp Arg Ser
 1
 aaa cgg aat tca att gca gga ttt cct cca cgt gtg gag cgt ctt gaa 461
 Lys Arg Asn Ser Ile Ala Gly Phe Pro Pro Arg Val Glu Arg Leu Glu
 5 10 15 20
 gag ttt gaa gga ggt ggt gga gga gaa gga aat gtg agc cag gtg gga 509
 Glu Phe Glu Gly Gly Gly Gly Gly Glu Gly Asn Val Ser Gln Val Gly
 21 26 31 36
 aga gtt tgg cca tct tcg tat cga gct ctt ata agt gcc ttt tcc aga 557
 Arg Val Trp Pro Ser Ser Tyr Arg Ala Leu Ile Ser Ala Phe Ser Arg
 37 42 47 52
 ctg acg cgt ttg gat gat ttc acc tgt gaa aaa ata ggg tct ggc ttc 605
 Leu Thr Arg Leu Asp Asp Phe Thr Cys Glu Lys Ile Gly Ser Gly Phe
 53 58 63 68
 ttt tct gaa gtg ttc aag gta cga cac cga gct tct ggt cag gtg atg 653
 Phe Ser Glu Val Phe Lys Val Arg His Arg Ala Ser Gly Gln Val Met
 69 74 79 84
 gct ctt aag atg aac aca ttg agc agt aac cgg gca aac atg ctg aaa 701
 Ala Leu Lys Met Asn Thr Leu Ser Ser Asn Arg Ala Asn Met Leu Lys
 85 90 95 100
 gaa gta cag ctc atg aat aga ctc tcc cat ccc aac atc ctt agg tat 749
 Glu Val Gln Leu Met Asn Arg Leu Ser His Pro Asn Ile Leu Arg Tyr
 101 106 111 116
 atc aac tcc ggg aac ctg gaa cag ttg cta gac agt aac ctg cat ttg 797
 Ile Asn Ser Gly Asn Leu Glu Gln Leu Leu Asp Ser Asn Leu His Leu
 117 122 127 132

cct tgg act gtg agg gta aaa ctg gcc tat gac ata gca gtg ggc ctc	845
Pro Trp Thr Val Arg Val Lys Leu Ala Tyr Asp Ile Ala Val Gly Leu	
133 138 143 148	
agc tac ctt cac ttc aaa ggc att ttt cat cgg gac ctc aca tct aag	893
Ser Tyr Leu His Phe Lys Gly Ile Phe His Arg Asp Leu Thr Ser Lys	
149 154 159 164	
aac tgc ctg ata aag agg gat gag aat ggt tac tct gca gtg gta gct	941
Asn Cys Leu Ile Lys Arg Asp Glu Asn Gly Tyr Ser Ala Val Val Ala	
165 170 175 180	
gac ttt ggc ctg gct gag aag atc ccc gat gtc agc atg ggg agt gag	989
Asp Phe Gly Leu Ala Glu Lys Ile Pro Asp Val Ser Met Gly Ser Glu	
181 186 191 196	
aag ctg gcc gtg gtg ggt tcc cca ttc tgg atg gca cct gag gtt ctc	1037
Lys Leu Ala Val Val Gly Ser Pro Phe Trp Met Ala Pro Glu Val Leu	
197 202 207 212	
cga gat gag ccc tat aat gaa aag gca gat gtg ttc tct tat ggt atc	1085
Arg Asp Glu Pro Tyr Asn Glu Lys Ala Asp Val Phe Ser Tyr Gly Ile	
213 218 223 228	
atc ctc tgc gag atc atc gcc cgc atc cag gcc gat ccg gac tat ctt	1133
Ile Leu Cys Glu Ile Ile Ala Arg Ile Gln Ala Asp Pro Asp Tyr Leu	
229 234 239 244	
ccc cgc aca gag aat ttc ggg ctg gac tat gat gct ttc cag cac atg	1181
Pro Arg Thr Glu Asn Phe Gly Leu Asp Tyr Asp Ala Phe Gln His Met	
245 250 255 260	
gtg gga gac tgt ccc cca gat ttt ctg caa ctt act ttc aac tgc tgt	1229
Val Gly Asp Cys Pro Pro Asp Phe Leu Gln Leu Thr Phe Asn Cys Cys	
261 266 271 276	
aac atg gat ccc aaa ctg cgc cca tct ttt gtg gag att ggg aag acc	1277
Asn Met Asp Pro Lys Leu Arg Pro Ser Phe Val Glu Ile Gly Lys Thr	
277 282 287 292	
ctg gag gaa att ctg agc cgc cta cag gaa gaa gag cag gag agg gat	1325
Leu Glu Glu Ile Leu Ser Arg Leu Gln Glu Glu Glu Gln Glu Arg Asp	
293 298 303 308	
agg aag ctg cag ccc aca gcc agg gga ctc ttg gag aaa gca cct ggg	1373
Arg Lys Leu Gln Pro Thr Ala Arg Gly Leu Leu Glu Lys Ala Pro Gly	
309 314 319 324	
gtg aag cga cta agc tca ctg gat gac aag atc ccc cac aag tca cca	1421
Val Lys Arg Leu Ser Ser Leu Asp Asp Lys Ile Pro His Lys Ser Pro	
325 330 335 340	
tgc cca aga cgt acc atc tgg ctg tct cga agc cag tca gat atc ttt	1469
Cys Pro Arg Arg Thr Ile Trp Leu Ser Arg Ser Gln Ser Asp Ile Phe	
341 346 351 356	

tcc cgt aag ccc cca cgt aca gtg agt gtc ttg gac cca tac tac cgg	1517
Ser Arg Lys Pro Pro Arg Thr Val Ser Val Leu Asp Pro Tyr Tyr Arg	
357 362 367 372	
cca cga gat ggt gct gcc cgc acc ccc aaa gtc aac cct ttt agt gct	1565
Pro Arg Asp Gly Ala Ala Arg Thr Pro Lys Val Asn Pro Phe Ser Ala	
373 378 383 388	
cgc cag gac ctc atg ggg ggc aag atc aag ttt ttt gac ctg ccc agc	1613
Arg Gln Asp Leu Met Gly Gly Lys Ile Lys Phe Phe Asp Leu Pro Ser	
389 394 399 404	
aag tct gtc atc tct ctg gta ttt gac ctg gat gca cca ggg ccc gga	1661
Lys Ser Val Ile Ser Leu Val Phe Asp Leu Asp Ala Pro Gly Pro Gly	
405 410 415 420	
act atg ccc ctg gct gac tgg cag gag ccc ctg gcc cca cct att cgc	1709
Thr Met Pro Leu Ala Asp Trp Gln Glu Pro Leu Ala Pro Pro Ile Arg	
421 426 431 436	
cgg tgg cgt tcc ttg cct ggt tcg cct gag ttc ttg cat caa gag gct	1757
Arg Trp Arg Ser Leu Pro Gly Ser Pro Glu Phe Leu His Gln Glu Ala	
437 442 447 452	
tgt cca ttt gtg ggc cgg gaa gaa tcg cta tct gat ggg ccc cca cca	1805
Cys Pro Phe Val Gly Arg Glu Glu Ser Leu Ser Asp Gly Pro Pro Pro	
453 458 463 468	
cgc cta agt agt ctc aag tac aga gtt aaa gag atc cca cca ttc cgg	1853
Arg Leu Ser Ser Leu Lys Tyr Arg Val Lys Glu Ile Pro Pro Phe Arg	
469 474 479 484	
gca tct gcc cta cca gct gct caa gcc cat gag gct atg gac tgc tcc	1901
Ala Ser Ala Leu Pro Ala Ala Gln Ala His Glu Ala Met Asp Cys Ser	
485 490 495 500	
att ctc cag gaa gaa aat ggt ttt ggg tcc agg ccc cag ggg acc agt	1949
Ile Leu Gln Glu Glu Asn Gly Phe Gly Ser Arg Pro Gln Gly Thr Ser	
501 506 511 516	
cca tgc cct gcg ggt gct tct gag gag atg gag gta gaa gaa agg cca	1997
Pro Cys Pro Ala Gly Ala Ser Glu Glu Met Glu Val Glu Glu Arg Pro	
517 522 527 532	
gca ggc tca act cca gcc acc ttc tcc acc tca ggc ata ggc ctg caa	2045
Ala Gly Ser Thr Pro Ala Thr Phe Ser Thr Ser Gly Ile Gly Leu Gln	
533 538 543 548	
acc cag gga aag cag gat ggg tga ggggggttag tccctgcctc accttgggga	2099
Thr Gln Gly Lys Gln Asp Gly *	
549 554	
tggaccttca gctgaaacca tatggcccc taggtgcaca gccttgattc ttccttgagg	2159
cctacagagc aggcaggcta ggccaagcca ggctcaactt ctgggctccc agtgccatt	2219
ggctgtgtat gacgggaggc agcagtgaga ggcttccta gttagggccca acagctgata	2279

```

ccaagcctct gaaatccagc aaggaggtct gcctcccacc agaccctctc cagtgtactt 2339
ccccagatag gaccagagga tgtctagttc taggctgagc tggcaggcag ctattacccc 2399
ggttctttcc ccaccccagg tctgtctctt gccttttctt ggggcatata agctactgag 2459
tggaacatgg agctgatcaa gaggccgtaa tggatcatggc tgtttcccag acctgaatat 2519
tggggtgctt cttgccagta ttctaagaca tttgagtaat tgctgtttgc acttactgca 2579
tggtcagacc acgtcactac atttctatgc aaggggacag caaggcagcg tgggtggcat 2639
ggctcttagc taacctattc aaagaccttt tcctgttgat taatctattt tcatatttat 2699
aaaggagtct taatgttctg ccccataaga ctttcaacct tgtggttggg agtggggctg 2759
gttttgtagg ccctagggcc tgcttctatg tatttatcaa catgtgatac attcaattgg 2819
ttaaatggtt tatacagga ctgatttgct tcccttctctg ccatggctgg agctttggga 2879
acagtctgtc cttacagagc tgcaataaga aataaccaa gatgaagctg gtcaaatatt 2939
ttcataactt gcttctgttg attttttttt tgtaaaactt tccaagaca ttttcagact 2999
taaaaataaa gtcagtgtta caggtaaaaa aaaaaagtcg acg 3042

```

```

<210> 145
<211> 2958
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (402) .. (1985)

```

```

<400> 145
gaattcgagg ccgctcgagc ctcagcagag ctaccagctg ccctgttggc ttcgctggtc 60
ggatcgctct cctggccccg ccaaacaggc ggggggagcg gccccgactg tggggccatg 120
gcagtagtct cctcgttctc cgccgccgct agcctagctg agtcgccggc ttctgcgcta 180
ggggctccca ccgcctccgc aggctaagga gccgctgcc ccaacgagct gtgaggggta 240
ctatgctccc tctttgccgc cgtctctctc tcttgcccgc gcaggcacc ctctggctgc 300
tcagtcctgc ctgagtgtca aaccagaaga gaagtaaaat tcaacaaaaa tttatgtgtg 360
gagttccttc ttaaaagaag aaaaaagtga ttatttagac t atg gat cgg agc 413
Met Asp Arg Ser
1
aaa cgg aat tca att gca gga ttt cct cca cgt gtg gag cgt ctt gaa 461

```

Lys	Arg	Asn	Ser	Ile	Ala	Gly	Phe	Pro	Pro	Arg	Val	Glu	Arg	Leu	Glu	
5					10					15					20	
gag	ttt	gaa	gga	ggt	ggt	gga	gga	gaa	gga	aat	gtg	agc	cag	gtg	gga	509
Glu	Phe	Glu	Gly	Gly	Gly	Gly	Gly	Glu	Gly	Asn	Val	Ser	Gln	Val	Gly	
21					26					31					36	
aga	gtt	tgg	cca	tct	tcg	tat	cga	gct	ctt	ata	agt	gcc	ttt	tcc	aga	557
Arg	Val	Trp	Pro	Ser	Ser	Tyr	Arg	Ala	Leu	Ile	Ser	Ala	Phe	Ser	Arg	
37					42					47					52	
ctg	acg	cgt	ttg	gat	gat	ttc	acc	tgt	gaa	aaa	ata	ggg	tct	ggc	ttc	605
Leu	Thr	Arg	Leu	Asp	Asp	Phe	Thr	Cys	Glu	Lys	Ile	Gly	Ser	Gly	Phe	
53					58					63					68	
ttt	tct	gaa	gtg	ttc	aag	gta	cga	cac	cga	gct	tct	ggg	cag	gtg	atg	653
Phe	Ser	Glu	Val	Phe	Lys	Val	Arg	His	Arg	Ala	Ser	Gly	Gln	Val	Met	
69					74					79					84	
gct	ctt	aag	atg	aac	aca	ttg	agc	agt	aac	cgg	gca	aac	atg	ctg	aaa	701
Ala	Leu	Lys	Met	Asn	Thr	Leu	Ser	Ser	Asn	Arg	Ala	Asn	Met	Leu	Lys	
85					90					95					100	
gaa	gta	cag	ctc	atg	aat	aga	ctc	tcc	cat	ccc	aac	atc	ctt	agg	tat	749
Glu	Val	Gln	Leu	Met	Asn	Arg	Leu	Ser	His	Pro	Asn	Ile	Leu	Arg	Tyr	
101					106					111					116	
atc	aac	tcc	ggg	aac	ctg	gaa	cag	ttg	cta	gac	agt	aac	ctg	cat	ttg	797
Ile	Asn	Ser	Gly	Asn	Leu	Glu	Gln	Leu	Leu	Asp	Ser	Asn	Leu	His	Leu	
117					122					127					132	
cct	tgg	act	gtg	agg	gta	aaa	ctg	gcc	tat	gac	ata	gca	gtg	ggc	ctc	845
Pro	Trp	Thr	Val	Arg	Val	Lys	Leu	Ala	Tyr	Asp	Ile	Ala	Val	Gly	Leu	
133					138					143					148	
agc	tac	ctt	cac	ttc	aaa	ggc	att	ttt	cat	cgg	gac	ctc	aca	tct	aag	893
Ser	Tyr	Leu	His	Phe	Lys	Gly	Ile	Phe	His	Arg	Asp	Leu	Thr	Ser	Lys	
149					154					159					164	
aac	tgc	ctg	ata	aag	agg	gat	gag	aat	ggg	tac	tct	gca	gtg	gta	gct	941
Asn	Cys	Leu	Ile	Lys	Arg	Asp	Glu	Asn	Gly	Tyr	Ser	Ala	Val	Val	Ala	
165					170					175					180	
gac	ttt	ggc	ctg	gct	gag	aag	atc	ccc	gat	gtc	agc	atg	ggg	agt	gag	989
Asp	Phe	Gly	Leu	Ala	Glu	Lys	Ile	Pro	Asp	Val	Ser	Met	Gly	Ser	Glu	
181					186					191					196	
aag	ctg	gcc	gtg	gtg	ggt	tcc	cca	ttc	tgg	atg	gca	cct	gag	gtt	ctc	1037
Lys	Leu	Ala	Val	Val	Gly	Ser	Pro	Phe	Trp	Met	Ala	Pro	Glu	Val	Leu	
197					202					207					212	
cga	gat	gag	ccc	tat	aat	gaa	aag	aat	ttc	ggg	ctg	gac	tat	gat	gct	1085
Arg	Asp	Glu	Pro	Tyr	Asn	Glu	Lys	Asn	Phe	Gly	Leu	Asp	Tyr	Asp	Ala	
213					218					223					228	
ttc	cag	cac	atg	gtg	gga	gac	tgt	ccc	cca	gat	ttt	ctg	caa	ctt	act	1133
Phe	Gln	His	Met	Val	Gly	Asp	Cys	Pro	Pro	Asp	Phe	Leu	Gln	Leu	Thr	

229		234		239		244	
ttc aac tgc tgt aac atg gat ccc aaa ctg cgc cca tct ttt gtg gag	1181						
Phe Asn Cys Cys Asn Met Asp Pro Lys Leu Arg Pro Ser Phe Val Glu							
245		250		255		260	
att ggg aag acc ctg gag gaa att ctg agc cgc cta cag gaa gaa gag	1229						
Ile Gly Lys Thr Leu Glu Glu Ile Leu Ser Arg Leu Gln Glu Glu Glu							
261		266		271		276	
cag gag agg gat agg aag ctg cag ccc aca gcc agg gga ctc ttg gag	1277						
Gln Glu Arg Asp Arg Lys Leu Gln Pro Thr Ala Arg Gly Leu Leu Glu							
277		282		287		292	
aaa gca cct ggg gtg aag cga cta agc tca ctg gat gac aag atc ccc	1325						
Lys Ala Pro Gly Val Lys Arg Leu Ser Ser Leu Asp Asp Lys Ile Pro							
293		298		303		308	
cac aag tca cca tgc cca aga cgt acc atc tgg ctg tct cga agc cag	1373						
His Lys Ser Pro Cys Pro Arg Arg Thr Ile Trp Leu Ser Arg Ser Gln							
309		314		319		324	
tca gat atc ttt tcc cgt aag ccc cca cgt aca gtg agt gtc ttg gac	1421						
Ser Asp Ile Phe Ser Arg Lys Pro Pro Arg Thr Val Ser Val Leu Asp							
325		330		335		340	
cca tac tac cgg cca cga gat ggt gct gcc cgc acc ccc aaa gtc aac	1469						
Pro Tyr Tyr Arg Pro Arg Asp Gly Ala Ala Arg Thr Pro Lys Val Asn							
341		346		351		356	
cct ttt agt gct cgc cag gac ctc atg ggg ggc aag atc aag ttt ttt	1517						
Pro Phe Ser Ala Arg Gln Asp Leu Met Gly Gly Lys Ile Lys Phe Phe							
357		362		367		372	
gac ctg ccc agc aag tct gtc atc tct ctg gta ttt gac ctg gat gca	1565						
Asp Leu Pro Ser Lys Ser Val Ile Ser Leu Val Phe Asp Leu Asp Ala							
373		378		383		388	
cca ggg ccc gga act atg ccc ctg gct gac tgg cag gag ccc ctg gcc	1613						
Pro Gly Pro Gly Thr Met Pro Leu Ala Asp Trp Gln Glu Pro Leu Ala							
389		394		399		404	
cca cct att cgc cgg tgg cgt tcc ttg cct ggt tcg cct gag ttc ttg	1661						
Pro Pro Ile Arg Arg Trp Arg Ser Leu Pro Gly Ser Pro Glu Phe Leu							
405		410		415		420	
cat caa gag gct tgt cca ttt gtg ggc cgg gaa gaa tcg cta tct gat	1709						
His Gln Glu Ala Cys Pro Phe Val Gly Arg Glu Glu Ser Leu Ser Asp							
421		426		431		436	
ggg ccc cca cca cgc cta agt agt ctc aag tac aga gtt aaa gag atc	1757						
Gly Pro Pro Pro Arg Leu Ser Ser Leu Lys Tyr Arg Val Lys Glu Ile							
437		442		447		452	
cca cca ttc cgg gca tct gcc cta cca gct gct caa gcc cat gag gct	1805						
Pro Pro Phe Arg Ala Ser Ala Leu Pro Ala Ala Gln Ala His Glu Ala							
453		458		463		468	

atg gac tgc tcc att ctc cag gaa gaa aat ggt ttt ggg tcc agg ccc	1853
Met Asp Cys Ser Ile Leu Gln Glu Glu Asn Gly Phe Gly Ser Arg Pro	
469 474 479 484	
cag ggg acc agt cca tgc cct gcg ggt gct tct gag gag atg gag gta	1901
Gln Gly Thr Ser Pro Cys Pro Ala Gly Ala Ser Glu Glu Met Glu Val	
485 490 495 500	
gaa gaa agg cca gca ggc tca act cca gcc acc ttc tcc acc tca ggc	1949
Glu Glu Arg Pro Ala Gly Ser Thr Pro Ala Thr Phe Ser Thr Ser Gly	
501 506 511 516	
ata ggc ctg caa acc cag gga aag cag gat ggg tga gggg gtttagtccc	1999
Ile Gly Leu Gln Thr Gln Gly Lys Gln Asp Gly *	
517 522 527	
tgccctcacct tgggggatgga ccttcagctg aaaccatatg gccccctagg tgcacagcct	2059
tgattcttcc ctggagccta cagagcaggc aggctaggcc aagccaggct caacttctgg	2119
gctcccagtg ccattgggt gtgtatgacg ggaggcagca gtgagaggcc ttcctagtta	2179
gggccaacag ctgataccaa gcctctgaaa tccagcaagg aggtctgcct cccaccagac	2239
cctctccagt gtacttcccc agataggacc agaggatgtc tagttctagg ctgagctggc	2299
aggcagctat taccocgggt ctttccccac ccaggtctg tctcttgcct tttcttgggg	2359
catataagct actgagtgga acatggagct gatcaagagg ccgtaatgggt catggctggt	2419
tcccagacct gaatatggg gtgcttcttg ccagtattct aagacatttg agtaattgct	2479
gtttgcactt actgcatggt cagaccacgt cactacattt ctatgcaagg ggacagcaag	2539
gcagcgtgggt ggtcatggct cttagctaac ctattcaaag accttttctt gttgattaat	2599
ctattttcat atttataaag gagtcttaat gttctgcccc ataagacttt caaccttggtg	2659
gttgggagtg gggctgggtt tgtaggccct agggcctgct tctatgtatt tatcaacatg	2719
tgatacattc aattgggttaa atggtttata cagggactga tttgcttccc ttcttgccat	2779
ggctggagct ttgggaacag tctgtcctta cagagctgca ataagaaata accaaagatg	2839
aagctgggtca aatattttca taacttgctt ctgttgattt tttttttgta aaactttccc	2899
aagacatfff cagacttaaa aataaagtca gtgttacagg taaaaaaaaa aagtcgacg	2958

<210> 146
 <211> 3353
 <212> DNA
 <213> Homo sapiens

[illegible]

515

act gaa ggc aaa cgg act atc gtc cgg cag gga aag cag gtg gtg ttc	681
Thr Glu Gly Lys Arg Thr Ile Val Arg Gln Gly Lys Gln Val Val Phe	
194 199 204 209	
cga gat gag gac agc act ggc aat gat gag gac atc atg gtg gac tca	729
Arg Asp Glu Asp Ser Thr Gly Asn Asp Glu Asp Ile Met Val Asp Ser	
210 215 220 225	
gat gac gat tcc tgg gac ctc gtg acc tgc ttc tgc atg aag cca ttt	777
Asp Asp Asp Ser Trp Asp Leu Val Thr Cys Phe Cys Met Lys Pro Phe	
226 231 236 241	
gcc ggc cgc ccc atg atc gag tgt aat gag tgc cac acc tgg att cac	825
Ala Gly Arg Pro Met Ile Glu Cys Asn Glu Cys His Thr Trp Ile His	
242 247 252 257	
ctg tcc tgt gcg aaa atc cgg aaa tcc aat gtt cca gaa gtg ttt gtc	873
Leu Ser Cys Ala Lys Ile Arg Lys Ser Asn Val Pro Glu Val Phe Val	
258 263 268 273	
tgc caa aag tgc cgg gac tcc aag ttt gac atc cgc cgt tcc aac cgc	921
Cys Gln Lys Cys Arg Asp Ser Lys Phe Asp Ile Arg Arg Ser Asn Arg	
274 279 284 289	
tcg cgg acg ggc tcc cgg aag ctg ttc ctg gac tga ctgc tggctggcga	971
Ser Arg Thr Gly Ser Arg Lys Leu Phe Leu Asp *	
290 295 300	
ggaggctgcg agcgtggaat cggaagcgac cgcgggcttt tttgcccttc tcttagttga	1031
gcacagaacc ctacgtctctg gtgcggggcag atccctgcca tttaggtgcc taagcaaaag	1091
gacaggctgt ccaaggtaga aactgtacat agccggtgac cgaatgcgac ctttgccagc	1151
cagagctgct gccagagctg cgttccctgc agtggaggtg gactggacac ccacgtgcag	1211
cgggttttggc tcatttgaaa atgaggggtcc gtggttagctg tgcgttttgc tatcattgct	1271
aagagattcc cgctgattgg gctcagtgcc agctgttatt ctgcttcac tgtgttgggg	1331
agaggtgttc ggtttcccca gcctgttaat gaacagccat acgtgtaagc tttttcttga	1391
gtgttaagtc ttttacaaa agtgtctgta cagcagccat ccaagttgcc cctacttagt	1451
ggcttgccct ctgcctgcct cagctgctgc ctgaccggct gggggaggca ctggcgggag	1511
gcctcgggct cccctggaag ggcgctgggc tggcgggtca gctggtggtt cttaggtttc	1571
cttctgtttg ttaaaaaggga caatgtggcc acttctctgt ggaaaggag ttggttgggg	1631
ggttgagatg gcccggtgttc ataactcagt ttctgtttt gcacgatgta aaaaccctgt	1691
ctttttgcac gatacagcca aaagtattgg ctgatttctt gctgagtgcc ctcttagttg	1751
gtgtgtgagg tcttggtggg ctcaggccag ctgtttgcga gtgtgggaac tcataggttc	1811
tgtctttgtc tcttcctttc acctcattct ggtagcagca taaaggttag gcaatcactg	1871

ggacccgcat ggtgttcctc caaagaatag ggtaaaggag agctgggagg gagccctctc	1931
cgttggggtga ctcttggtg ccctttagac aggctggcct gccggttcca caggggtacag	1991
ttaggacttg agtctttctt tttctgtttt gagttgggtga gtgagtgata gggtaacatg	2051
ggccttcagg atgacccctt ggaactgtgc cgagttcctt aaatctcagc tgggatcctg	2111
gacctgggag gccctgtga gggccagctc tggaaaaacc tgggagttga tgccggaggc	2171
tgtggaagaa ctctgctcga gggcaggggtg ccctggaaca ctggtagttc tggggctggg	2231
agggagaggg gctccggctt tctctgaaat gaacactgct cttcagcagt tcaagtactt	2291
gttctcaaaa cattttctaa ttgattggta ggttttcata agcattgttt ctttaaggca	2351
tggaaaggga agaatgctca agcaagtcac gtttgttttc agtgggatgg gcccgcgctc	2411
tcactgctgg gggcttcccc ttcattgtggc acctttgtgc caggccacca ggcagactct	2471
tcccaccttc tcccactgaa gcaccaaggg gcttgaaccg taatttggtt aatcagaggc	2531
atTTTTTTTg tcttagtatt tttcacactt gtccaaccgt cttatTTTTt taaaagttct	2591
gttgcttgta ttaacacgaa actagagaga aatagtttct gaagccagtt tattgtgaag	2651
atcccccaagg gggaggttcg gtagagaaaa atagtaagct ggtttagaaa ctgacgaggg	2711
caaacagcca ggacgcattg gagaggaatt tgccaaagat ctaccctgag ataacgcctg	2771
tccagtgtct tcaccacgtg aataaccagc gtcctcaaagt gtttttctgc tttgaaaaaa	2831
aaaaattcca caagctttta aagggtgcatt taagaatcca tgtgacttta gaatggaact	2891
gccggccctg gcaactgtca cgtgtgctag aaggttcgat gcctctggaa tgcattgtgat	2951
actcatctcc attttgtttc cttgattgca tttttgttct tttagcagat ctgtccctgt	3011
gggtggtgtc taagaagtcg gacaccttgg tttttgtgtt agattgagct gggcagctgc	3071
aatcagcttc tttatatgca aattaggcac gacccatctg tggttcctgg ttggtggcta	3131
atgaagtgag gggagggagg gatgtcacc caaaagtagg ccctccatt ggctttggcc	3191
aggccagaca cttcacatcg tttacatggg tctgtgtaat tttaaagttt atgtgtataa	3251
agcgaagctg tttctgtgaa actgtatat ttgtaaataa atatattgct actttgaggt	3311
tcattgattca aggttcaggc gattgctgtc tgtgctgaag ga	3353

<210> 147
 <211> 7838
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (673) .. (2616)

<400> 147

tgaatgagtc	tcatcctgca	cttgcagaat	ggtgcagttt	gggcagatat	agtcttcccc	60
attcctttcc	aaaagcctcc	ctcgagcctc	agaaatgccc	acacaatcgc	catgaaacca	120
ttcttcacag	cggtcacagc	aaatcataaa	cctgttggtg	tgaggctggc	ggcaaagtca	180
atacagggcg	ttggggtcgt	accctcacat	tcaggcttcg	tattttcaac	aactcagatt	240
atctagaggc	tgttcccgtg	gagtaagctc	cttcgcctcc	gactcagtgt	agacgtcgcc	300
atcccgggtc	cagatttccg	cgctccaacg	cctccgcagc	agccatcttg	ccagagggcc	360
gacgcccttt	tgactctggc	gccaacccgt	agtgcgtggt	cgccgcgagg	ggagttctgc	420
gcaagtacgg	aagctgaggt	tccgcgcttc	cgggagaccg	tccgctccgc	cccctcgcgg	480
gggcgcttca	ttggtcacg	gctcgcgtc	tcgcgtctc	ttgctgtcgc	gagagcccag	540
gagaggctgc	ggagccgcag	ccgccagac	cgcgcagcgc	gggaggcagg	ttccgcacgt	600
gggaggcagc	ccaagcgcac	tgagcgcgtg	gagcagttcc	tgaccattgc	gcggcgccgc	660
ggcaggagga	gc	atg cct gtc tcc ctg gag gat tct ggt gag ccc acg				708
		Met Pro Val Ser Leu Glu Asp Ser Gly Glu Pro Thr				
		1 5 10				
tcc tgc ccc gcc aca gac gcc gag aca gcc tcc gag ggc agc gtg gaa						756
Ser Cys Pro Ala Thr Asp Ala Glu Thr Ala Ser Glu Gly Ser Val Glu						
13 18 23 28						
agc gct tct gag acc aga agc ggc ccc cag tct gct tcc aca gct gtg						804
Ser Ala Ser Glu Thr Arg Ser Gly Pro Gln Ser Ala Ser Thr Ala Val						
29 34 39 44						
aag gaa cga cca gcc tct tct gaa aag gtg aaa gga ggg gat gac cac						852
Lys Glu Arg Pro Ala Ser Ser Glu Lys Val Lys Gly Gly Asp Asp His						
45 50 55 60						
gat gac acc tcc gat agt gac agc gat ggc ctg acc ttg aaa gag ctt						900
Asp Asp Thr Ser Asp Ser Asp Ser Asp Gly Leu Thr Leu Lys Glu Leu						
61 66 71 76						
cag aat cgc ctt cgc agg aag cgg gaa cag gag ccc act gag agg ccc						948
Gln Asn Arg Leu Arg Arg Lys Arg Glu Gln Glu Pro Thr Glu Arg Pro						
77 82 87 92						
ctg aaa ggg atc cag agt cgc ctg cgg aag aag cgc cgg gag gag ggt						996
Leu Lys Gly Ile Gln Ser Arg Leu Arg Lys Lys Arg Arg Glu Glu Gly						
93 98 103 108						

ccc gcc gag act gtg ggc tcc gag gcc agt gac act gtg gag ggc gtc	1044
Pro Ala Glu Thr Val Gly Ser Glu Ala Ser Asp Thr Val Glu Gly Val	
109 114 119 124	
ctg ccc agt aag cag gag ccc gag aac gat cag ggg gtt gtg tcc cag	1092
Leu Pro Ser Lys Gln Glu Pro Glu Asn Asp Gln Gly Val Val Ser Gln	
125 130 135 140	
gct ggg aaa gat gac aga gag agt aag ttg gag gga aag gcg gct cag	1140
Ala Gly Lys Asp Asp Arg Glu Ser Lys Leu Glu Gly Lys Ala Ala Gln	
141 146 151 156	
gac atc aaa gat gag gag cct gga gac ttg ggc cga ccg aag cct gaa	1188
Asp Ile Lys Asp Glu Glu Pro Gly Asp Leu Gly Arg Pro Lys Pro Glu	
157 162 167 172	
tgt gag ggt tac gac ccc aac gcc ctg tat tgc att tgc cgc cag cct	1236
Cys Glu Gly Tyr Asp Pro Asn Ala Leu Tyr Cys Ile Cys Arg Gln Pro	
173 178 183 188	
cac aac aac agg ttt atg att tgc tgt gac cgc tgt gaa gaa tgg ttt	1284
His Asn Asn Arg Phe Met Ile Cys Cys Asp Arg Cys Glu Glu Trp Phe	
189 194 199 204	
cat ggc gat tgt gtg ggc att tct gag gct cga ggg agg ctt ttg gaa	1332
His Gly Asp Cys Val Gly Ile Ser Glu Ala Arg Gly Arg Leu Leu Glu	
205 210 215 220	
agg aat ggg gaa gac tat atc tgc cca aac tgc acc att ctg caa gtg	1380
Arg Asn Gly Glu Asp Tyr Ile Cys Pro Asn Cys Thr Ile Leu Gln Val	
221 226 231 236	
cag gat gag act cat tca gaa acg gca gat cag cag gaa gct aaa tgg	1428
Gln Asp Glu Thr His Ser Glu Thr Ala Asp Gln Gln Glu Ala Lys Trp	
237 242 247 252	
aga cct gga gat gct gat ggc acc gat tgt aca agt ata gga aca ata	1476
Arg Pro Gly Asp Ala Asp Gly Thr Asp Cys Thr Ser Ile Gly Thr Ile	
253 258 263 268	
gag cag aag tct agc gaa gac caa ggg ata aag ggt aga att gag aaa	1524
Glu Gln Lys Ser Ser Glu Asp Gln Gly Ile Lys Gly Arg Ile Glu Lys	
269 274 279 284	
gct gca aat cca agt ggc aag aag aaa ctc aag atc ttc cag cct ggt	1572
Ala Ala Asn Pro Ser Gly Lys Lys Lys Leu Lys Ile Phe Gln Pro Gly	
285 290 295 300	
ccc ggg cct gtc ccc acc cag ctg cct gtc ctc tgg cag gta ttg gaa	1620
Pro Gly Pro Val Pro Thr Gln Leu Pro Val Leu Trp Gln Val Leu Glu	
301 306 311 316	
att gct gtg tct aga agc atc tct gcc ttc aca ctc ttg cac tgc att	1668
Ile Ala Val Ser Arg Ser Ile Ser Ala Phe Thr Leu Leu His Cys Ile	
317 322 327 332	
agc tgc aag gtg ata gag gcg cct ggt gcc tca aaa tgt att ggc ccc	1716

Ser Cys Lys Val Ile Glu Ala Pro Gly Ala Ser Lys Cys Ile Gly Pro	
333 338 343 348	
ggg tgc tgt cac gtg gcg cag ccc gac tcg gtg tac tgc agt aat gac	1764
Gly Cys Cys His Val Ala Gln Pro Asp Ser Val Tyr Cys Ser Asn Asp	
349 354 359 364	
tgt atc ctc aaa cac gcc gca gcg aca atg aag ttt cta agc tca ggt	1812
Cys Ile Leu Lys His Ala Ala Ala Thr Met Lys Phe Leu Ser Ser Gly	
365 370 375 380	
aaa gaa cag aag cca aag cct aaa gaa aag atg aag atg aag cca gag	1860
Lys Glu Gln Lys Pro Lys Pro Lys Glu Lys Met Lys Met Lys Pro Glu	
381 386 391 396	
aag ccc agt ctt ccg aaa tgc ggt gct cag gca ggt att aaa atc tct	1908
Lys Pro Ser Leu Pro Lys Cys Gly Ala Gln Ala Gly Ile Lys Ile Ser	
397 402 407 412	
tct gtg cac aag aga cca gct cca gaa aaa aaa gag acc aca gtg aag	1956
Ser Val His Lys Arg Pro Ala Pro Glu Lys Lys Glu Thr Thr Val Lys	
413 418 423 428	
aag gca gtg gtg gtc cct gcg cgg agt gaa gca ctc ggg aag gaa gca	2004
Lys Ala Val Val Val Pro Ala Arg Ser Glu Ala Leu Gly Lys Glu Ala	
429 434 439 444	
gct tgt gag agc agc acg ccg tcg tgg gcg agc gat cac aat tac aat	2052
Ala Cys Glu Ser Ser Thr Pro Ser Trp Ala Ser Asp His Asn Tyr Asn	
445 450 455 460	
gca gta aag cca gaa aag act gct gct ccc tcg ccg tca ctg ttg tat	2100
Ala Val Lys Pro Glu Lys Thr Ala Ala Pro Ser Pro Ser Leu Leu Tyr	
461 466 471 476	
aaa tcc acg aag gaa gac agg agg tcc gag gag aaa gcg gca gcc acg	2148
Lys Ser Thr Lys Glu Asp Arg Arg Ser Glu Glu Lys Ala Ala Ala Thr	
477 482 487 492	
gca gcc tca aag aaa aca gcc cct cca ggc tcc acg gtg ggc aag cag	2196
Ala Ala Ser Lys Lys Thr Ala Pro Pro Gly Ser Thr Val Gly Lys Gln	
493 498 503 508	
cct gca cct aga aac ctc gtg cca aag aag tct tct ttt gct aat gtg	2244
Pro Ala Pro Arg Asn Leu Val Pro Lys Lys Ser Ser Phe Ala Asn Val	
509 514 519 524	
gca gca gcc aca cca gcc att aaa aag cca ccc tca ggt ttc aag ggc	2292
Ala Ala Ala Thr Pro Ala Ile Lys Lys Pro Pro Ser Gly Phe Lys Gly	
525 530 535 540	
acc atc ccc aag agg cca tgg ctc tcc gct acc cca tcg agt ggt gct	2340
Thr Ile Pro Lys Arg Pro Trp Leu Ser Ala Thr Pro Ser Ser Gly Ala	
541 546 551 556	
tca gct gcc agg cag gcc gga ccg gca cct gca gcg gcg acg gct gcc	2388
Ser Ala Ala Arg Gln Ala Gly Pro Ala Pro Ala Ala Ala Thr Ala Ala	

557	562	567	572	
tcc aag aag ttc cct ggc tcc gct gct ttg gtg gga gcc gta agg aag				2436
Ser Lys Lys Phe Pro Gly Ser Ala Ala Leu Val Gly Ala Val Arg Lys				
573	578	583	588	
cca gtg gta cct tct gtt cca atg gcc tcg cca gcc cca gga cgc ctt				2484
Pro Val Val Pro Ser Val Pro Met Ala Ser Pro Ala Pro Gly Arg Leu				
589	594	599	604	
ggg gct atg agt gct gca cca tcg cag cca aat tca caa att cgg caa				2532
Gly Ala Met Ser Ala Ala Pro Ser Gln Pro Asn Ser Gln Ile Arg Gln				
605	610	615	620	
aat atc aga cgc tcc tta aaa gag att ttg tgg aaa agt tcc ttt ttt				2580
Asn Ile Arg Arg Ser Leu Lys Glu Ile Leu Trp Lys Ser Ser Phe Phe				
621	626	631	636	
tta ttc tgt tca gag tca atg aca gcg atg act taa tcat gacagaaaac				2630
Leu Phe Cys Ser Glu Ser Met Thr Ala Met Thr *				
637	642	647		
gaagtaggaa aaattgccct ccatattgag aaggagatgt ttaacttggt tcaagttaca				2690
gataatcgct acaagagtaa atatcgacgc atcatgttca acctgaagga ccctaaaaat				2750
cagggactct tccatcgtgt tctgcgtgag gaaatctctt tggcgaaact tgtgagactg				2810
aagccagaag aacttgatc taaagagctt tccacgtgga aagagaggcc agcgagatct				2870
gtgatggagt ccagaactaa actgcacaat gaaagcaaga agacggcccc caggcaggag				2930
gccatccccg atctggagga ctctccgcca gtgtcggatt cagaggaaca gcaagagtca				2990
gcacgtgctg tccctgagaa gagcacagcg ccgcttctcg acgtcttcag cagcatgttg				3050
aaagacacca ccagtcagca ccgcgcacac ctcttcgacg tcaactgtaa aatttgcaca				3110
ggccagggtc cctccgcaga agatgagcca gctccgaaaa aacaaaaatt gtcagcttct				3170
gttaagaaag aagacttaaa atcaaagcat gacagctctg cacctgaccc agctccggat				3230
tcagctgatg aggtgatgcc ggaggctgtg cctgaagttg cctctgagcc aggcctagaa				3290
agtgttctc atccaaatgt ggacagaacg tatttccctg ggccctcagg agatggccat				3350
cccgagccct ccccgctgga agacctgtcc ccctgccag cctcctgtgg gagcgggggtg				3410
gtcaccaccg tcacagtgtc cggccgggac ccaggaccg ctccaagcag ttcattgcaca				3470
gccgtggcct ccgcagcatc ccgcccagac agcaccaca tgggtggaagc cagacaggat				3530
gtgccgaagc ctgtcttgac ttctgtgatg gtgcccaagt ccatactagc taagccatcc				3590
tcattctctg acccaagata cctgtcagtt cctccgtcac caaatatcag cacttcagaa				3650
tcacgttccc ctccagaggg agacacgacc ctctttttgt ctcgactcag caccatttgg				3710

aaaggattta ttaacatgca gagtgtggca aaatttgtca ctaaggcgta tcctgtctct	3770
gggtgttttg attacctcag tgaggatttg cctgacacaa ttcacattgg tgggaggatc	3830
gcaccgaaga cagtttggga ttatgttggc aaactcaagt cttctgtgtc taaggagctc	3890
tgtctgatcc gcttccaccc cgccacagag gaagaggagg tgcctatat ctctctctac	3950
tcctatttca gcagccgtgg ccgctttggt gttgtagcta ataacaacag gcacgtcaag	4010
gacctctacc tgatcccgt gagcgcccag gacctgttc catccaaact cttgcccttt	4070
gagggaccag gtaagcgccg gctttctggg tggagggtgag gccacactgc acctgcaccc	4130
ctcctccac tgacatgcc tgctgagtcc tgaccagccc agggctctct gggagcagga	4190
gttaggagca cagacgcagc ggtagcaat aggattcatc tttgagggcg taggactgtg	4250
gcacgagaag taccctgat tcacagcata aattgtctta ggagagtttt ttagagaggg	4310
aaaaaccac agcctgcaac cagctcatct tggcctcagg tcagagaaga ctcagtgcc	4370
aggagcccaa ggctcagcca gaaaggagg tgacactccc agcgccctg ctctttctc	4430
tagacagact cgggagccag cacacaccgg gaagtggctc catcagggat cacttctcta	4490
acagggatgg atttccagga gacttaacaa taatgacata gaaaactatt tctagaaata	4550
attattttta aatctgcagc tcaaattgta atagttcatt catctttggc aagctatttt	4610
gtgtttgcac gttccttgga aagtactgta tttaaacgat tatttacaaa tagcctaaaa	4670
tacatctttg tcaagggtg agggtgattc caggggccac gtgctctgtt agtgaccagc	4730
tctttcatag ccccttagaa gaagctgatg tgacttcagt taggggttag tatctgatgc	4790
ccaactgaag tgtctccgtg gccatgcagt cccagagga ttggtgttct ctcaaagcgg	4850
gtgtgtggat cacacagtgt cctctaaagt gcttcgtcat aaaggcagg gctgtctgga	4910
ccctgtgcct cagtgcctc tgtccctgtc accaggcctc ggcggtgtt cctgccatag	4970
ctgtgcaggg tgttccacc cacaccctc atgccgcacc ctagctagct ggggtcctgt	5030
aggggccact ccacatcttg ggcgggactt ctgtcgcccc aggcacagcc cacgttccta	5090
ctggagccca ttcttcacag ctggagtggg ctcagcctat gcctgtgttg tgggaattata	5150
tgtccataaa gggattgggt ggtatcagta atttcagggt taaatatttg ctggcggtgt	5210
gcattaaatt attttagtgc cagataaatt tttaaaagca aagtgcctta gtgtgtcccc	5270
tcaaatecta cttgggataa agagatgcc cctaattgggt ggcagaaagg accctggtag	5330
aggttcttgg tgttgcttgt gaagagctct ggccagctcc acgtgaccag ggagaggaaa	5390

agccccggccc	tcctggaggt	gaagaccgag	aagctggcct	ctccgcacct	gtgaagaccc	5450
actggtcagt	tgcaagtgcg	acagtgtgtg	cactcagtgc	agacactgca	gcacctcagc	5510
acctccctac	cggggtgga	agagcacttt	ttcttttacag	aaacatgatt	cttagatagc	5570
gagcctcccc	tttttaaaac	aattgaagcg	atatttcac	ctttcttgag	cttctctccc	5630
tgctcatctc	caaacttgga	gctgtcaggt	gagcacaggt	tgtaggggtgt	tgagcgagcc	5690
ccggcgcatg	ccgggcaccg	gggttcccca	cacttgggca	gtgacggggc	ccagggaggc	5750
caccagagga	gcgggcgctc	cattctcccc	acagcaaggg	ctggctgtgc	aggtgcagcc	5810
ccggggcaga	gggaaaggac	aggtctccca	gcacctcccg	gatggcaccg	ggacaaggag	5870
ggctgggctg	gggtcactca	ccttgtctgc	tgagtgcgat	ggcaccaacc	acctcactg	5930
tcagctccgc	gaccagctgg	gggaacgtca	cactcgccca	ccaaggcact	tgctgaggcc	5990
acgacgccgc	ctgacgggga	cacacaaaag	cccaggggac	tttgatccac	gataaagagc	6050
agaggcgtct	gggtaaagta	acacagggca	agggacttta	gaaaagtaac	agctagttaa	6110
acctttccat	acacttcaga	aatgttttaa	cttaagactt	cagtataatg	ttactttctc	6170
ctgatgtcct	tggtgacatg	aatgcgtgtg	cgtgaaatct	cacacacttc	catggtcact	6230
aaacagcctt	caccccgggc	caggccatcg	ggtactcggc	ccgcttcacg	tactgattac	6290
ttgacttggc	gttttctaga	tataaacatg	tacatgtgtg	tcctggcttt	gtggtgtaaa	6350
tgtgtagtgc	gtgtgcatgt	gcgcgcgtgt	gtgtgtgtaa	ggctaggtcc	tggcatgttt	6410
cccctgtctc	agcggaccct	gtcctcacgg	agatagccca	gaagcccttg	gacagcacag	6470
gccacacctg	aggggtgctga	tggtggtgac	tccacagagc	tgtggtcagg	ggtgagcgtg	6530
tgctgcgcag	cttggagtca	cgccccaga	agtgtgggt	gagggctctgc	aggaccagc	6590
tccattccac	agcctcagtt	ctctgcggca	catgcagcac	aggcctgaag	gagacctggc	6650
gccccagcct	tgagctgccc	gtctgcatca	gggcactgat	gtgggagcat	cttcccctgg	6710
ggatgttaag	gagaagggtcc	tggtgggggt	agagattcac	gcagaaaaga	gtgactgact	6770
cgtccgtgtg	cctcagttta	taccacacaa	ttgcagggtgt	ccatgcctcc	cacacatggg	6830
gacctagtgg	gttttgacag	cgtgggtgtcc	agtcctagcc	ccctcagtgc	ttgtgtttca	6890
cacttaagca	agtgaaggcc	tgaagggtgcc	cagctgtgcc	ctcaggggaa	acttaagtca	6950
cccgccctgt	cagcacttgg	cccttgtcgg	gcagtgagag	tggagctgcc	cccgagcac	7010
cctcaggagc	catgcagttc	acagcagtag	ctggatctcc	ctgaggacat	ttgtccttgc	7070
atatottaat	gatttgtcca	cagaaacacc	gggttgtctt	cctctgcccc	tctgccccgc	7130

```

agtgggggca ctctctgtaa ctcagcatca cgggtggggg cagctgggag gcctggttcc 7190
aggtgacctt ctccacctag atgttcaccc cactcagttc cagctttacc aacagggccc 7250
cccgagggga cttggggtcg cagagtcccg gcctgtctca gggccttggt catggaaggg 7310
agatgagtca ggttgaaagc tcctcgtgta gggttctgtg cggggccctt acaggactgg 7370
accgcagcca agatgcctgc ctgttaacca tgcccagccc ccgtcatttc cgcgtgaagc 7430
cgcaggcctc ggagccttgg tctgaaatgc ctgtggagta acctcgggcc ataaacatgg 7490
gtgcacagtc tgttctcccc aagtacaggg caggaggaaa caccgccctc tgtagctgct 7550
cgaatggaaa gggctctttt ctctgaggtc ttatatacatt agaaagctct tctgggaaga 7610
atgtttgaat ccatagtgtc tttctgtatt cacttttaat tgctttctaa attagctgag 7670
aaattctgac ttgaaatatt gtcaggttaag catttcttca gttttcatgt gtgtatgtaa 7730
cagtagcttt gcatggaaat tgtaatcaga gtcaaataca gtattgaatg gaatgtactg 7790
ccttctcttc ctaaatacat aaacatcttt catggaaaaa aaaaaaaa 7838

```

```

<210> 148
<211> 3484
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (131) .. (3178)

```

```

<400> 148
cgcccagcag cccgtgggca ggcgcgggcg agcgagcggg gccggcgggcg ggcgcagagg 60
gacgcagagg cctcggggcg gggctggccc ggggttccag gtctccagtg ggggctgcag 120
actaagcaaa atg agg cgg ttc ctg agg cca ggg cat gac cct gtg cgg 169
          Met Arg Arg Phe Leu Arg Pro Gly His Asp Pro Val Arg
            1             5             10

gag agg ctc aag cgg gac ctg ttc cag ttt aac aag acg gtg gag cat 217
Glu Arg Leu Lys Arg Asp Leu Phe Gln Phe Asn Lys Thr Val Glu His
  14             19             24             29

ggc ttc ccg cac cag ccc agc gcc ctc ggc tac agc ccg tcc ctg cgc 265
Gly Phe Pro His Gln Pro Ser Ala Leu Gly Tyr Ser Pro Ser Leu Arg
  30             35             40             45

atc ctg gcc atc ggc acc cgt tct gga gcc atc aag ctc tac gga gcc 313
Ile Leu Ala Ile Gly Thr Arg Ser Gly Ala Ile Lys Leu Tyr Gly Ala
  46             51             56             61

```

cca ggc gtg gag ttc atg ggg ctg cac cag gag aac aac gct gtg acg	361
Pro Gly Val Glu Phe Met Gly Leu His Gln Glu Asn Asn Ala Val Thr	
62 67 72 77	
cag atc cac ctc ctg ccc ggc cag tgc cag ctg gtc acc ctg ctg gat	409
Gln Ile His Leu Leu Pro Gly Gln Cys Gln Leu Val Thr Leu Leu Asp	
78 83 88 93	
gac aac agc ctg cac ctt tgg agc ctg aag gtc aag ggc ggg gca tcg	457
Asp Asn Ser Leu His Leu Trp Ser Leu Lys Val Lys Gly Gly Ala Ser	
94 99 104 109	
gag ctg cag gag gat gag agc ttc aca ctg cgt gga ccc cca ggg gct	505
Glu Leu Gln Glu Asp Glu Ser Phe Thr Leu Arg Gly Pro Pro Gly Ala	
110 115 120 125	
gcc ccc agt gcc aca cag atc acc gtg gtc ctg cca cat tcc tcc tgc	553
Ala Pro Ser Ala Thr Gln Ile Thr Val Val Leu Pro His Ser Ser Cys	
126 131 136 141	
gag ctg ctc tac ctg ggc acc gag agt ggc aac gtg ttt gtg gtg cag	601
Glu Leu Leu Tyr Leu Gly Thr Glu Ser Gly Asn Val Phe Val Val Gln	
142 147 152 157	
ctg cca gct ttt cgt gcg ctg gag gac cgg acc atc agc tcg gac gcg	649
Leu Pro Ala Phe Arg Ala Leu Glu Asp Arg Thr Ile Ser Ser Asp Ala	
158 163 168 173	
gtg ctg cag cgg ttg cca gag gag gcc cgc cac cgg cgt gtg ttc gag	697
Val Leu Gln Arg Leu Pro Glu Glu Ala Arg His Arg Arg Val Phe Glu	
174 179 184 189	
atg gtg gag gca ctg cag gag cac cct cga gac ccc aac cag atc ctg	745
Met Val Glu Ala Leu Gln Glu His Pro Arg Asp Pro Asn Gln Ile Leu	
190 195 200 205	
atc ggc tac agc cga ggc ctc gtt gtc atc tgg gac cta cag ggc agc	793
Ile Gly Tyr Ser Arg Gly Leu Val Val Ile Trp Asp Leu Gln Gly Ser	
206 211 216 221	
cgc gtg ctc tac cac ttc ctc agc agc cag caa ctg gag aac atc tgg	841
Arg Val Leu Tyr His Phe Leu Ser Ser Gln Gln Leu Glu Asn Ile Trp	
222 227 232 237	
tgg cag cgg gac ggc cgc ctg ctc gtc agc tgt cac tct gac ggc agc	889
Trp Gln Arg Asp Gly Arg Leu Leu Val Ser Cys His Ser Asp Gly Ser	
238 243 248 253	
tac tgc cag tgg ccc gtg tcc agc gaa gcc cag caa cca gag ccc ctc	937
Tyr Cys Gln Trp Pro Val Ser Ser Glu Ala Gln Gln Pro Glu Pro Leu	
254 259 264 269	
cgc agc ctc gtg cct tac ggt ccc ttt cct tgc aaa gcg att acc aga	985
Arg Ser Leu Val Pro Tyr Gly Pro Phe Pro Cys Lys Ala Ile Thr Arg	
270 275 280 285	

atc Ile 286	ctc Leu	tgg Trp	ctg Leu	acc Thr	act Thr 291	agg Arg	cag Gln	ggg Gly	ttg Leu	ccc Pro 296	ttc Phe	acc Thr	atc Ile	ttc Phe	cag Gln 301	1033
ggg Gly 302	ggc Gly	atg Met	cca Pro	cgg Arg	gcc Ala 307	agc Ser	tac Tyr	ggg Gly	gac Asp	cgc Arg 312	cac His	tgc Cys	atc Ile	tca Ser	gtg Val 317	1081
atc Ile 318	cac His	gat Asp	ggc Gly	cag Gln	cag Gln 323	acg Thr	gcc Ala	ttc Phe	gac Asp	ttc Phe 328	acc Thr	tcc Ser	cgt Arg	gtc Val	atc Ile 333	1129
ggc Gly 334	ttc Phe	act Thr	gtc Val	ctc Leu	aca Thr 339	gag Glu	gca Ala	gac Asp	cct Pro	gca Ala 344	gcc Ala	acc Thr	ttt Phe	gac Asp	gac Asp 349	1177
ccc Pro 350	tat Tyr	gcc Ala	ctg Leu	gtg Val	gtg Val 355	ctg Leu	gct Ala	gag Glu	gag Glu	gag Glu 360	ctg Leu	gtg Val	gtg Val	att Ile	gac Asp 365	1225
ctg Leu 366	cag Gln	aca Thr	gca Ala	ggc Gly	tgg Trp 371	cca Pro	ccg Pro	gtc Val	cag Gln	ctg Leu 376	ccc Pro	tac Tyr	ctg Leu	gct Ala	tct Ser 381	1273
ctg Leu 382	cac His	tgt Cys	tcc Ser	gcc Ala	atc Ile 387	acc Thr	tgc Cys	tct Ser	cac His	cac His 392	gtc Val	tcc Ser	aac Asn	atc Ile	ccg Pro 397	1321
ctg Leu 398	aag Lys	ctg Leu	tgg Trp	gag Glu	cgg Arg 403	atc Ile	att Ile	gcc Ala	gcc Ala	ggc Gly 408	agc Ser	cgg Arg	cag Gln	aac Asn	gca Ala 413	1369
cac His 414	ttc Phe	tcc Ser	acc Thr	atg Met	gag Glu 419	tgg Trp	cca Pro	att Ile	gat Asp	ggg Gly 424	ggc Gly	acc Thr	agc Ser	ctg Leu	acc Thr 429	1417
cca Pro 430	gcc Ala	cca Pro	ccc Pro	cag Gln	agg Arg 435	gac Asp	ctg Leu	ctg Leu	ctc Leu	aca Thr 440	ggg Gly	cac His	gag Glu	gac Asp	ggc Gly 445	1465
acg Thr 446	gtg Val	cgg Arg	ttc Phe	tgg Trp	gat Asp 451	gcc Ala	tcg Ser	ggg Gly	gtc Val	tgc Cys 456	ctg Leu	cgg Arg	ctg Leu	ctc Leu	tac Tyr 461	1513
aaa Lys 462	ctc Leu	agc Ser	act Thr	gtg Val	cgc Arg 467	gtg Val	ttc Phe	ctc Leu	acc Thr	gac Asp 472	acg Thr	gac Asp	ccc Pro	aac Asn	gag Glu 477	1561
aac Asn 478	ttc Phe	agt Ser	gcc Ala	cag Gln	ggc Gly 483	gag Glu	gac Asp	gag Glu	tgg Trp	ccc Pro 488	cca Pro	ctc Leu	cgc Arg	aag Lys	gtg Val 493	1609
ggc Gly 494	tcc Ser	ttt Phe	gac Asp	ccc Pro	tac Tyr 499	agt Ser	gat Asp	gac Asp	ccc Pro	cgg Arg 504	ctg Leu	ggc Gly	atc Ile	cag Gln	aag Lys 509	1657
atc	ttc	ctc	tgc	aag	tac	agc	ggc	tac	ctg	gct	gtg	gca	ggc	acg	gca	1705

Ile Phe Leu Cys Lys Tyr Ser Gly Tyr Leu Ala Val Ala Gly Thr Ala	
510 515 520 525	
ggg cag gtg ctg gta ctg gaa ctg aat gac gag gca gcg gag cag gct	1753
Gly Gln Val Leu Val Leu Glu Leu Asn Asp Glu Ala Ala Glu Gln Ala	
526 531 536 541	
gtg gag cag gtg gag gcc gac ctg ctg cag gac caa gag ggc tac cgc	1801
Val Glu Gln Val Glu Ala Asp Leu Leu Gln Asp Gln Glu Gly Tyr Arg	
542 547 552 557	
tgg aag ggg cac gag cgc ctg gca gcc cgc tca ggg ccc gtg cgc ttt	1849
Trp Lys Gly His Glu Arg Leu Ala Ala Arg Ser Gly Pro Val Arg Phe	
558 563 568 573	
gag cct ggc ttt cag ccc ttc gtg ttg gtg cag tgt cag ccc ccg gct	1897
Glu Pro Gly Phe Gln Pro Phe Val Leu Val Gln Cys Gln Pro Pro Ala	
574 579 584 589	
gtg gtc acc tcc ttg gcc ctg cac tct gag tgg cgg ctc gtg gcc ttc	1945
Val Val Thr Ser Leu Ala Leu His Ser Glu Trp Arg Leu Val Ala Phe	
590 595 600 605	
ggc acc agc cat ggc ttt ggc ctc ttt gac cac cag cag cgg cgg cag	1993
Gly Thr Ser His Gly Phe Gly Leu Phe Asp His Gln Gln Arg Arg Gln	
606 611 616 621	
gtc ttt gtt aag tgc aca ctg cac ccc agt gac cag ctg gcc ttg gag	2041
Val Phe Val Lys Cys Thr Leu His Pro Ser Asp Gln Leu Ala Leu Glu	
622 627 632 637	
ggc cca ctc tcc cgc gtc aag tcc ctc aag aag tcc ttg cgt cag tca	2089
Gly Pro Leu Ser Arg Val Lys Ser Leu Lys Lys Ser Leu Arg Gln Ser	
638 643 648 653	
ttc cgc cgg atg cgt cgg agc cgg gtg tcc agc cgg aag cgg cac ccg	2137
Phe Arg Arg Met Arg Arg Ser Arg Val Ser Ser Arg Lys Arg His Pro	
654 659 664 669	
gct ggc ccc cca gga gag gca cag gag ggg agt gcc aag gct gag cgg	2185
Ala Gly Pro Pro Gly Glu Ala Gln Glu Gly Ser Ala Lys Ala Glu Arg	
670 675 680 685	
cca ggc ctc cag aac atg gag ctg gcg cct gtg cag cgc aag atc gag	2233
Pro Gly Leu Gln Asn Met Glu Leu Ala Pro Val Gln Arg Lys Ile Glu	
686 691 696 701	
gct cgc tcg gca gag gac tcc ttc aca ggc ttc gtc cgg acc ctg tac	2281
Ala Arg Ser Ala Glu Asp Ser Phe Thr Gly Phe Val Arg Thr Leu Tyr	
702 707 712 717	
ttt gct gac acc tac ctg aag gac agc tcc cgg cac tgc ccc tcg ctg	2329
Phe Ala Asp Thr Tyr Leu Lys Asp Ser Ser Arg His Cys Pro Ser Leu	
718 723 728 733	
tgg gct ggc acc aat ggg ggc acc atc tat gcc ttc tcc ctg cgt gtg	2377
Trp Ala Gly Thr Asn Gly Gly Thr Ile Tyr Ala Phe Ser Leu Arg Val	

734		739		744		749	
cct ccc gcc gag cgg aga atg gat gag cct gtg cgg gca gag cag gcc	2425						
Pro Pro Ala Glu Arg Arg Met Asp Glu Pro Val Arg Ala Glu Gln Ala							
750		755		760		765	
aag gag atc cag ctg atg cac cgg gcg ccg gtg gtg ggc atc ctg gtg	2473						
Lys Glu Ile Gln Leu Met His Arg Ala Pro Val Val Gly Ile Leu Val							
766		771		776		781	
ctc gac gga cac agc gta ccc ctt ccc gag ccc ctc gaa gtg gcc cat	2521						
Leu Asp Gly His Ser Val Pro Leu Pro Glu Pro Leu Glu Val Ala His							
782		787		792		797	
gat ctg tcg aag agc cct gac atg cag gga agc cac cag ctg ctc gtc	2569						
Asp Leu Ser Lys Ser Pro Asp Met Gln Gly Ser His Gln Leu Leu Val							
798		803		808		813	
gta tca gag gag cag ttc aag gtg ttc acg ctg ccc aag gtg agt gcc	2617						
Val Ser Glu Glu Gln Phe Lys Val Phe Thr Leu Pro Lys Val Ser Ala							
814		819		824		829	
aag ctg aag ttg aag ctg acg gcc ctg gag ggc tca aga gtg cgg cgg	2665						
Lys Leu Lys Leu Lys Leu Thr Ala Leu Glu Gly Ser Arg Val Arg Arg							
830		835		840		845	
gtc agc gtg gcc cac ttc ggc agt cgt cga gcc gag gac tac ggg gag	2713						
Val Ser Val Ala His Phe Gly Ser Arg Arg Ala Glu Asp Tyr Gly Glu							
846		851		856		861	
cac cac ctg gca gtc ctt acc aac ctg ggc gac atc cag gtg gtc tcg	2761						
His His Leu Ala Val Leu Thr Asn Leu Gly Asp Ile Gln Val Val Ser							
862		867		872		877	
ctg ccc ctg ctc aag ccc cag gtg cgc tac agc tgc atc cgc cgg gag	2809						
Leu Pro Leu Leu Lys Pro Gln Val Arg Tyr Ser Cys Ile Arg Arg Glu							
878		883		888		893	
gac gtc agt ggc atc gcc tcc tgc gtc ttc acc aaa tat ggc caa ggc	2857						
Asp Val Ser Gly Ile Ala Ser Cys Val Phe Thr Lys Tyr Gly Gln Gly							
894		899		904		909	
ttc tac ctg atc tca ccc tcg gag ttt gag cgc ttc tct ctc tcc acc	2905						
Phe Tyr Leu Ile Ser Pro Ser Glu Phe Glu Arg Phe Ser Leu Ser Thr							
910		915		920		925	
aag tgg ctg gtg gag ccc cgg tgt ctg gtg gat tca gca gaa acc aag	2953						
Lys Trp Leu Val Glu Pro Arg Cys Leu Val Asp Ser Ala Glu Thr Lys							
926		931		936		941	
aac cac cgc cct ggt aac ggt gcg ggc ccc aag aag gcc ccg agc cga	3001						
Asn His Arg Pro Gly Asn Gly Ala Gly Pro Lys Lys Ala Pro Ser Arg							
942		947		952		957	
gcc agg aac tca ggg act cag agt gat ggc gag gag aag cag ccc ggc	3049						
Ala Arg Asn Ser Gly Thr Gln Ser Asp Gly Glu Glu Lys Gln Pro Gly							
958		963		968		973	

ctg gtg atg gag cgc gct ctg ctc agt gat gag aga gcg gca act ggc	3097
Leu Val Met Glu Arg Ala Leu Leu Ser Asp Glu Arg Ala Ala Thr Gly	
974 979 984 989	
ggt cac atc gag ccg ccg tgg ggt gca gcc tca gca atg gcg gag cag	3145
Val His Ile Glu Pro Pro Trp Gly Ala Ala Ser Ala Met Ala Glu Gln	
990 995 1000 1005	
agt gag tgg ctg agc gtc cag gct gcg cga tga gcacacac tactactgat	3196
Ser Glu Trp Leu Ser Val Gln Ala Ala Arg *	
1006 1011 1016	
ggccttttcgg gggtcctgc cccaaccgga gaggccggtg cacagggccc cgccaggggc	3256
tgggggcatc ccggcttcca caatgcagct gctctgggcc tcgggagagg agagacccca	3316
gtcccctggg ctgcccttcc cgggcctcgt ctgtctgggt cctttggtca atgttgaca	3376
gtttttattg ctcccatccc tttttgtagt gggctggggt ttaagttata aatgttaact	3436
gcctctgggt gaaaaagttt ttaataaaca cctattacct cttgaaaa	3484
<210> 149	
<211> 3274	
<212> DNA	
<213> Homo sapiens	
<220>	
<221> CDS	
<222> (131)..(2968)	
<400> 149	
cgcccagcag cccgtgggca ggcgcggcgg agcgagcggg gccggcggcg ggcgccgagg	60
gacgccgagg cctcgggcgg gggctggccc ggggttcag gtctccagtg ggggctgcag	120
actaagcaaa atg agg cgg ttc ctg agg cca ggg cat gac cct gtg cgg	169
Met Arg Arg Phe Leu Arg Pro Gly His Asp Pro Val Arg	
1 5 10	
gag agg ctc aag cgg gac ctg ttc cag ttt aag acg gtg gag cat	217
Glu Arg Leu Lys Arg Asp Leu Phe Gln Phe Asn Lys Thr Val Glu His	
14 19 24 29	
ggc ttc ccg cac cag ccc agc gcc ctc ggc tac agc ccg tcc ctg cgc	265
Gly Phe Pro His Gln Pro Ser Ala Leu Gly Tyr Ser Pro Ser Leu Arg	
30 35 40 45	
atc ctg gcc atc ggc acc cgt tct gga gcc atc aag ctc tac gga gcc	313
Ile Leu Ala Ile Gly Thr Arg Ser Gly Ala Ile Lys Leu Tyr Gly Ala	
46 51 56 61	
cca ggc gtg gag ttc atg ggg ctg cac cag gag aac aac gct gtg acg	361

Pro	Gly	Val	Glu	Phe	Met	Gly	Leu	His	Gln	Glu	Asn	Asn	Ala	Val	Thr	
62					67					72					77	
cag	atc	cac	ctc	ctg	ccc	ggc	cag	tgc	cag	ctg	gtc	acc	ctg	ctg	gat	409
Gln	Ile	His	Leu	Leu	Pro	Gly	Gln	Cys	Gln	Leu	Val	Thr	Leu	Leu	Asp	
78					83					88					93	
gac	aac	agc	ctg	cac	ctt	tgg	agc	ctg	aag	gtc	aag	ggc	ggg	gca	tcg	457
Asp	Asn	Ser	Leu	His	Leu	Trp	Ser	Leu	Lys	Val	Lys	Gly	Gly	Ala	Ser	
94					99					104					109	
gag	ctg	cag	gag	gat	gag	agc	ttc	aca	ctg	cgt	gga	ccc	cca	ggg	gct	505
Glu	Leu	Gln	Glu	Asp	Glu	Ser	Phe	Thr	Leu	Arg	Gly	Pro	Pro	Gly	Ala	
110					115					120					125	
gcc	ccc	agt	gcc	aca	cag	atc	acc	gtg	gtc	ctg	cca	cat	tcc	tcc	tgc	553
Ala	Pro	Ser	Ala	Thr	Gln	Ile	Thr	Val	Val	Leu	Pro	His	Ser	Ser	Cys	
126					131					136					141	
gag	ctg	ctc	tac	ctg	ggc	acc	gag	agt	ggc	aac	gtg	ttt	gtg	gtg	cag	601
Glu	Leu	Leu	Tyr	Leu	Gly	Thr	Glu	Ser	Gly	Asn	Val	Phe	Val	Val	Gln	
142					147					152					157	
ctg	cca	gct	ttt	cgt	gcg	ctg	gag	gac	cgg	acc	atc	agc	tcg	gac	gcg	649
Leu	Pro	Ala	Phe	Arg	Ala	Leu	Glu	Asp	Arg	Thr	Ile	Ser	Ser	Asp	Ala	
158					163					168					173	
gtg	ctg	cag	cgg	ttg	cca	gag	gag	gcc	cgc	cac	cgg	cgt	gtg	ttc	gag	697
Val	Leu	Gln	Arg	Leu	Pro	Glu	Glu	Ala	Arg	His	Arg	Arg	Val	Phe	Glu	
174					179					184					189	
atg	gtg	gag	gca	ctg	cag	gag	cac	cct	cga	gac	ccc	aac	cag	atc	ctg	745
Met	Val	Glu	Ala	Leu	Gln	Glu	His	Pro	Arg	Asp	Pro	Asn	Gln	Ile	Leu	
190					195					200					205	
atc	ggc	tac	agc	cga	ggc	ctc	gtt	gtc	atc	tgg	gac	cta	cag	ggc	agc	793
Ile	Gly	Tyr	Ser	Arg	Gly	Leu	Val	Val	Ile	Trp	Asp	Leu	Gln	Gly	Ser	
206					211					216					221	
cgc	gtg	ctc	tac	cac	ttc	ctc	agc	agc	cag	caa	ctg	gag	aac	atc	tgg	841
Arg	Val	Leu	Tyr	His	Phe	Leu	Ser	Ser	Gln	Gln	Leu	Glu	Asn	Ile	Trp	
222					227					232					237	
tgg	cag	cgg	gac	ggc	cgc	ctg	ctc	gtc	agc	tgt	cac	tct	gac	ggc	agc	889
Trp	Gln	Arg	Asp	Gly	Arg	Leu	Leu	Val	Ser	Cys	His	Ser	Asp	Gly	Ser	
238					243					248					253	
tac	tgc	cag	tgg	ccc	gtg	tcc	agc	gaa	gcc	cag	caa	cca	gag	ccc	ctc	937
Tyr	Cys	Gln	Trp	Pro	Val	Ser	Ser	Glu	Ala	Gln	Gln	Pro	Glu	Pro	Leu	
254					259					264					269	
cgc	agc	ctc	gtg	cct	tac	gcc	ttt	gac	gac	ccc	tat	gcc	ctg	gtg	gtg	985
Arg	Ser	Leu	Val	Pro	Tyr	Ala	Phe	Asp	Asp	Pro	Tyr	Ala	Leu	Val	Val	
270					275					280					285	
ctg	gct	gag	gag	gag	ctg	gtg	gtg	att	gac	ctg	cag	aca	gca	ggc	tgg	1033
Leu	Ala	Glu	Glu	Glu	Leu	Val	Val	Ile	Asp	Leu	Gln	Thr	Ala	Gly	Trp	

286						291						296						301	
cca	ccg	gtc	cag	ctg	ccc	tac	ctg	gct	tct	ctg	cac	tgt	tcc	gcc	atc	1081			
Pro	Pro	Val	Gln	Leu	Pro	Tyr	Leu	Ala	Ser	Leu	His	Cys	Ser	Ala	Ile				
302						307						312						317	
acc	tgc	tct	cac	cac	gtc	tcc	aac	atc	ccg	ctg	aag	ctg	tgg	gag	cgg	1129			
Thr	Cys	Ser	His	His	Val	Ser	Asn	Ile	Pro	Leu	Lys	Leu	Trp	Glu	Arg				
318						323						328						333	
atc	att	gcc	gcc	ggc	agc	cgg	cag	aac	gca	cac	ttc	tcc	acc	atg	gag	1177			
Ile	Ile	Ala	Ala	Gly	Ser	Arg	Gln	Asn	Ala	His	Phe	Ser	Thr	Met	Glu				
334						339						344						349	
tgg	cca	att	gat	ggg	ggc	acc	agc	ctg	acc	cca	gcc	cca	ccc	cag	agg	1225			
Trp	Pro	Ile	Asp	Gly	Gly	Thr	Ser	Leu	Thr	Pro	Ala	Pro	Pro	Gln	Arg				
350						355						360						365	
gac	ctg	ctg	ctc	aca	ggg	cac	gag	gac	ggc	acg	gtg	cgg	ttc	tgg	gat	1273			
Asp	Leu	Leu	Leu	Thr	Gly	His	Glu	Asp	Gly	Thr	Val	Arg	Phe	Trp	Asp				
366						371						376						381	
gcc	tcg	ggt	gtc	tgc	ctg	cgg	ctg	ctc	tac	aaa	ctc	agc	act	gtg	cgc	1321			
Ala	Ser	Gly	Val	Cys	Leu	Arg	Leu	Leu	Tyr	Lys	Leu	Ser	Thr	Val	Arg				
382						387						392						397	
gtg	ttc	ctc	acc	gac	acg	gac	ccc	aac	gag	aac	ttc	agt	gcc	cag	ggc	1369			
Val	Phe	Leu	Thr	Asp	Thr	Asp	Pro	Asn	Glu	Asn	Phe	Ser	Ala	Gln	Gly				
398						403						408						413	
gag	gac	gag	tgg	ccc	cca	ctc	cgc	aag	gtg	ggc	tcc	ttt	gac	ccc	tac	1417			
Glu	Asp	Glu	Trp	Pro	Pro	Leu	Arg	Lys	Val	Gly	Ser	Phe	Asp	Pro	Tyr				
414						419						424						429	
agt	gat	gac	ccc	cgg	ctg	ggc	atc	cag	aag	atc	ttc	ctc	tgc	aag	tac	1465			
Ser	Asp	Asp	Pro	Arg	Leu	Gly	Ile	Gln	Lys	Ile	Phe	Leu	Cys	Lys	Tyr				
430						435						440						445	
agc	ggc	tac	ctg	gct	gtg	gca	ggc	acg	gca	ggg	cag	gtg	ctg	gta	ctg	1513			
Ser	Gly	Tyr	Leu	Ala	Val	Ala	Gly	Thr	Ala	Gly	Gln	Val	Leu	Val	Leu				
446						451						456						461	
gaa	ctg	aat	gac	gag	gca	gcg	gag	cag	gct	gtg	gag	cag	gtg	gag	gcc	1561			
Glu	Leu	Asn	Asp	Glu	Ala	Ala	Glu	Gln	Ala	Val	Glu	Gln	Val	Glu	Ala				
462						467						472						477	
gac	ctg	ctg	cag	gac	caa	gag	ggc	tac	cgc	tgg	aag	ggg	cac	gag	cgc	1609			
Asp	Leu	Leu	Gln	Asp	Gln	Glu	Gly	Tyr	Arg	Trp	Lys	Gly	His	Glu	Arg				
478						483						488						493	
ctg	gca	gcc	cgc	tca	ggg	ccc	gtg	cgc	ttt	gag	cct	ggc	ttt	cag	ccc	1657			
Leu	Ala	Ala	Arg	Ser	Gly	Pro	Val	Arg	Phe	Glu	Pro	Gly	Phe	Gln	Pro				
494						499						504						509	
ttc	gtg	ttg	gtg	cag	tgt	cag	ccc	ccg	gct	gtg	gtc	acc	tcc	ttg	gcc	1705			
Phe	Val	Leu	Val	Gln	Cys	Gln	Pro	Pro	Ala	Val	Val	Thr	Ser	Leu	Ala				
510						515						520						525	

ctg cac tct gag tgg cgg ctc gtg gcc ttc ggc acc agc cat ggc ttt	1753
Leu His Ser Glu Trp Arg Leu Val Ala Phe Gly Thr Ser His Gly Phe	
526 531 536 541	
ggc ctc ttt gac cac cag cag cgg cgg cag gtc ttt gtt aag tgc aca	1801
Gly Leu Phe Asp His Gln Gln Arg Arg Gln Val Phe Val Lys Cys Thr	
542 547 552 557	
ctg cac ccc agt gac cag ctg gcc ttg gag ggc cca ctc tcc cgc gtc	1849
Leu His Pro Ser Asp Gln Leu Ala Leu Glu Gly Pro Leu Ser Arg Val	
558 563 568 573	
aag tcc ctc aag aag tcc ttg cgt cag tca ttc cgc cgg atg cgt cgg	1897
Lys Ser Leu Lys Lys Ser Leu Arg Gln Ser Phe Arg Arg Met Arg Arg	
574 579 584 589	
agc cgg gtg tcc agc cgg aag cgg cac ccg gct ggc ccc cca gga gag	1945
Ser Arg Val Ser Ser Arg Lys Arg His Pro Ala Gly Pro Pro Gly Glu	
590 595 600 605	
gca cag gag ggg agt gcc aag gct gag cgg cca ggc ctc cag aac atg	1993
Ala Gln Glu Gly Ser Ala Lys Ala Glu Arg Pro Gly Leu Gln Asn Met	
606 611 616 621	
gag ctg gcg cct gtg cag cgc aag atc gag gct cgc tcg gca gag gac	2041
Glu Leu Ala Pro Val Gln Arg Lys Ile Glu Ala Arg Ser Ala Glu Asp	
622 627 632 637	
tcc ttc aca ggc ttc gtc cgg acc ctg tac ttt gct gac acc tac ctg	2089
Ser Phe Thr Gly Phe Val Arg Thr Leu Tyr Phe Ala Asp Thr Tyr Leu	
638 643 648 653	
aag gac agc tcc cgg cac tgc ccc tcg ctg tgg gct ggc acc aat ggg	2137
Lys Asp Ser Ser Arg His Cys Pro Ser Leu Trp Ala Gly Thr Asn Gly	
654 659 664 669	
ggc acc atc tat gcc ttc tcc ctg cgt gtg cct ccc gcc gag cgg aga	2185
Gly Thr Ile Tyr Ala Phe Ser Leu Arg Val Pro Pro Ala Glu Arg Arg	
670 675 680 685	
atg gat gag cct gtg cgg gca gag cag gcc aag gag atc cag ctg atg	2233
Met Asp Glu Pro Val Arg Ala Glu Gln Ala Lys Glu Ile Gln Leu Met	
686 691 696 701	
cac cgg gcg ccg gtg gtg ggc atc ctg gtg ctc gac gga cac agc gta	2281
His Arg Ala Pro Val Val Gly Ile Leu Val Leu Asp Gly His Ser Val	
702 707 712 717	
ccc ctt ccc gag ccc ctc gaa gtg gcc cat gat ctg tcg aag agc cct	2329
Pro Leu Pro Glu Pro Leu Glu Val Ala His Asp Leu Ser Lys Ser Pro	
718 723 728 733	
gac atg cag gga agc cac cag ctg ctc gtc gta tca gag gag cag ttc	2377
Asp Met Gln Gly Ser His Gln Leu Leu Val Val Ser Glu Glu Gln Phe	
734 739 744 749	

aag gtg ttc acg ctg ccc aag gtg agt gcc aag ctg aag ttg aag ctg Lys Val Phe Thr Leu Pro Lys Val Ser Ala Lys Leu Lys Leu Lys Leu 750 755 760 765	2425
acg gcc ctg gag ggc tca aga gtg cgg cgg gtc agc gtg gcc cac ttc Thr Ala Leu Glu Gly Ser Arg Val Arg Arg Val Ser Val Ala His Phe 766 771 776 781	2473
ggc agt cgt cga gcc gag gac tac ggg gag cac cac ctg gca gtc ctt Gly Ser Arg Arg Ala Glu Asp Tyr Gly Glu His His Leu Ala Val Leu 782 787 792 797	2521
acc aac ctg ggc gac atc cag gtg gtc tcg ctg ccc ctg ctc aag ccc Thr Asn Leu Gly Asp Ile Gln Val Val Ser Leu Pro Leu Leu Lys Pro 798 803 808 813	2569
cag gtg cgc tac agc tgc atc cgc cgg gag gac gtc agt ggc atc gcc Gln Val Arg Tyr Ser Cys Ile Arg Arg Glu Asp Val Ser Gly Ile Ala 814 819 824 829	2617
tcc tgc gtc ttc acc aaa tat ggc caa ggc ttc tac ctg atc tca ccc Ser Cys Val Phe Thr Lys Tyr Gly Gln Gly Phe Tyr Leu Ile Ser Pro 830 835 840 845	2665
tcg gag ttt gag cgc ttc tct ctc tcc acc aag tgg ctg gtg gag ccc Ser Glu Phe Glu Arg Phe Ser Leu Ser Thr Lys Trp Leu Val Glu Pro 846 851 856 861	2713
cgg tgt ctg gtg gat tca gca gaa acc aag aac cac cgc cct ggt aac Arg Cys Leu Val Asp Ser Ala Glu Thr Lys Asn His Arg Pro Gly Asn 862 867 872 877	2761
ggt gcg ggc ccc aag aag gcc ccg agc cga gcc agg aac tca ggg act Gly Ala Gly Pro Lys Lys Ala Pro Ser Arg Ala Arg Asn Ser Gly Thr 878 883 888 893	2809
cag agt gat ggc gag gag aag cag ccc ggc ctg gtg atg gag cgc gct Gln Ser Asp Gly Glu Glu Lys Gln Pro Gly Leu Val Met Glu Arg Ala 894 899 904 909	2857
ctg ctc agt gat gag aga gcg gca act ggc gtt cac atc gag ccg ccg Leu Leu Ser Asp Glu Arg Ala Ala Thr Gly Val His Ile Glu Pro Pro 910 915 920 925	2905
tgg ggt gca gcc tca gca atg gcg gag cag agt gag tgg ctg agc gtc Trp Gly Ala Ala Ser Ala Met Ala Glu Gln Ser Glu Trp Leu Ser Val 926 931 936 941	2953
cag gct gcg cga tga gcacacacta ctactgatgg cctttcgggg gtccttcccc Gln Ala Ala Arg * 942	3008
caaccggaga ggccggtgca caggggcccc ccaggggctg ggggcatccc ggcttccaca	3068
atgcagctgc tctgggcctc gggagaggag agaccccagt cccctgggct gcccttcccc	3128
ggcctcgtct gtctgggtcc tttgtgcaat gttgcacagt ttttattgct cccatccctt	3188

tttgtagtgg gctgggtttt aagttataaa tgttaactgc ctctgggtga aaaagttttt 3248
aataaacacc tattacctct tgaaaa 3274

<210> 150
<211> 5250
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (166)..(2499)

<400> 150
ggtgactcag gaggaccctt ggtctgcgag gagccctctg gccgggttctt tctggctggc 60
atcgtgagct ggggaatcgg gtgtgcggaa gcccggcgtc caggggtcta tgcccgagtc 120
accaggctac gtgactggat cctggaggcc accaccaaag ccagc atg cct ctg 174
Met Pro Leu
1
gcc ccc acc atg gct cct gcc cct gcc gcc ccc agc aca gcc tgg ccc 222
Ala Pro Thr Met Ala Pro Ala Pro Ala Ala Pro Ser Thr Ala Trp Pro
4 9 14 19
acc agt cct gag agc cct gtg gtc agc acc ccc acc aaa tcg atg cag 270
Thr Ser Pro Glu Ser Pro Val Val Ser Thr Pro Thr Lys Ser Met Gln
20 25 30 35
gcc ctc agt acc gtg cct ctt gac tgg gtc acc gtt cct aag cta caa 318
Ala Leu Ser Thr Val Pro Leu Asp Trp Val Thr Val Pro Lys Leu Gln
36 41 46 51
gaa tgt ggg gcc agg cct gca atg gag aag ccc acc cgg gtc gtg ggc 366
Glu Cys Gly Ala Arg Pro Ala Met Glu Lys Pro Thr Arg Val Val Gly
52 57 62 67
ggg ttc gga gct gcc tcc ggg gag gtg ccc tgg cag gtc agc ctg aag 414
Gly Phe Gly Ala Ala Ser Gly Glu Val Pro Trp Gln Val Ser Leu Lys
68 73 78 83
gaa ggg tcc cgg cac ttc tgc gga gca act gtg gtg ggg gac cgc tgg 462
Glu Gly Ser Arg His Phe Cys Gly Ala Thr Val Val Gly Asp Arg Trp
84 89 94 99
ctg ctg tct gcc gcc cac tgc ttc aac cac acg aag gtg gag cag gtt 510
Leu Leu Ser Ala Ala His Cys Phe Asn His Thr Lys Val Glu Gln Val
100 105 110 115
cgg gcc cac ctg ggc act gcg tcc ctc ctg ggc ctg ggc ggg agc ccg 558
Arg Ala His Leu Gly Thr Ala Ser Leu Leu Gly Leu Gly Gly Ser Pro
116 121 126 131

gtg aag atc ggg ctg cgg cgg gta gtg ctg cac ccc ctc tac aac cct	606
Val Lys Ile Gly Leu Arg Arg Val Val Leu His Pro Leu Tyr Asn Pro	
132 137 142 147	
ggc atc ctg gac ttc gac ctg gct gtc ctg gag ctg gcc agc ccc ctg	654
Gly Ile Leu Asp Phe Asp Leu Ala Val Leu Glu Leu Ala Ser Pro Leu	
148 153 158 163	
gcc ttc aac aaa tac atc cag cct gtc tgc ctg ccc ctg gcc atc cag	702
Ala Phe Asn Lys Tyr Ile Gln Pro Val Cys Leu Pro Leu Ala Ile Gln	
164 169 174 179	
aag ttc cct gtg ggc cgg aag tgc atg atc tcc gga tgg gga aat acg	750
Lys Phe Pro Val Gly Arg Lys Cys Met Ile Ser Gly Trp Gly Asn Thr	
180 185 190 195	
cag gaa gga aat gcc acc aag ccc gag ctc ctg cag aag gcg tcc gtg	798
Gln Glu Gly Asn Ala Thr Lys Pro Glu Leu Leu Gln Lys Ala Ser Val	
196 201 206 211	
ggc atc ata gac cag aaa acc tgt agt gtg ctc tac aac ttc tcc ctc	846
Gly Ile Ile Asp Gln Lys Thr Cys Ser Val Leu Tyr Asn Phe Ser Leu	
212 217 222 227	
aca gac cgc atg atc tgc gca ggc ttc ctg gaa ggc aaa gtc gac tcc	894
Thr Asp Arg Met Ile Cys Ala Gly Phe Leu Glu Gly Lys Val Asp Ser	
228 233 238 243	
tgc cag gtg agt ggc atc aag gcg ctg tac gag tgc gag ctg gcc gat	942
Cys Gln Val Ser Gly Ile Lys Ala Leu Tyr Glu Ser Glu Leu Ala Asp	
244 249 254 259	
gcc cgg aga gtc ctg gat gag acg gct cga gag cgt gcc cgg ctg cag	990
Ala Arg Arg Val Leu Asp Glu Thr Ala Arg Glu Arg Ala Arg Leu Gln	
260 265 270 275	
ata gag att ggg aag ctg agg gca gag ttg gac gag gtc aac aag agc	1038
Ile Glu Ile Gly Lys Leu Arg Ala Glu Leu Asp Glu Val Asn Lys Ser	
276 281 286 291	
gcc aag aag agg gag ggc gag ctt acg gtg gcc cag ggc cgt gtg aag	1086
Ala Lys Lys Arg Glu Gly Glu Leu Thr Val Ala Gln Gly Arg Val Lys	
292 297 302 307	
gac ctg gag tcc ctg ttc cac cgg agc gag gtg gag ctg gca gct gcc	1134
Asp Leu Glu Ser Leu Phe His Arg Ser Glu Val Glu Leu Ala Ala Ala	
308 313 318 323	
ctc agc gac aag cgc ggc ctg gag agt gac gtg gct gag ctg cgg gcc	1182
Leu Ser Asp Lys Arg Gly Leu Glu Ser Asp Val Ala Glu Leu Arg Ala	
324 329 334 339	
cag ctg gcc aag gcc gag gac ggt cat gca gtg gcc aaa aag cag ctg	1230
Gln Leu Ala Lys Ala Glu Asp Gly His Ala Val Ala Lys Lys Gln Leu	
340 345 350 355	

gag aag gag acg ctg atg cgt gtg gac ctg gag aac cgc tgc cag agc Glu Lys Glu Thr Leu Met Arg Val Asp Leu Glu Asn Arg Cys Gln Ser 356 361 366 371	1278
ctg cag gag gag ctg gac ttc cgg aag agt gtg ttc gag gag gag gtg Leu Gln Glu Glu Leu Asp Phe Arg Lys Ser Val Phe Glu Glu Glu Val 372 377 382 387	1326
cgg gag acg cgg cgg cgg cac gag cgg cgc ctg gtg gag gtg gac agc Arg Glu Thr Arg Arg Arg His Glu Arg Arg Leu Val Glu Val Asp Ser 388 393 398 403	1374
agc cgg cag cag gag tac gac ttc aag atg gca cag gcg ctg gag gag Ser Arg Gln Gln Glu Tyr Asp Phe Lys Met Ala Gln Ala Leu Glu Glu 404 409 414 419	1422
ctg cgg agc cag cac gac gag caa gtg cgg ctc tac aag ctg gag ctg Leu Arg Ser Gln His Asp Glu Gln Val Arg Leu Tyr Lys Leu Glu Leu 420 425 430 435	1470
gag cag acc tac cag gcc aag ctg gac agc gcc aag ctg agc tct gac Glu Gln Thr Tyr Gln Ala Lys Leu Asp Ser Ala Lys Leu Ser Ser Asp 436 441 446 451	1518
cag aac gac aag gcg gcc agt gcg gct cgc gag gag ctg aag gag gcc Gln Asn Asp Lys Ala Ala Ser Ala Ala Arg Glu Glu Leu Lys Glu Ala 452 457 462 467	1566
cgc atg cgc ctg gag tcc ctc agc tac cag ctc tcc ggc ctc cag aag Arg Met Arg Leu Glu Ser Leu Ser Tyr Gln Leu Ser Gly Leu Gln Lys 468 473 478 483	1614
cag gcc agt gcc gct gaa gat cgc att cgg gag ctg gag gag gcc atg Gln Ala Ser Ala Ala Glu Asp Arg Ile Arg Glu Leu Glu Glu Ala Met 484 489 494 499	1662
gcc ggg gag cgg gac aag ttc cgg aag atg ctg gac gcc aag gag cag Ala Gly Glu Arg Asp Lys Phe Arg Lys Met Leu Asp Ala Lys Glu Gln 500 505 510 515	1710
gag atg acg gag atg cgg gac gtg atg cag cag cag ctg gcc gag tac Glu Met Thr Glu Met Arg Asp Val Met Gln Gln Gln Leu Ala Glu Tyr 516 521 526 531	1758
cag gag ctg ctg gac gtg aag ctg gcc ctg gac atg gag atc aac gcc Gln Glu Leu Leu Asp Val Lys Leu Ala Leu Asp Met Glu Ile Asn Ala 532 537 542 547	1806
tac cgg aag ctc ctg gag ggc gag gag gag agg ctg aag ctg tcc ccc Tyr Arg Lys Leu Leu Glu Gly Glu Glu Glu Arg Leu Lys Leu Ser Pro 548 553 558 563	1854
agc cca tcc tcg cgc gtc acc gtc tca cga gcc acc tcg agc agc agc Ser Pro Ser Ser Arg Val Thr Val Ser Arg Ala Thr Ser Ser Ser Ser 564 569 574 579	1902
ggc agc ttg tcc gcc acc ggg cgc ctg ggc cgc agt aag cgg aag cgg	1950

Gly 580	Ser	Leu	Ser	Ala	Thr 585	Gly	Arg	Leu	Gly	Arg 590	Ser	Lys	Arg	Lys	Arg 595	
ctg	gag	gtg	gag	gag	ccc	ttg	ggc	agc	ggc	cca	agc	gtc	ctg	ggc	acg	1998
Leu 596	Glu	Val	Glu	Glu	Pro 601	Leu	Gly	Ser	Gly	Pro 606	Ser	Val	Leu	Gly	Thr 611	
ggc	acg	ggt	ggc	agc	ggt	ggc	ttc	cac	ctg	gcc	cag	cag	gcc	tcg	gcc	2046
Gly 612	Thr	Gly	Gly	Ser	Gly 617	Gly	Phe	His	Leu	Ala 622	Gln	Gln	Ala	Ser	Ala 627	
tcg	ggc	agc	gtc	agc	atc	gag	gag	atc	gac	ctg	gag	ggc	aag	ttt	gtg	2094
Ser 628	Gly	Ser	Val	Ser	Ile 633	Glu	Glu	Ile	Asp	Leu 638	Glu	Gly	Lys	Phe	Val 643	
cag	ctc	aag	aac	aac	tcg	gac	aag	gat	cag	tct	ctg	ggg	aac	tgg	aga	2142
Gln 644	Leu	Lys	Asn	Asn	Ser 649	Asp	Lys	Asp	Gln	Ser 654	Leu	Gly	Asn	Trp	Arg 659	
atc	aag	agg	cag	gtc	ttg	gag	ggg	gag	gag	atc	gcc	tac	aag	ttc	acg	2190
Ile 660	Lys	Arg	Gln	Val	Leu 665	Glu	Gly	Glu	Glu	Ile 670	Ala	Tyr	Lys	Phe	Thr 675	
ccc	aag	tac	atc	ctg	cgc	gcc	ggc	cag	atg	gtc	acg	gtg	tgg	gca	gct	2238
Pro 676	Lys	Tyr	Ile	Leu	Arg 681	Ala	Gly	Gln	Met	Val 686	Thr	Val	Trp	Ala	Ala 691	
ggt	gcg	ggg	gtg	gcc	cac	agc	ccc	ccc	tcg	acg	ctg	gtg	tgg	aag	ggc	2286
Gly 692	Ala	Gly	Val	Ala	His 697	Ser	Pro	Pro	Ser	Thr 702	Leu	Val	Trp	Lys	Gly 707	
cag	agc	agc	tgg	ggc	acg	ggc	gag	agc	ttc	cgc	acc	gtc	ctg	gtt	aac	2334
Gln 708	Ser	Ser	Trp	Gly	Thr 713	Gly	Glu	Ser	Phe	Arg 718	Thr	Val	Leu	Val	Asn 723	
gcg	gat	ggc	gag	gaa	gtg	gcc	atg	agg	act	gtg	aag	aag	tcc	tcg	gtg	2382
Ala 724	Asp	Gly	Glu	Glu	Val 729	Ala	Met	Arg	Thr	Val 734	Lys	Lys	Ser	Ser	Val 739	
atg	cgt	gag	aat	gag	aat	ggg	gag	gaa	gag	gag	gag	gaa	gcc	gag	ttt	2430
Met 740	Arg	Glu	Asn	Glu	Asn 745	Gly	Glu	Glu	Glu	Glu 750	Glu	Glu	Ala	Glu	Phe 755	
ggc	gag	gag	gat	ctt	ttc	cac	caa	cag	ggg	gac	ccg	agg	acc	acc	tca	2478
Gly 756	Glu	Glu	Asp	Leu	Phe 761	His	Gln	Gln	Gly	Asp 766	Pro	Arg	Thr	Thr	Ser 771	
aga	ggc	tgc	tac	gtg	atg	tga	ac	ccacactcct	catccacaca	cctttcttta						2531
Arg 772	Gly	Cys	Tyr	Val	Met 777	*										
cccagagcca	ctgaaaacta	tttttatatc	attggctttc	tttagttctt	gatacatttc											2591
tagagaattt	ctaagcgaac	tgccagaacg	tgtgggtggg	tctccccag	ccctccctcc											2651
tggcgggtct	cctccagcct	cacttcgctg	ccacttcgcc	gctgccccgg	agacttttca											2711

atcccccccc	actcctcatc	tcaccatttg	gtcaaattgg	aagcccaggg	ccaggacccc	2771
gaggtttaga	agatgcttgg	gcttgagggg	aggagggccg	gcgaggctag	cgaggggaca	2831
ggagacggcc	ctgctgcgga	cggagcgcgg	aaactgcgta	ggaattcagt	ggtggtgggt	2891
ttttttaagg	ctttctacaa	aaccaaattc	agaatccagg	cgtcgacctg	gtggggcccg	2951
gggccaagcc	tgcattctgg	ctgcccagct	tccgacagcg	ggaactcctc	aggcagccac	3011
gcagcgggtg	tgggccagca	tggggatggc	gtggccccc	gggcggggtt	tcactccgct	3071
gcctgggctt	ccagattccc	gttctggcag	cgcaccggcc	gggtttctcg	gaccgttgac	3131
tttatttggg	ggagttttcc	cgcagttcag	ttcctgactg	tgcagggcca	acagggcagg	3191
ggaggggaag	acctggggaa	ggaagaatga	ggacagtccc	gtcgtaagac	ctgtcacaac	3251
aataagcagg	gaggggagat	gtggagggga	cacatctggt	tgccttgagg	gcagaagctg	3311
tgagtttcag	aacagctgtc	tgcagggaac	gccaccatgt	tgaccctctg	gaggagagcg	3371
ctgtggagcc	cctcccgtgt	tccagctccg	tctgccctgt	gcctatatat	acacatgcgt	3431
ctatccatac	tgtgctttta	tctgtgattt	tctcgtgaa	accatgtttc	tcagacaggc	3491
caagggcacc	tgactcctat	cacgacgcac	ccaagcccct	cagtccagct	tcccaatgcc	3551
tggcaccccc	cttcggcaat	agctcaccgt	ttacaccctc	cctcatagat	acacagaagt	3611
tattttttta	atggatattt	atttttttac	attggtcagt	acacaggtca	ggagctcacg	3671
ccagggcctt	gaggacaggc	tgaccctcct	ccccgggggtg	gcgtggggct	ggggcaccct	3731
ccgacggcag	agcctccttc	agaaagtgca	gctcaagtct	taaagacacc	aaaactgagc	3791
catgggcacg	cgccgtctcc	gggccatggc	gttcaactgca	gggcgggggc	ggcaccgctc	3851
ccctgtgact	gcaccccgcc	tccctgggga	cctgcctgtg	gcaggaagga	atggggggcc	3911
ccagcccagg	ccgggaagga	gccagcggcc	gacaaagcag	aaacacccgc	tgctccacgt	3971
agcccctgct	ggctgtcctt	gctctcagaa	gtcccggctc	catgtagata	gagcccggcg	4031
gatcttacca	aagcatttcc	tcctggaggc	tacgccgctt	ggtgctccca	gtgaggcggc	4091
tggtagggag	ctttgcctgc	cccggggata	ccctctacca	gccgctggaa	gtgggaatgc	4151
tggcgacaga	ctgtgtctgt	ttcccacctt	catagcagga	atcacccgga	cccgactggc	4211
tgggcttcgt	gctagcaggg	gttttctggg	ggtgggtctt	ggtgatcttg	tcctatgggg	4271
atctctgcag	tggctctcagc	cacatcctag	tatatatttg	ctctggagga	gcaaagctgt	4331
atcctggagt	tggctctgtga	tttgccgaca	gacttgacag	ctgggctcag	caaagtcccc	4391
cccaaaaccc	gcaggtcctc	atgtccagac	gctgccagtc	ctgtcctgaa	aacagcacgc	4451


```

cccaggccca cagaaccccc caccctacat ttgccttggg tggagctggg ggtggctcta 4511
ggactgcggg tgcccttagc tgaagggggc ccgcagaagc gtgagctggg ccgcctgtgg 4571
gtcattggag gttcattgag aattgagtct ttggaaacac taagaaaatc aaatttttaa 4631
aagttattta tggcctggga aacaatttgc atttgtcccc aaatacgctt agctgtgtgc 4691
cgcttagaac gatgcgaaac catccctctg tgtaagcccg tgccgtgtga ctcgaagcct 4751
agcgccctcc ctgcgaagca tcagacgcca ccagccctg gggggaggcc cacgcctgct 4811
ggaccaacgc gggttctggg gtgcacagcg ccagggttaac gctgaagcct gccccgctga 4871
gcccaggagc cgggaggcct gcgggctgac ccagaatccg atcatgcacc tgtcctcatg 4931
ccagcggtt tggctggggt tggctgaag cctgcacgcg gcagttcttt gttaaagatc 4991
tgagggactc ctcagtcctg gggcgctgcc gcctgcagcc tcttccaagc cctgcgtcca 5051
gcgagcgtca cagcacaacc tgcaaaaacg gagctgggct gcagctgggg ctggcatgga 5111
ctttcatttc agagattcgg tttttaagaa gatgcatgcc taatgtgttc tttttttttt 5171
ccaatgattt gtaatataca ttttatgact ggaaactttt ttgtacaaca ctccaataaa 5231
cattttgatt ttaaaaaaa 5250

```

```

<210> 151
<211> 2066
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (85) .. (1932)

```

```

<400> 151
aggtaccgcg ccggaattcc cggggacggt cgcaaggatt acattcgcct gaccggccc 60

ggcttgacct tgccggggcg cgcc    atg ttc gcg cgt ggg tcc cgg agg cgc 111
                               Met Phe Ala Arg Gly Ser Arg Arg Arg
                               1                      5

cgc tcc ggg cgt gcg cct cca gag gca gag gac cca gac cgg ggc cag 159
Arg Ser Gly Arg Ala Pro Pro Glu Ala Glu Asp Pro Asp Arg Gly Gln
 10                      15                      20                      25

ccc tgc aac tcc tgt agg gag cag tgc cct ggc ttc ctg ctc cac ggc 207
Pro Cys Asn Ser Cys Arg Glu Gln Cys Pro Gly Phe Leu Leu His Gly
 26                      31                      36                      41

tgg aga aag atc tgc cag cat tgc aaa tgc ccg cgg gag gag cat gca 255

```

Trp	Arg	Lys	Ile	Cys	Gln	His	Cys	Lys	Cys	Pro	Arg	Glu	Glu	His	Ala	
42					47					52					57	
gtg	cac	gcg	gtg	cct	gtg	gac	ctg	gaa	cgc	atc	atg	tgt	cgg	cta	atc	303
Val	His	Ala	Val	Pro	Val	Asp	Leu	Glu	Arg	Ile	Met	Cys	Arg	Leu	Ile	
58					63					68					73	
tcg	gac	ttc	cag	cgc	cac	tcc	atc	tcc	gac	gac	gac	tca	ggc	tgt	gca	351
Ser	Asp	Phe	Gln	Arg	His	Ser	Ile	Ser	Asp	Asp	Asp	Ser	Gly	Cys	Ala	
74					79					84					89	
tcg	gag	gag	tat	gcc	tgg	gtg	ccc	cca	ggc	ctt	aag	ccg	gag	cag	gta	399
Ser	Glu	Glu	Tyr	Ala	Trp	Val	Pro	Pro	Gly	Leu	Lys	Pro	Glu	Gln	Val	
90					95					100					105	
tat	caa	ttt	ttc	agc	tgc	ctc	cca	gag	gac	aag	gtc	ccc	tac	gtc	aac	447
Tyr	Gln	Phe	Phe	Ser	Cys	Leu	Pro	Glu	Asp	Lys	Val	Pro	Tyr	Val	Asn	
106					111					116					121	
agt	cct	ggg	gag	aaa	tac	agg	atc	aag	cag	ctg	ctg	cac	cag	ctg	ccc	495
Ser	Pro	Gly	Glu	Lys	Tyr	Arg	Ile	Lys	Gln	Leu	Leu	His	Gln	Leu	Pro	
122					127					132					137	
cca	cac	gac	agt	gag	gca	cag	tac	tgc	aca	gca	ctg	gaa	gag	gag	gaa	543
Pro	His	Asp	Ser	Glu	Ala	Gln	Tyr	Cys	Thr	Ala	Leu	Glu	Glu	Glu	Glu	
138					143					148					153	
aag	aaa	gag	ctc	cga	gcc	ttt	agc	cag	cag	cgg	aag	cgg	gag	aat	ctg	591
Lys	Lys	Glu	Leu	Arg	Ala	Phe	Ser	Gln	Gln	Arg	Lys	Arg	Glu	Asn	Leu	
154					159					164					169	
ggg	cgt	ggc	atc	gtg	cgc	atc	ttc	ccg	gtg	acc	atc	act	ggg	gcc	atc	639
Gly	Arg	Gly	Ile	Val	Arg	Ile	Phe	Pro	Val	Thr	Ile	Thr	Gly	Ala	Ile	
170					175					180					185	
tgt	gag	gag	tgc	gga	aag	cag	att	gga	ggt	ggg	gac	atc	gca	gtg	ttt	687
Cys	Glu	Glu	Cys	Gly	Lys	Gln	Ile	Gly	Gly	Gly	Asp	Ile	Ala	Val	Phe	
186					191					196					201	
gcc	agc	cgt	gca	ggc	ctg	ggt	gcc	tgc	tgg	cac	cca	cag	tgc	ttc	gtg	735
Ala	Ser	Arg	Ala	Gly	Leu	Gly	Ala	Cys	Trp	His	Pro	Gln	Cys	Phe	Val	
202					207					212					217	
tgt	acc	acg	tgc	cag	gaa	ctg	ctg	ggt	gac	ctc	atc	tac	ttc	tac	cat	783
Cys	Thr	Thr	Cys	Gln	Glu	Leu	Leu	Val	Asp	Leu	Ile	Tyr	Phe	Tyr	His	
218					223					228					233	
gtt	ggc	aag	gtc	tac	tgc	ggg	cgt	cac	cat	gcc	gaa	tgc	ctg	cgt	cca	831
Val	Gly	Lys	Val	Tyr	Cys	Gly	Arg	His	His	Ala	Glu	Cys	Leu	Arg	Pro	
234					239					244					249	
cgc	tgc	caa	gcc	tgt	gac	gag	atc	atc	ttc	tcc	cct	gag	tgc	acg	gag	879
Arg	Cys	Gln	Ala	Cys	Asp	Glu	Ile	Ile	Phe	Ser	Pro	Glu	Cys	Thr	Glu	
250					255					260					265	
gct	gag	ggc	cgc	cac	tgg	cac	atg	gat	cac	ttc	tgc	tgc	ttt	gag	tgt	927
Ala	Glu	Gly	Arg	His	Trp	His	Met	Asp	His	Phe	Cys	Cys	Phe	Glu	Cys	

266		271		276		281	
gaa gct tca cta gga ggg cag cgc tat gtc atg cgt cag agc cgc ccc	975						
Glu Ala Ser Leu Gly Gly Gln Arg Tyr Val Met Arg Gln Ser Arg Pro							
282		287		292		297	
cac tgc tgc gcc tgc tac gag gcc cgc cac gcg gag tac tgt gat ggc	1023						
His Cys Cys Ala Cys Tyr Glu Ala Arg His Ala Glu Tyr Cys Asp Gly							
298		303		308		313	
tgt ggg gag cac atc ggc ctg gac caa ggc cag atg gct tac gag ggc	1071						
Cys Gly Glu His Ile Gly Leu Asp Gln Gly Gln Met Ala Tyr Glu Gly							
314		319		324		329	
cag cac tgg cat gcc tca gac cgc tgc ttc tgc tgt agt cgc tgt ggc	1119						
Gln His Trp His Ala Ser Asp Arg Cys Phe Cys Cys Ser Arg Cys Gly							
330		335		340		345	
cgg gcc ctg ctg ggc cgc cca ttc ctg cca cgc cga ggc cta atc ttc	1167						
Arg Ala Leu Leu Gly Arg Pro Phe Leu Pro Arg Arg Gly Leu Ile Phe							
346		351		356		361	
tgc tct cga gcc tgc agc ctt ggg tcc gag ccc aca gct cca ggc ccg	1215						
Cys Ser Arg Ala Cys Ser Leu Gly Ser Glu Pro Thr Ala Pro Gly Pro							
362		367		372		377	
agc cgc cgc agc tgg agt gcc ggc cct gtc aca gcc cca ctt gca gcc	1263						
Ser Arg Arg Ser Trp Ser Ala Gly Pro Val Thr Ala Pro Leu Ala Ala							
378		383		388		393	
tcc aca gcc tct ttc tct gct gtg aag ggg gca tca gag acc acc acc	1311						
Ser Thr Ala Ser Phe Ser Ala Val Lys Gly Ala Ser Glu Thr Thr Thr							
394		399		404		409	
aaa ggc acc agc aca gag tta gcg cca gct aca ggc cct gag gag ccc	1359						
Lys Gly Thr Ser Thr Glu Leu Ala Pro Ala Thr Gly Pro Glu Glu Pro							
410		415		420		425	
tcc cgc ttt ctg aga ggg gct ccc cac cgc cac tcc atg ccg gaa ctg	1407						
Ser Arg Phe Leu Arg Gly Ala Pro His Arg His Ser Met Pro Glu Leu							
426		431		436		441	
ggg ctc cgc agt gtc ccc gag ccg ccc cca gag tcc ccc ggc cag cct	1455						
Gly Leu Arg Ser Val Pro Glu Pro Pro Pro Glu Ser Pro Gly Gln Pro							
442		447		452		457	
aac ctg cgc cca gat gat agt gcc ttc ggt cgt cag agc acc cca cgc	1503						
Asn Leu Arg Pro Asp Asp Ser Ala Phe Gly Arg Gln Ser Thr Pro Arg							
458		463		468		473	
gtc agc ttc cgc gac cct ctg gtg tct gaa gga ggc ccg cgc cgg acc	1551						
Val Ser Phe Arg Asp Pro Leu Val Ser Glu Gly Gly Pro Arg Arg Thr							
474		479		484		489	
ctg agt gca ccc ccg gcc cag cgc cgc agg cca cgc agt ccc cca ccc	1599						
Leu Ser Ala Pro Pro Ala Gln Arg Arg Arg Pro Arg Ser Pro Pro Pro							
490		495		500		505	

```

agg gcc ccc agc cgt cgc cgc cac cat cat cat aat cac cat cac cat      1647
Arg Ala Pro Ser Arg Arg Arg His His His His Asn His His His His
506                      511                      516                      521

cac aac cgc cac cca agc aga cgt cgc cac tat caa tgt gac gcg gga      1695
His Asn Arg His Pro Ser Arg Arg Arg His Tyr Gln Cys Asp Ala Gly
522                      527                      532                      537

tca ggg tca gac tcg gaa tct tgc tcc agc tcg ccc tcc agt tcc agt      1743
Ser Gly Ser Asp Ser Glu Ser Cys Ser Ser Ser Pro Ser Ser Ser Ser
538                      543                      548                      553

tcc gaa tca tca gag gat gat ggc ttc ttc cta gga gag cgc atc cct      1791
Ser Glu Ser Ser Glu Asp Asp Gly Phe Phe Leu Gly Glu Arg Ile Pro
554                      559                      564                      569

ctg ccc ccg cat ttg tgc agg ccc atg cct gct cag gac act gca atg      1839
Leu Pro Pro His Leu Cys Arg Pro Met Pro Ala Gln Asp Thr Ala Met
570                      575                      580                      585

gag acc ttc aac tcc cca tct tta tcg ctc ccc agg gac tct cgc gca      1887
Glu Thr Phe Asn Ser Pro Ser Leu Ser Leu Pro Arg Asp Ser Arg Ala
586                      591                      596                      601

ggg atg cct cgt cag gcc cga gac aag aac tgc atc gtg gct tga agg      1935
Gly Met Pro Arg Gln Ala Arg Asp Lys Asn Cys Ile Val Ala *
602                      607                      612

caggccgtcc tggagggggc tccattctcc agtcagagta gatgatgagg cccatgcccc      1995

tcacccccac gccccgcccc tacaacctaa gtcataaatc ctcttctctcc ctcttttaaa      2055

aaaaaaaaaa a                                                                2066

<210> 152
<211> 7137
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (47)..(3793)

<400> 152
ctatgcacgc gtacgtaagc ttggatcctc tagagcggcc gcggtg      atg atg acg      55
                                   Met Met Thr
                                   1

ggc tac aat aat ggt cgc tgt ccc cgg aat tct ctc tac agt gac tgc      103
Gly Tyr Asn Asn Gly Arg Cys Pro Arg Asn Ser Leu Tyr Ser Asp Cys
4                      9                      14                      19

att att gag gag aag acg gtg gtc ctg cag aaa aaa gac aat gag ggc      151

```

Ile	Ile	Glu	Glu	Lys	Thr	Val	Val	Leu	Gln	Lys	Lys	Asp	Asn	Glu	Gly	
20					25					30					35	
ttt	gga	ttc	gtg	ctt	cga	ggg	gcc	aaa	gct	gac	aca	ccc	att	gaa	gaa	199
Phe	Gly	Phe	Val	Leu	Arg	Gly	Ala	Lys	Ala	Asp	Thr	Pro	Ile	Glu	Glu	
36					41					46					51	
ttc	aca	cca	aca	ccg	gct	ttc	cca	gcc	cta	cag	tac	ctg	gag	tcc	gtg	247
Phe	Thr	Pro	Thr	Pro	Ala	Phe	Pro	Ala	Leu	Gln	Tyr	Leu	Glu	Ser	Val	
52					57					62					67	
gat	gaa	ggt	ggg	gtg	gcg	tgg	caa	gcc	gga	cta	agg	acc	ggg	gac	ttc	295
Asp	Glu	Gly	Gly	Val	Ala	Trp	Gln	Ala	Gly	Leu	Arg	Thr	Gly	Asp	Phe	
68					73					78					83	
ttg	att	gag	gtt	aac	aat	gag	aat	gtt	gtc	aaa	gtc	ggc	cac	agg	cag	343
Leu	Ile	Glu	Val	Asn	Asn	Glu	Asn	Val	Val	Lys	Val	Gly	His	Arg	Gln	
84					89					94					99	
gtg	gtg	aac	atg	atc	cgg	cag	gga	ggg	aat	cac	ctg	gtc	ctt	aag	gtg	391
Val	Val	Asn	Met	Ile	Arg	Gln	Gly	Gly	Asn	His	Leu	Val	Leu	Lys	Val	
100					105					110					115	
gtc	acg	gtg	acc	agg	aat	ctg	gac	ccc	gac	gac	acc	gcc	agg	aag	aaa	439
Val	Thr	Val	Thr	Arg	Asn	Leu	Asp	Pro	Asp	Asp	Thr	Ala	Arg	Lys	Lys	
116					121					126					131	
gct	ccc	ccg	cct	cca	aag	cgg	gca	ccg	acc	aca	gcc	ctc	acc	ctg	cgc	487
Ala	Pro	Pro	Pro	Pro	Lys	Arg	Ala	Pro	Thr	Thr	Ala	Leu	Thr	Leu	Arg	
132					137					142					147	
tcc	aag	tcc	atg	acc	tcg	gag	ctg	gag	gag	ctc	gtg	gat	aaa	gcc	tcg	535
Ser	Lys	Ser	Met	Thr	Ser	Glu	Leu	Glu	Glu	Leu	Val	Asp	Lys	Ala	Ser	
148					153					158					163	
gtc	cgg	aag	aag	aag	gat	aaa	ccc	gag	gag	ata	gtc	ccg	gcc	tcc	aag	583
Val	Arg	Lys	Lys	Lys	Asp	Lys	Pro	Glu	Glu	Ile	Val	Pro	Ala	Ser	Lys	
164					169					174					179	
ccc	tcc	cgc	gct	gct	gag	aac	atg	gct	gtg	gaa	ccg	agg	gtg	gcg	acc	631
Pro	Ser	Arg	Ala	Ala	Glu	Asn	Met	Ala	Val	Glu	Pro	Arg	Val	Ala	Thr	
180					185					190					195	
atc	aag	cag	cgg	ccc	agc	agc	cgg	tgc	ttc	ccg	gcg	ggc	tca	gac	atg	679
Ile	Lys	Gln	Arg	Pro	Ser	Ser	Arg	Cys	Phe	Pro	Ala	Gly	Ser	Asp	Met	
196					201					206					211	
aac	tct	gtg	tac	gaa	cgc	caa	gga	atc	gcc	gtg	atg	acg	ccc	act	gtt	727
Asn	Ser	Val	Tyr	Glu	Arg	Gln	Gly	Ile	Ala	Val	Met	Thr	Pro	Thr	Val	
212					217					222					227	
cct	ggg	agc	cca	aaa	gcc	ccg	ttt	ctg	ggc	atc	cct	cga	ggt	acg	atg	775
Pro	Gly	Ser	Pro	Lys	Ala	Pro	Phe	Leu	Gly	Ile	Pro	Arg	Gly	Thr	Met	
228					233					238					243	
cga	agg	cag	aaa	tca	ata	gac	agc	aga	atc	ttt	cta	tca	gga	ata	aca	823
Arg	Arg	Gln	Lys	Ser	Ile	Asp	Ser	Arg	Ile	Phe	Leu	Ser	Gly	Ile	Thr	

244	249	254	259	
gag gaa gag cgg cag ttt ctg gct cct cca atg ctg aag ttc acc aga	871			
Glu Glu Glu Arg Gln Phe Leu Ala Pro Pro Met Leu Lys Phe Thr Arg				
260	265	270	275	
agc ctg tcc atg ccg gac acc tct gag gac atc ccc cct cca ccg cag	919			
Ser Leu Ser Met Pro Asp Thr Ser Glu Asp Ile Pro Pro Pro Pro Gln				
276	281	286	291	
tct gtg ccc ccg tcc cca cca cca cct tcc cca acc act tac aac tgc	967			
Ser Val Pro Pro Ser Pro Pro Pro Pro Ser Pro Thr Thr Tyr Asn Cys				
292	297	302	307	
ccc aag tcc cca act cca aga gtc tac ggg acg att aag cct gcg ttc	1015			
Pro Lys Ser Pro Thr Pro Arg Val Tyr Gly Thr Ile Lys Pro Ala Phe				
308	313	318	323	
aat cag aat tct gcc gcc aag gtg tcc ccc gcc acc agg tcc gac acc	1063			
Asn Gln Asn Ser Ala Ala Lys Val Ser Pro Ala Thr Arg Ser Asp Thr				
324	329	334	339	
gtg gcc acc atg atg agg gag aag ggg atg tac ttc agg aga gag ctg	1111			
Val Ala Thr Met Met Arg Glu Lys Gly Met Tyr Phe Arg Arg Glu Leu				
340	345	350	355	
gac cgc tac tcc ttg gac tct gaa gac ctc tac agt cgg aat gcc ggc	1159			
Asp Arg Tyr Ser Leu Asp Ser Glu Asp Leu Tyr Ser Arg Asn Ala Gly				
356	361	366	371	
ccg caa gcc aac ttc cgc aac aag aga ggc cag atg cca gaa aac cca	1207			
Pro Gln Ala Asn Phe Arg Asn Lys Arg Gly Gln Met Pro Glu Asn Pro				
372	377	382	387	
tac tca gag gtg ggg aag atc gcc agc aaa gcc gtc tac gtc ccc gcc	1255			
Tyr Ser Glu Val Gly Lys Ile Ala Ser Lys Ala Val Tyr Val Pro Ala				
388	393	398	403	
aag ccc gcc agg cgg aag ggg atg ctg gtg aag cag tcc aac gtg gag	1303			
Lys Pro Ala Arg Arg Lys Gly Met Leu Val Lys Gln Ser Asn Val Glu				
404	409	414	419	
gac agc ccc gag aag acg tgc tcc atc cct atc ccg acc atc atc gtg	1351			
Asp Ser Pro Glu Lys Thr Cys Ser Ile Pro Ile Pro Thr Ile Ile Val				
420	425	430	435	
aag gag ccg tcc acc agc agc agc ggc aag agc agc cag ggc agc agc	1399			
Lys Glu Pro Ser Thr Ser Ser Ser Gly Lys Ser Ser Gln Gly Ser Ser				
436	441	446	451	
atg gag atc gac ccc cag gcc ccg gag cca ccg agc cag ctg ccg cct	1447			
Met Glu Ile Asp Pro Gln Ala Pro Glu Pro Pro Ser Gln Leu Arg Pro				
452	457	462	467	
gac gaa agc ctg acc gtc agc agc ccc ttt gcc gcc gcc atc gcc gga	1495			
Asp Glu Ser Leu Thr Val Ser Ser Pro Phe Ala Ala Ala Ile Ala Gly				
468	473	478	483	

gcc gtc cgc gac cgt gag aag cgg ctg gaa gcc agg agg aac tcc ccg	1543
Ala Val Arg Asp Arg Glu Lys Arg Leu Glu Ala Arg Arg Asn Ser Pro	
484 489 494 499	
gcc ttc ctc tcc aca gac ctg ggg gat gag gat gtg ggc ctg ggg cca	1591
Ala Phe Leu Ser Thr Asp Leu Gly Asp Glu Asp Val Gly Leu Gly Pro	
500 505 510 515	
ccc gcc ccc agg acg cgg ccc tcc atg ttc ccc gag gag ggg gat ttt	1639
Pro Ala Pro Arg Thr Arg Pro Ser Met Phe Pro Glu Glu Gly Asp Phe	
516 521 526 531	
gct gac gag gac agc gct gag cag ctg tca tcc ccc atg ccg agt gcc	1687
Ala Asp Glu Asp Ser Ala Glu Gln Leu Ser Ser Pro Met Pro Ser Ala	
532 537 542 547	
acg ccc agg gag ccc gaa aac cat ttc gtg ggt ggc gcc gag gcc agt	1735
Thr Pro Arg Glu Pro Glu Asn His Phe Val Gly Gly Ala Glu Ala Ser	
548 553 558 563	
gct ccg ggt gag gct ggg agg ccg ctg aat tcc acg tcc aaa gcc cag	1783
Ala Pro Gly Glu Ala Gly Arg Pro Leu Asn Ser Thr Ser Lys Ala Gln	
564 569 574 579	
ggg ccc gag agc agc cca gca gtg ccc tcc gcg agc agc ggc aca gcc	1831
Gly Pro Glu Ser Ser Pro Ala Val Pro Ser Ala Ser Ser Gly Thr Ala	
580 585 590 595	
ggc ccc ggg aat tat gtc cac cca ctc aca ggg cgg ctg ctt gat ccc	1879
Gly Pro Gly Asn Tyr Val His Pro Leu Thr Gly Arg Leu Leu Asp Pro	
596 601 606 611	
agc tcc ccg ctg gcc ctg gca ctc tcc gca agg gac cga gcc atg aag	1927
Ser Ser Pro Leu Ala Leu Ala Leu Ser Ala Arg Asp Arg Ala Met Lys	
612 617 622 627	
gag tct caa cag gga ccc aaa ggg gag gcc ccc aag gcc gac ctc aac	1975
Glu Ser Gln Gln Gly Pro Lys Gly Glu Ala Pro Lys Ala Asp Leu Asn	
628 633 638 643	
aaa cct ctt tac att gat acc aaa atg cgg ccc agc ctg gat gcc ggc	2023
Lys Pro Leu Tyr Ile Asp Thr Lys Met Arg Pro Ser Leu Asp Ala Gly	
644 649 654 659	
ttc cct acg gtc acc agg cag aac acc cgg gga ccc ctg agg cgg cag	2071
Phe Pro Thr Val Thr Arg Gln Asn Thr Arg Gly Pro Leu Arg Arg Gln	
660 665 670 675	
gag acg gag aac aag tac gag acc gac ctg ggc cga gac cgg aaa ggc	2119
Glu Thr Glu Asn Lys Tyr Glu Thr Asp Leu Gly Arg Asp Arg Lys Gly	
676 681 686 691	
gat gac aag aag aac atg ctg atc gac atc atg gac acg tcc cag cag	2167
Asp Asp Lys Lys Asn Met Leu Ile Asp Ile Met Asp Thr Ser Gln Gln	
692 697 702 707	

aag tcg gct ggc ctg ctg atg gtg cac acc gtg gac gcc act aag ctg Lys Ser Ala Gly Leu Leu Met Val His Thr Val Asp Ala Thr Lys Leu 708 713 718 723	2215
gac aac gcc ctg cag gaa gag gac gag aag gca gag gtg gag atg aag Asp Asn Ala Leu Gln Glu Glu Asp Glu Lys Ala Glu Val Glu Met Lys 724 729 734 739	2263
cca gac agc tcg ccg tcc gag gtg cca gaa ggt gtt tcc gaa acc gaa Pro Asp Ser Ser Pro Ser Glu Val Pro Glu Gly Val Ser Glu Thr Glu 740 745 750 755	2311
ggg gct tta cag atc tcc gct gcc ccc gag ccc acc acc gtg ccc ggc Gly Ala Leu Gln Ile Ser Ala Ala Pro Glu Pro Thr Thr Val Pro Gly 756 761 766 771	2359
aga acc atc gtc gcg gtg ggc tcc atg gaa gag gcg gtg att ttg cca Arg Thr Ile Val Ala Val Gly Ser Met Glu Glu Ala Val Ile Leu Pro 772 777 782 787	2407
ttc cgc atc cct cct ccc cct ctg gca tcc gtg gac ttg gat gag gat Phe Arg Ile Pro Pro Pro Pro Leu Ala Ser Val Asp Leu Asp Glu Asp 788 793 798 803	2455
ttt att ttt aca gag cca ttg cct cct ccc ctg gaa ttt gca aat agt Phe Ile Phe Thr Glu Pro Leu Pro Pro Pro Leu Glu Phe Ala Asn Ser 804 809 814 819	2503
ttt gat atc ccc gat gac cgg gca gct tct gtc ccg gct ctc tca gac Phe Asp Ile Pro Asp Asp Arg Ala Ala Ser Val Pro Ala Leu Ser Asp 820 825 830 835	2551
tta gtg aag cag aag aaa agc gac acc cct cag tcc cct tcg ttg aac Leu Val Lys Gln Lys Lys Ser Asp Thr Pro Gln Ser Pro Ser Leu Asn 836 841 846 851	2599
tcc agc caa cca acc aac tct gca gac agc aag aag cca gcc agt ctt Ser Ser Gln Pro Thr Asn Ser Ala Asp Ser Lys Lys Pro Ala Ser Leu 852 857 862 867	2647
tca aac tgt ctg cct gcc tca ttc ctg cca ccc cct gaa agc ttt gac Ser Asn Cys Leu Pro Ala Ser Phe Leu Pro Pro Pro Glu Ser Phe Asp 868 873 878 883	2695
gcc gtc gcc gac tct ggg atc gag gag gtg gac agc cgg agt agc agc Ala Val Ala Asp Ser Gly Ile Glu Glu Val Asp Ser Arg Ser Ser Ser 884 889 894 899	2743
gac cac cac ctc gag acg acc agc act atc tcc acc gtg tct agc atc Asp His His Leu Glu Thr Thr Ser Thr Ile Ser Thr Val Ser Ser Ile 900 905 910 915	2791
tcc acc ctg tct tcc gaa ggt gga gag aat gtg gac acc tgc aca gtc Ser Thr Leu Ser Ser Glu Gly Gly Glu Asn Val Asp Thr Cys Thr Val 916 921 926 931	2839
tat gca gat ggg caa gca ttt atg gtt gac aaa ccc cca gta cct cct	2887

Tyr	Ala	Asp	Gly	Gln	Ala	Phe	Met	Val	Asp	Lys	Pro	Pro	Val	Pro	Pro		
932					937					942					947		
aag	cca	aaa	atg	aag	ccc	atc	att	cac	aaa	agc	aat	gca	ctt	tat	caa	2935	
Lys	Pro	Lys	Met	Lys	Pro	Ile	Ile	His	Lys	Ser	Asn	Ala	Leu	Tyr	Gln		
948					953					958					963		
gac	gcg	ctc	gtg	gaa	gaa	gat	gta	gat	agc	ttt	gtt	atc	ccc	ccg	ccc	2983	
Asp	Ala	Leu	Val	Glu	Glu	Asp	Val	Asp	Ser	Phe	Val	Ile	Pro	Pro	Pro		
964					969					974					979		
gct	ccc	ccg	ccc	ccg	ccg	ggc	agt	gcc	cag	cct	ggg	atg	gcc	aag	gtt	3031	
Ala	Pro	Pro	Pro	Pro	Pro	Gly	Ser	Ala	Gln	Pro	Gly	Met	Ala	Lys	Val		
980					985					990					995		
ctc	cag	cca	agg	acc	tcc	aag	ttg	tgg	ggc	gac	gtc	aca	gag	atc	aaa	3079	
Leu	Gln	Pro	Arg	Thr	Ser	Lys	Leu	Trp	Gly	Asp	Val	Thr	Glu	Ile	Lys		
996					1001					1006					1011		
agc	ccg	att	ctc	tca	ggc	cca	aag	gca	aac	gtt	att	agt	gaa	ttg	aac	3127	
Ser	Pro	Ile	Leu	Ser	Gly	Pro	Lys	Ala	Asn	Val	Ile	Ser	Glu	Leu	Asn		
1012					1017					1022					1027		
tct	atc	cta	cag	caa	atg	aac	cga	gag	aaa	ttg	gca	aag	ccg	ggg	gaa	3175	
Ser	Ile	Leu	Gln	Gln	Met	Asn	Arg	Glu	Lys	Leu	Ala	Lys	Pro	Gly	Glu		
1028					1033					1038					1043		
gga	ctg	gat	tca	cca	atg	gga	gcc	aag	tcc	gcc	agc	ctc	gct	cca	aga	3223	
Gly	Leu	Asp	Ser	Pro	Met	Gly	Ala	Lys	Ser	Ala	Ser	Leu	Ala	Pro	Arg		
1044					1049					1054					1059		
agc	ccg	gag	atc	atg	agc	acc	atc	tca	ggg	aca	cgg	agc	acg	acg	gtc	3271	
Ser	Pro	Glu	Ile	Met	Ser	Thr	Ile	Ser	Gly	Thr	Arg	Ser	Thr	Thr	Val		
1060					1065					1070					1075		
acc	ttc	act	gtt	cgc	ccc	ggc	acc	tcc	cag	ccc	atc	acc	ctg	cag	agc	3319	
Thr	Phe	Thr	Val	Arg	Pro	Gly	Thr	Ser	Gln	Pro	Ile	Thr	Leu	Gln	Ser		
1076					1081					1086					1091		
cgg	ccc	ccc	gac	tat	gaa	agc	agg	acc	tca	gga	aca	aga	cgt	gcc	cca	3367	
Arg	Pro	Pro	Asp	Tyr	Glu	Ser	Arg	Thr	Ser	Gly	Thr	Arg	Arg	Ala	Pro		
1092					1097					1102					1107		
agc	cct	gtg	gtc	tcg	cca	aca	gag	atg	aac	aaa	gag	acc	ctg	ccc	gcc	3415	
Ser	Pro	Val	Val	Ser	Pro	Thr	Glu	Met	Asn	Lys	Glu	Thr	Leu	Pro	Ala		
1108					1113					1118					1123		
ccc	ctg	tct	gct	gcc	acc	gcc	tct	cct	tct	ccc	gct	ctc	tca	gat	gtc	3463	
Pro	Leu	Ser	Ala	Ala	Thr	Ala	Ser	Pro	Ser	Pro	Ala	Leu	Ser	Asp	Val		
1124					1129					1134					1139		
ttt	agc	ctt	cca	agc	cag	ccc	cct	tct	ggg	gat	cta	ttt	ggc	ttg	aac	3511	
Phe	Ser	Leu	Pro	Ser	Gln	Pro	Pro	Ser	Gly	Asp	Leu	Phe	Gly	Leu	Asn		
1140					1145					1150					1155		
cca	gcg	gga	cgc	agt	agg	tcg	cca	tcc	ccc	tcg	ata	ctg	caa	cag	cca	3559	
Pro	Ala	Gly	Arg	Ser	Arg	Ser	Pro	Ser	Pro	Ser	Ile	Leu	Gln	Gln	Pro		

ccagccaagg gtgagcatct ctgctgagac agtccttttg ctctcggagg ccaggggaaga	4940
tggtacttag aggcttttcc cctatcgctc tgggtgtcta ggaatcccac cagcttgtct	5000
taacagtaca acagcttctt tgaggaccca gtgggtatgg agtatagaca gaaccagg	5060
ttgagaacag aaggtgggcg gcaggatcag agtgaaagca gaggcgtgag gagaggaaag	5120
caggagggtc tcctgggctg ccaggtcagc ctctctggca aggctttctt gagccccgcc	5180
cctttctttc cccggagtcc ctccacccca taacaatacc tcgaatttcc aaaagaggtc	5240
accagatgca catgggcccgc aaaacacaca gtcaggcttc cagcacattc tccccattt	5300
ggaggatact cgaatgtcag gtttttggtt ttattattat ttcagaacta gctcagccca	5360
tctctaatta taaaacatgg ttttgttttt ttttttctt tttttcttg attaggctctg	5420
gaacagctct agaatgaaca cataaaattt agcaatttaa aatctttctt tactgcaagt	5480
ttaaatagtt gtacagatag tttataagca caatatttta agaaaaaaaa gtggctggtc	5540
tactaggcag cctttgtgcc acttcagtgc tagaaagtta aagaaaaaaaa aacttttgtg	5600
atttaataat actatttctg tggaataatt ataaaagtat gaccttttta aatcaacctt	5660
at ttggatgc atctgaacca gcagagctgt gttatatattt ctatctttgc tagaacttcg	5720
tcattgaagg acaatttctt caaagtgggtt acaattcata atgcagcagt ttctccaaaa	5780
acaaaaacaa aacacacacc acacacacgc gcttttccag tcacacaccc ctgatgttgg	5840
aaccaagttt ttggaccttc tgttccaaaa ccttttgcag gtcaatcttt gtatttgaaa	5900
tgatccaatc caacttgaag tcaattgaat attaaggcgc tttacttccg tgtgctttca	5960
gtttttccat catgagatga atgagcatta ctctagataa atttcaagac aggatactac	6020
aggtggcctg ctgaggctgc cccatatttt agaaaatgta aaaatgggtg tttggccatt	6080
aatttgtctt ccatttgatg ataccgcaaa attccgtgag tccattcctt tggcatggca	6140
ctttccctgg gcctacagtt ggtattacct ctgtgctcag tgccaggcaa aacactagct	6200
caaaggagag tcaaggaaac cgctggcaga cgataaccag tcgaaactcg tgacttcggt	6260
ttgttgaact ttggcagcca gttggtgagg gccagatgtt attccctttc ttaaagatac	6320
tccaagccac atgccactaa ccacaagcaa gctggctgca agactaaaga gctgacaaca	6380
tagtttattt ttacactgtc ttattataga gaagtaatag acctatcaga acctgcactg	6440
accaacaaat aaacacatgt tgccaagatg aatcgggtctc tatctctatc tgcttatttt	6500
ggtactgaaa gcaatagttc ctcatcctaa tcaccaccca ctgttctccc cctttgggac	6560

```

atgttaggac gaggcctat tccatgcccc tctttaatgg tggaacaaat gttaaactgc 6620
tcatctaaag atcatgttga tattattcca ggttttaaga tcaacttttg ttacatactg 6680
taatttaaam aaactgcatt tacatgccta gtttctgtaa tattgtgtat acaaaaccca 6740
aatctctcaa aatgtaaatt atgtatacct gccaaagatac cttttccagg gtgtctgcgc 6800
acattttaag ttaattcaca taatataaaa attactcaat gtgactgttg atttgctgaa 6860
ctttacatat cacaaagtga attatttgtg atacttttagt taataaaatg gttaaattttt 6920
ttctcagtta ttgaacaagc aagcattatc cagttgatct ggcaatgact ttttgtgtgt 6980
gggccacaat attgattttc ccattaacaa tttttttttg ttttttaaat actaatatgt 7040
ttcacactat agtttgtgta acaacacgtg ttcgcattat ctatgttget gttacttttg 7100
tgcttttatt ctttttagac tttataaaaa aaaaaaa 7137

```

```

<210> 153
<211> 2212
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (227) .. (1294)

```

```

<400> 153
aatactttat aagtgaata ttacttgaat cctttgagat gttacaagtt ttttttttcc 60
ttgagtcatg ctaatagatg gttcaataca tgaatgagtc ccttgctgaa atgctttagg 120
acttcagact accctgaacg ttgattactc tttatactga aataggcatt attcagtgga 180
agagagggaa gaccaaattg atagactgga ctttattcga aaccag atg aac ctt 235
Met Asn Leu
1

tta aca ctg gat gtt aag aaa aaa atc aag gag gtt acc gag gag gtg 283
Leu Thr Leu Asp Val Lys Lys Lys Ile Lys Glu Val Thr Glu Glu Val
4 9 14 19

gca aac aaa gtt tca tgt gca atg aca gat gaa att tgt cga ctg tct 331
Ala Asn Lys Val Ser Cys Ala Met Thr Asp Glu Ile Cys Arg Leu Ser
20 25 30 35

gtt ttg gtt gat gaa ttt tgt tca gag ttt cat cct aat cca gat gta 379
Val Leu Val Asp Glu Phe Cys Ser Glu Phe His Pro Asn Pro Asp Val
36 41 46 51

tta aaa ata tat aaa agt gaa tta aat aag cac ata gag gat ggt atg 427
Leu Lys Ile Tyr Lys Ser Glu Leu Asn Lys His Ile Glu Asp Gly Met

```

52	57	62	67	
gga aga aat ttg gct gat cga tgc acc gat gaa gta aac gcc tta gtg				475
Gly Arg Asn Leu Ala Asp Arg Cys Thr Asp Glu Val Asn Ala Leu Val				
68	73	78	83	
ctt cag acc cag caa gaa att att gaa aat ttg aag cca tta ctt cca				523
Leu Gln Thr Gln Gln Glu Ile Ile Glu Asn Leu Lys Pro Leu Leu Pro				
84	89	94	99	
gct ggt ata cag gat aaa cta cat aca ctg atc cct tgc aag aaa ttt				571
Ala Gly Ile Gln Asp Lys Leu His Thr Leu Ile Pro Cys Lys Lys Phe				
100	105	110	115	
gat ctc agt tat aat cta aat tac cac aag tta tgt tca gat ttt caa				619
Asp Leu Ser Tyr Asn Leu Asn Tyr His Lys Leu Cys Ser Asp Phe Gln				
116	121	126	131	
gag gat att gta ttt cgt ttt tcc ctg ggc tgg tct tcc ctt gta cat				667
Glu Asp Ile Val Phe Arg Phe Ser Leu Gly Trp Ser Ser Leu Val His				
132	137	142	147	
cga ttt ttg ggc cct aga aat gct caa agg gtg ctc cta gga tta tca				715
Arg Phe Leu Gly Pro Arg Asn Ala Gln Arg Val Leu Leu Gly Leu Ser				
148	153	158	163	
gag cct atc ttt cag ctc cct aga tct tta gct tct act ccc act gct				763
Glu Pro Ile Phe Gln Leu Pro Arg Ser Leu Ala Ser Thr Pro Thr Ala				
164	169	174	179	
cct acc act cca gca acg cca gat aat gca tca cag gaa gaa ctc atg				811
Pro Thr Thr Pro Ala Thr Pro Asp Asn Ala Ser Gln Glu Glu Leu Met				
180	185	190	195	
att aca tta gta aca gga ttg gcg tcc gtt aca tct aga act tct atg				859
Ile Thr Leu Val Thr Gly Leu Ala Ser Val Thr Ser Arg Thr Ser Met				
196	201	206	211	
ggc atc att att gtt gga gga gtg att tgg aaa act ata ggc tgg aaa				907
Gly Ile Ile Ile Val Gly Gly Val Ile Trp Lys Thr Ile Gly Trp Lys				
212	217	222	227	
ctc cta tct gtt tca tta act atg tat gga gct ttg tat ctt tat gaa				955
Leu Leu Ser Val Ser Leu Thr Met Tyr Gly Ala Leu Tyr Leu Tyr Glu				
228	233	238	243	
aga ctg agc tgg acc acc cat gcc aag gag cga gcc ttt aaa cag cag				1003
Arg Leu Ser Trp Thr Thr His Ala Lys Glu Arg Ala Phe Lys Gln Gln				
244	249	254	259	
ttt gta aac tat gca act gaa aaa ctg agg atg att gtt agc tcc acg				1051
Phe Val Asn Tyr Ala Thr Glu Lys Leu Arg Met Ile Val Ser Ser Thr				
260	265	270	275	
agt gca aac tgc agt cac caa gta aaa caa caa ata gct acc act ttt				1099
Ser Ala Asn Cys Ser His Gln Val Lys Gln Gln Ile Ala Thr Thr Phe				
276	281	286	291	

gct cgc ctg tgc caa caa gtt gat att act caa aaa cag ctg gaa gaa	1147
Ala Arg Leu Cys Gln Gln Val Asp Ile Thr Gln Lys Gln Leu Glu Glu	
292 297 302 307	
gaa att gct aga tta ccc aaa gaa ata gat cag ttg gag aaa ata caa	1195
Glu Ile Ala Arg Leu Pro Lys Glu Ile Asp Gln Leu Glu Lys Ile Gln	
308 313 318 323	
aac aat tca aag ctc tta aga aat aaa gct gtt caa ctt gaa aat gag	1243
Asn Asn Ser Lys Leu Leu Arg Asn Lys Ala Val Gln Leu Glu Asn Glu	
324 329 334 339	
ctg gag aat ttt act aag cag ttt cta cct tca agc aat gaa gaa tcc	1291
Leu Glu Asn Phe Thr Lys Gln Phe Leu Pro Ser Ser Asn Glu Glu Ser	
340 345 350 355	
taa caat agagattgct ttggtgacca tgataggagg aaacgaaact tgtaagattg	1348
* 356	
gaacagttgt tatttttatg aaattacttt aaatatgaat tgtactaact gtacctaaat	1408
agcaaagccc tgtgtagatt ctggtaatga tctgtctcag ggtatgtgta tttttgaaga	1468
gtgttatgtc cttagtttta attttgagta aagaaaaggc taaaatcatg aattagttac	1528
aagcaacagt accaacttat gtgacccttg aggggtgggg ctgtgagctc ttaatttggt	1588
tttgattctg aaaaactctg ctccctggca tccaggagtt agagattgag cctttcatct	1648
tctttctcaa aactagtttt tgatgctttc tttcatggga atagtcactt ttttatttag	1708
taaatcgcat tgctggaacc accaaggagt gtggaatgtc cttgagtgtg ttatttatgc	1768
aagtcacagt cacgttgcca tcatggcagc tatgtgaaac actaataaat gtgtttttac	1828
tttttattcc cgtaaaaact gatgtaaaac aggataaagg cttgttatag tcacttataa	1888
gtatctgggt ctaagtaatt tccttagatg tttctaaaga aacattttca gctttgctcc	1948
cattatgatt ccaataagga acgctttcct agtgcaattt taggagtaaa gtttgaagag	2008
ataaaaaatag ccaaagatag gagacgtctg aattttgaat gataaacagt gatgttttaa	2068
aaaggctgtt gttcttcagg aggcatttgc ctaggatatt gctggattat accccattgg	2128
aggcttttaa ttttatttgt atgaattttc caggatttca ttaaaaatta ttattgtatt	2188
ttttacctta aaaaaaaaaa aaaa	2212

<210> 154
 <211> 2083
 <212> DNA

[illegible]

<221> CDS

<400> 154

553

89						94						99						104	
gtt gga gga gtg att tgg aaa act ata ggc tgg aaa ctc cta tct gtt						110						115						120	1107
Val Gly Gly Val Ile Trp Lys Thr Ile Gly Trp Lys Leu Leu Ser Val																			
105																			
tca tta act atg tat gga gct ttg tat ctt tat gaa aga ctg agc tgg						126						131						136	1155
Ser Leu Thr Met Tyr Gly Ala Leu Tyr Leu Tyr Glu Arg Leu Ser Trp																			
121																			
acc acc cat gcc aag gag cga gcc ttt aaa cag cag ttt gta aac tat						142						147						152	1203
Thr Thr His Ala Lys Glu Arg Ala Phe Lys Gln Gln Phe Val Asn Tyr																			
137																			
gca act gaa aaa ctg agg atg att gtt agc tcc acg agt gca aac tgc						158						163						168	1251
Ala Thr Glu Lys Leu Arg Met Ile Val Ser Ser Thr Ser Ala Asn Cys																			
153																			
agt cac caa gta aaa caa caa ata gct acc act ttt gct cgc ctg tgc						174						179						184	1299
Ser His Gln Val Lys Gln Gln Ile Ala Thr Thr Phe Ala Arg Leu Cys																			
169																			
caa caa gtt gat att acc cac aaa cag ctg gaa gaa gaa att gct aga						190						195						200	1347
Gln Gln Val Asp Ile Thr His Lys Gln Leu Glu Glu Glu Ile Ala Arg																			
185																			
tta ccc aaa gaa ata gat cag ttg gag aaa atc caa aac aat tca aag						206						211						216	1395
Leu Pro Lys Glu Ile Asp Gln Leu Glu Lys Ile Gln Asn Asn Ser Lys																			
201																			
ctc tta aga aat aaa gct gtt caa ctt gaa aat gag ctg gag aat ttt						222						227						232	1443
Leu Leu Arg Asn Lys Ala Val Gln Leu Glu Asn Glu Leu Glu Asn Phe																			
217																			
act aag cag ttt cta cct tca agc aat gaa gaa tcc taa caatagagat						238						243							1492
Thr Lys Gln Phe Leu Pro Ser Ser Asn Glu Glu Ser *																			
233																			
tgcttttggtg accatgatag gaggaaacga aacttgtaag attggaacag ttgttatttt																			1552
tatgaaatta ctttaaatat gaattgtact atctgtacct aaatagcaaa gccctgtgta																			1612
gattctggta atgatctgtc tcagggtatg tgtattttttg aagagtgtta tgtccttagt																			1672
tttaatttttg agtaaagaaa aggctaaaat catgaattag ttacaagcaa cagtaccaac																			1732
ttatgtgacc cctgaggggt ggggctgtga gctcttaatt tgtttttgat tctgaaaaac																			1792
tctgcttcct ggcatccagg agttagagat tgagcctttc atcttctttc tcaacactag																			1852
tttttgatgc tttctttcat gggaatagtc acttttttat ttagtaaadc gcattgctgg																			1912
aaccaccca aggagtgtgg aatgtccttg agtgtattat ttatgcaagt cacagtcacg																			1972
ttgccatcat ggcagctatg tgaaacacta ataaatgtgt ttttactttt tattcccgtt																			2032
aaaactgatg taaaacagga taaaggcttg ttatagtcaa aaaaaaaaaa a																			2083

<210> 155
 <211> 3231
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (331)..(1158)

<400> 155

```
gcacgagtgg acttggtg cgctgccagg gctccgcagc gttgccgggt gtattcgctg      60
gataccagag ggcggaagtg cagcagggtt cagctccgac ctccgcgccg gtgctttttg      120
cggtcgcgcg ggcttctctg agtcctgcta ccgcgtcccc gcaggacagt gtgtcaggcg      180
ggcagcttgc cccgccgccc caccggagcg cggaatctgg gcgtccccac cagtgcgggg      240
agccggaagg aggagccata gcttggagta ggtttggtt tggttgaaat aagaatttag      300
cctgtatgta ctgctttaac tcctggaaga      atg aca gat gac aaa gat gtg      351
                                   Met Thr Asp Asp Lys Asp Val
                                   1                      5

ctt cga gat gtg tgg ttt gga cga att cca act tgt ttc acg cta tat      399
Leu Arg Asp Val Trp Phe Gly Arg Ile Pro Thr Cys Phe Thr Leu Tyr
  8                      13                      18                      23

cag gat gag ata act gaa agg gaa gca gaa cca tac tat ttg ctt ttg      447
Gln Asp Glu Ile Thr Glu Arg Glu Ala Glu Pro Tyr Tyr Leu Leu Leu
  24                      29                      34                      39

cca aga gta agt tat ttg acg ttg gta act gac aaa gtg aaa aag cac      495
Pro Arg Val Ser Tyr Leu Thr Leu Val Thr Asp Lys Val Lys Lys His
  40                      45                      50                      55

ttt cag aag gtt atg aga caa gaa gac att agt gag ata tgg ttt gaa      543
Phe Gln Lys Val Met Arg Gln Glu Asp Ile Ser Glu Ile Trp Phe Glu
  56                      61                      66                      71

tat gaa ggc aca cca ctg aaa tgg cat tat cca att ggt ttg cta ttt      591
Tyr Glu Gly Thr Pro Leu Lys Trp His Tyr Pro Ile Gly Leu Leu Phe
  72                      77                      82                      87

gat ctt ctt gca tca agt tca gct ctt cct tgg aac atc aca gta cat      639
Asp Leu Leu Ala Ser Ser Ser Ala Leu Pro Trp Asn Ile Thr Val His
  88                      93                      98                      103

ttt aag agt ttt cca gaa aaa gac ctt ctg cac tgt cca tct aag gat      687
Phe Lys Ser Phe Pro Glu Lys Asp Leu Leu His Cys Pro Ser Lys Asp
  104                      109                      114                      119

gca att gaa gct cat ttt atg tca tgt atg aaa gaa gct gat gct tta      735
```

Ala Ile Glu Ala His Phe Met Ser Cys Met Lys Glu Ala Asp Ala Leu	
120 125 130 135	
aaa cat aaa agt caa gta atc aat gaa atg cag aaa aaa gat cac aag	783
Lys His Lys Ser Gln Val Ile Asn Glu Met Gln Lys Lys Asp His Lys	
136 141 146 151	
caa ctc tgg atg gga ttg caa aat gac aga ttt gac cag ttt tgg gcc	831
Gln Leu Trp Met Gly Leu Gln Asn Asp Arg Phe Asp Gln Phe Trp Ala	
152 157 162 167	
atc aat cgg aaa ctc atg gaa tat cct gca gaa gaa aat gga ttt cgt	879
Ile Asn Arg Lys Leu Met Glu Tyr Pro Ala Glu Glu Asn Gly Phe Arg	
168 173 178 183	
tat atc ccc ttt aga ata tat cag aca acg act gaa aga cct ttc att	927
Tyr Ile Pro Phe Arg Ile Tyr Gln Thr Thr Thr Glu Arg Pro Phe Ile	
184 189 194 199	
cag aag ctg ttt cgt cct gtg gct gca gat gga cag ttg cac aca cta	975
Gln Lys Leu Phe Arg Pro Val Ala Ala Asp Gly Gln Leu His Thr Leu	
200 205 210 215	
gga gat ctc ctc aaa gaa gtt tgt cct tct gct att gat cct gaa gat	1023
Gly Asp Leu Leu Lys Glu Val Cys Pro Ser Ala Ile Asp Pro Glu Asp	
216 221 226 231	
ggg gaa aaa aag aat caa gtg atg att cat gga att gag cca atg ttg	1071
Gly Glu Lys Lys Asn Gln Val Met Ile His Gly Ile Glu Pro Met Leu	
232 237 242 247	
gaa aca cct ctg cag tgg ctg agt gaa cat ctg agc tac ccg gat aat	1119
Glu Thr Pro Leu Gln Trp Leu Ser Glu His Leu Ser Tyr Pro Asp Asn	
248 253 258 263	
ttt ctt cat att agt atc atc cca cag cca aca gat tga aggatcaact	1168
Phe Leu His Ile Ser Ile Ile Pro Gln Pro Thr Asp *	
264 269 274	
atttgctga acagaatcat ccttaaattg gatttatcag agcatgtcac ccttttgctt	1228
caatcagggtt tgggtggaggc aacctgacca gaaacacttc gctgctgcaa gccagacagg	1288
aaaaagattc catgtcagat aaggcaactg ggctgggtctt actttgcatc acctctgctt	1348
tcctccactg ccatcattaa acctcagctg tgacatgaaa gacttaccgg accactgaag	1408
gtcttctgta aaatataatg aagctgaaac ctttggccta agaagaaaat ggaagtatgt	1468
gccactcgat ttgtatttct gattaacaaa taaacagggg tatttcctaa ggtgaccatg	1528
gttgaacttt agctcatgaa agtggaacaa ttggtttaatt tttcaagaga attaagaaag	1588
taaaagagaa attctgttat caataacttg caagtaattt tttgtaaaag attgaattac	1648
agtaaaccga tctttcctta acgaaaattt cctatgttta cagtctgtct attggtatgc	1708

aatccttgtaa	ctttgataat	gaacagtgag	agatttttaa	ataaagcctc	taaatatggt	1768
ttgtcattta	ataacataca	gttttgtcac	ttttcaagta	ctttctgact	cacatacagt	1828
agatcacttt	ttactctgtg	ttaccatttt	gactggctgt	cattggcatg	gggtggatat	1888
agggcatagg	attacttgtc	tcagaagctg	tcatagaatt	tcttgctgcc	aattaaaaaa	1948
cctgtgttct	ttacacacta	cacgtataaa	tattgtaact	gttcactctt	gttgttttat	2008
cactgtaagc	ctgtcaaatc	atagtatcct	aagcatctgt	aaatgcta	tttgcatttt	2068
tggaaaaacc	cattccttcc	aagctagtgt	ttttcattgg	ctccaggtct	aatttttcac	2128
tgtggtccct	ggcagccagt	cttttgaagt	ttaaagatta	cctgtctctt	gactgcagta	2188
ccttttcttt	aattttttacc	aaaaatatcc	agaggttact	ggagttctta	ttcaatataa	2248
ggaaagtttg	ctgcacttta	ttaccaagcc	tctgggattt	taccagtcaa	acatatttgt	2308
gcattacatt	tcattttcttg	tgagctagct	ggctgtccat	attgaatggt	gaccatttgg	2368
agtacgctaa	aaggcttaca	gtatcagaca	cgatcatggg	tttagatccc	ataataaaaa	2428
tgaatgtttt	tcttataaaa	aattatacaa	atgctgaagt	gagattctac	tattgttcat	2488
tgcttccttt	tctttttcct	tttgcgattt	tcactgatta	atagcacatt	tcttcacaaa	2548
attagataaa	gttggtcaaa	gaccagatat	tctggaatgg	aaattgtaaa	gcttaatcaa	2608
aaagaatagc	cagtacagca	tacaatctca	gaaacttaga	agcaagtaga	aaataattgg	2668
ttgatgtaaa	cgaaagtgcc	atttttagtaa	aggcaggaaa	aaaatagcaa	tatttgagtt	2728
atgtaaggat	aaaaaatcca	ctgacttgta	tttttgcaca	agaggctggg	ctgaatatga	2788
ttgttcacat	taagagtgtt	tattcgtcgg	ttcattttgg	ggattttccc	ccttgatgtt	2848
ttgacagatt	gaagtgagct	ttagtgagca	aaaggatcag	aatgcaggga	acactaagct	2908
gtgatgaaga	aagtgtggta	aaaagccaga	gtagttttat	acagacaaaa	ccagtgtcag	2968
gcctttgcag	taggcttgag	tgaacttctg	atctagattt	gaaagtaaat	tttatgaaga	3028
cattgccc	ttttacttcc	tcattcatta	ttgtaccagc	atcatagctt	tattactcta	3088
atcccaggta	agtcaagcct	acaatgccct	agaggaagag	taaaaccaga	aattcatgct	3148
ggcttaaata	atctattttt	gtttcttttc	atttgaatat	ttaaatttta	tggtttatta	3208
aaaaattaaa	taaaaaaaaa	aaa				3231

<210>	156
<211>	1073

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (337)..(720)

<400> 156

```

accacatata tacccaactt ttatttgtca attacacttt aataaagctg ggggaagcca      60
ctctttttttt gggcacagca tccggctttt atttactaac tttgagaaca gagtaccttg      120
atcaattaaa tggtagggag cgctgtggag acagcatcct cccagtcg ggaagagagg      180
cctaggatgc ctggggccca ggggcctctt cctcctgggc gtccccggct gccctcgctc      240
ccaggccccg cagtctcatt tgccgcttcc gacgcgtgac cccggcgcgc tagcgtccgg      300
gaccggtgac aggcgcgggg tgccccaagc agtccc  atg tgt ccc ctc cct ctc      354
                                         Met Cys Pro Leu Pro Leu
                                         1

gca gcc gcc gca gtc gct gcg ccc cga gcc cct ctc cgg ctc ctc aac      402
Ala Ala Ala Ala Val Ala Ala Pro Arg Ala Pro Leu Arg Leu Leu Asn
  7                      12                      17                      22

aga ggg ctc gcc gcc gcc atg tct acc gcc cag tca ctc aaa tcc gtg      450
Arg Gly Leu Ala Ala Ala Met Ser Thr Ala Gln Ser Leu Lys Ser Val
 23                      28                      33                      38

gac tac gag gtg ttc gga aga gtg cag ggt gtt tgc ttc aga atg tat      498
Asp Tyr Glu Val Phe Gly Arg Val Gln Gly Val Cys Phe Arg Met Tyr
 39                      44                      49                      54

aca gaa gat gaa gct agg aaa ata gga gtg gtt ggc tgg gtg aag aat      546
Thr Glu Asp Glu Ala Arg Lys Ile Gly Val Val Gly Trp Val Lys Asn
 55                      60                      65                      70

acc agc aaa ggc acc gtg aca ggc caa gtg cag ggg cca gaa gac aaa      594
Thr Ser Lys Gly Thr Val Thr Gly Gln Val Gln Gly Pro Glu Asp Lys
 71                      76                      81                      86

gtc aat tcc atg aag tcc tgg ctg agc aag gtt gga agc cct agt tct      642
Val Asn Ser Met Lys Ser Trp Leu Ser Lys Val Gly Ser Pro Ser Ser
 87                      92                      97                      102

cgc att gac cgc aca aac ttt tct aat gaa aaa acc atc tct aag ctt      690
Arg Ile Asp Arg Thr Asn Phe Ser Asn Glu Lys Thr Ile Ser Lys Leu
103                      108                      113                      118

gaa tac tct aat ttt agt att aga tac taa t agaagagaaa aattgtaaca      741
Glu Tyr Ser Asn Phe Ser Ile Arg Tyr *
119                      124

cactgaacaa tagatactgt atgttcttaa gactatgtat actagaataa tagtagcaga      801
gtagggtgaa aaggaaacttt ctgttctgaa agctaagcga ctgtacgtgc tactaaaaat      861

```

gtctgacact gaaataatTT tactcaacta tgTTTTcaac aagcaaaaat atagtattct 921
aagattaaaa tgtcattaca aaatatttag tgtgaacatt taatttaaac ttgttcatg 981
gaatctTTaa tttcaatgaa cattacagca tatatatgtt atttggcgag acatcaaata 1041
aagttaacca tttaaaaatt aaaaaaaaaa aa 1073

<210> 157
<211> 1246
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (218)..(1078)

<400> 157
atttggccct cgaggccaag aattcggcac gagcacggaa atgaaagtgg aagcaaacag 60
cctgcgagca gagcctcctg aggtgtatTT cgggtcttgc tggggctgag agagaccaca 120
gccctttggg gggtacaaac aagagttcag ttgctgtgaa ttctgccact gtgcccagct 180
ctgaagcctc agctcttgcc aaacagaccc gagaccc atg tca gcc cca ctg gat 235
Met Ser Ala Pro Leu Asp
1
gcc gcc ctc cac gcc ctt cag gag gag cag gcc aga ctc aag atg agg 283
Ala Ala Leu His Ala Leu Gln Glu Glu Gln Ala Arg Leu Lys Met Arg
7 12 17 22
ctg tgg gac ctg cag cag ctg aga aag gag ctc ggg gac tcc ccc aaa 331
Leu Trp Asp Leu Gln Gln Leu Arg Lys Glu Leu Gly Asp Ser Pro Lys
23 28 33 38
gac aag gtc cca ttt tca gtg ccc aag atc ccc ctg gta ttc cga gga 379
Asp Lys Val Pro Phe Ser Val Pro Lys Ile Pro Leu Val Phe Arg Gly
39 44 49 54
cac acc cag cag gac ccg gaa gtg cct aag tct tta gtt tcc aat ttg 427
His Thr Gln Gln Asp Pro Glu Val Pro Lys Ser Leu Val Ser Asn Leu
55 60 65 70
cgg atc cac tgc cct ctg ctt gcg ggc tct gct ctg atc acc ttt gat 475
Arg Ile His Cys Pro Leu Leu Ala Gly Ser Ala Leu Ile Thr Phe Asp
71 76 81 86
gac ccc aaa gtg gct gag cag gtg ctg caa caa aag gag cac acg atc 523
Asp Pro Lys Val Ala Glu Gln Val Leu Gln Gln Lys Glu His Thr Ile
87 92 97 102
aac atg gag gag tgc cgg ctg cgg gtg cag gtc cag ccc ttg gag ctg 571

Asn Met Glu Glu Cys Arg Leu Arg Val Gln Val Gln Pro Leu Glu Leu	
103 108 113 118	
ccc atg gtc acc acc atc cag gtg tcc agc cag ttg agt ggc cgg agg	619
Pro Met Val Thr Thr Ile Gln Val Ser Ser Gln Leu Ser Gly Arg Arg	
119 124 129 134	
gtg ttg gtc act gga ttt cct gcc agc ctc agg ctg agt gag gag gag	667
Val Leu Val Thr Gly Phe Pro Ala Ser Leu Arg Leu Ser Glu Glu Glu	
135 140 145 150	
ctg ctg gac aag cta gag atc ttc ttt ggc aag act agg aac gga ggt	715
Leu Leu Asp Lys Leu Glu Ile Phe Phe Gly Lys Thr Arg Asn Gly Gly	
151 156 161 166	
ggc gat gtg gac gtt cgg gag cta ctg cca ggg agt gtc atg ctg ggg	763
Gly Asp Val Asp Val Arg Glu Leu Leu Pro Gly Ser Val Met Leu Gly	
167 172 177 182	
ttt gct agg gat gga gtg gct cag cgt ctg tgc caa atc ggc cag ttc	811
Phe Ala Arg Asp Gly Val Ala Gln Arg Leu Cys Gln Ile Gly Gln Phe	
183 188 193 198	
aca gtg cca ctg ggt ggg cag caa gtc cct ctg aga gtc tct ccg tat	859
Thr Val Pro Leu Gly Gly Gln Gln Val Pro Leu Arg Val Ser Pro Tyr	
199 204 209 214	
gtg aat ggg gag atc cag aag gct gag atc agg tcg cag cca gtt ccc	907
Val Asn Gly Glu Ile Gln Lys Ala Glu Ile Arg Ser Gln Pro Val Pro	
215 220 225 230	
cgc tcg gta ctg gtg ctc aac att cct gat atc ttg gat ggc ccg gag	955
Arg Ser Val Leu Val Leu Asn Ile Pro Asp Ile Leu Asp Gly Pro Glu	
231 236 241 246	
ctg cat gac gtc ctg gag atc cac ttc cag aag ccc acc cgc ggg ggc	1003
Leu His Asp Val Leu Glu Ile His Phe Gln Lys Pro Thr Arg Gly Gly	
247 252 257 262	
ggg gag gta gag gcc ctg aca gtc gta ccc caa gga cag cag ggc cta	1051
Gly Glu Val Glu Ala Leu Thr Val Val Pro Gln Gly Gln Gln Gly Leu	
263 268 273 278	
gca gtc ttc acc tct gag tca ggc tag gggcc tcccccttctc atcctcccca	1103
Ala Val Phe Thr Ser Glu Ser Gly *	
279 284	
cccccccgcc aaggttctca cactggcctg ggcttggggtg cccatatagg aggtctgtat	1163
gttcaccaac agtgcagagg ggtcacacat tgcaaaacac tgcccagaac agtaaaaaga	1223
gcctgcatgc caaaaaaaaaaaa aaa	1246

<210> 158

Table 1. Demographic characteristics of the study population	
Age (years)	Mean (SD)
18-24	20.5 (2.5)
25-34	29.5 (4.5)
35-44	39.5 (5.5)
45-54	49.5 (6.5)
55-64	59.5 (7.5)
65-74	69.5 (8.5)
75-84	79.5 (9.5)
85-94	89.5 (10.5)
95-104	99.5 (11.5)
105-114	109.5 (12.5)
115-124	119.5 (13.5)
125-134	129.5 (14.5)
135-144	139.5 (15.5)
145-154	149.5 (16.5)
155-164	159.5 (17.5)
165-174	169.5 (18.5)
175-184	179.5 (19.5)
185-194	189.5 (20.5)
195-204	199.5 (21.5)
205-214	209.5 (22.5)
215-224	219.5 (23.5)
225-234	229.5 (24.5)
235-244	239.5 (25.5)
245-254	249.5 (26.5)
255-264	259.5 (27.5)
265-274	269.5 (28.5)
275-284	279.5 (29.5)
285-294	289.5 (30.5)
295-304	299.5 (31.5)
305-314	309.5 (32.5)
315-324	319.5 (33.5)
325-334	329.5 (34.5)
335-344	339.5 (35.5)
345-354	349.5 (36.5)
355-364	359.5 (37.5)
365-374	369.5 (38.5)
375-384	379.5 (39.5)
385-394	389.5 (40.5)
395-404	399.5 (41.5)
405-414	409.5 (42.5)
415-424	419.5 (43.5)
425-434	429.5 (44.5)
435-444	439.5 (45.5)
445-454	449.5 (46.5)
455-464	459.5 (47.5)
465-474	469.5 (48.5)
475-484	479.5 (49.5)
485-494	489.5 (50.5)
495-504	499.5 (51.5)
505-514	509.5 (52.5)
515-524	519.5 (53.5)
525-534	529.5 (54.5)
535-544	539.5 (55.5)
545-554	549.5 (56.5)
555-564	559.5 (57.5)
565-574	569.5 (58.5)
575-584	579.5 (59.5)
585-594	589.5 (60.5)
595-604	599.5 (61.5)
605-614	609.5 (62.5)
615-624	619.5 (63.5)
625-634	629.5 (64.5)
635-644	639.5 (65.5)
645-654	649.5 (66.5)
655-664	659.5 (67.5)
665-674	669.5 (68.5)
675-684	679.5 (69.5)
685-694	689.5 (70.5)
695-704	699.5 (71.5)
705-714	709.5 (72.5)
715-724	719.5 (73.5)
725-734	729.5 (74.5)
735-744	739.5 (75.5)
745-754	749.5 (76.5)
755-764	759.5 (77.5)
765-774	769.5 (78.5)
775-784	779.5 (79.5)
785-794	789.5 (80.5)
795-804	799.5 (81.5)
805-814	809.5 (82.5)
815-824	819.5 (83.5)
825-834	829.5 (84.5)
835-844	839.5 (85.5)
845-854	849.5 (86.5)
855-864	859.5 (87.5)
865-874	869.5 (88.5)
875-884	879.5 (89.5)
885-894	889.5 (90.5)
895-904	899.5 (91.5)
905-914	909.5 (92.5)
915-924	919.5 (93.5)
925-934	929.5 (94.5)
935-944	939.5 (95.5)
945-954	949.5 (96.5)
955-964	959.5 (97.5)
965-974	969.5 (98.5)
975-984	979.5 (99.5)
985-994	989.5 (100.5)
995-1004	999.5 (101.5)
1005-1014	1009.5 (102.5)
1015-1024	1019.5 (103.5)
1025-1034	1029.5 (104.5)
1035-1044	1039.5 (105.5)
1045-1054	1049.5 (106.5)
1055-1064	1059.5 (107.5)
1065-1074	1069.5 (108.5)
1075-1084	1079.5 (109.5)
1085-1094	1089.5 (110.5)
1095-1104	1099.5 (111.5)
1105-1114	1109.5 (112.5)
1115-1124	1119.5 (113.5)
1125-1134	

<400> 158

cca cag gct tta cta gct atc ttt tgg ctt cta ctg agc tgg gtg agc 104
Pro Gln Ala Leu Leu Ala Ile Phe Trp Leu Leu Leu Ser Trp Val Ser
5 10 15 20

gga gac acc gta act ctc aat tgc agt tat gaa gtg act aac ttt cga 200
Gly Asp Thr Val Thr Leu Asn Cys Ser Tyr Glu Val Thr Asn Phe Arg
37 42 47 52

agc cta cta tgg tac aag cag gaa aag aaa gct ccc aca ttt cta ttt 248
 Ser Leu Leu Trp Tyr Lys Gln Glu Lys Lys Ala Pro Thr Phe Leu Phe
 53 58 63 68

atg cta act tca agt gga att gaa aag aag tca gga aga cta agt agc 296
Met Leu Thr Ser Ser Gly Ile Glu Lys Lys Ser Gly Arg Leu Ser Ser
69 74 79 84

ata tta gat aag aaa gaa ctt tcc agc atc ctg aac atc aca gcc acc 344
Ile Leu Asp Lys Lys Glu Leu Ser Ser Ile Leu Asn Ile Thr Ala Thr
85 90 95 100

cag acc gga gac tcg gcc atc tac ctc tgt gct gtg gag gca cag tgc 392
Gln Thr Gly Asp Ser Ala Ile Tyr Leu Cys Ala Val Glu Ala Gln Cys
101 106 111 116

tcc cta gtc acc tgc agc ctg tac tca aat tct aca gct gag gct ctg 440
Ser Leu Val Thr Cys Ser Leu Tyr Ser Asn Ser Thr Ala Glu Ala Leu
117 122 127 132

caa ctg taa gatggggg aacttgctac attgagcaag ccctcaaaaa taaactatac 496
Gln Leu *
133

<210> 159
<211> 2243
<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (94)..(1341)

<400> 159

ccggaattcc cgggtcgacc cacgcgtccg cggacgcgtg ggcggaggtc tttggcgttc 60

agactcttag ctgaacgcgg agctgcggcg gct atg ctg tgg agc ggc tgc cgg 114
Met Leu Trp Ser Gly Cys Arg
1 5

cgt ttc ggg gcg cgc ctc ggc tgc ctg ccc ggc ggt ctc cgg gtc ctc 162
Arg Phe Gly Ala Arg Leu Gly Cys Leu Pro Gly Gly Leu Arg Val Leu
8 13 18 23

gtc cag acc ggc cac cgg agc ttg acc tcc tgc atc gac cct tcc atg 210
Val Gln Thr Gly His Arg Ser Leu Thr Ser Cys Ile Asp Pro Ser Met
24 29 34 39

gga ctt aat gaa gag cag aaa gaa ttt caa aaa gtg gcc ttt gac ttt 258
Gly Leu Asn Glu Glu Gln Lys Glu Phe Gln Lys Val Ala Phe Asp Phe
40 45 50 55

gct gcc cga gag atg gct cca aat atg gca gag tgg gac cag aag gag 306
Ala Ala Arg Glu Met Ala Pro Asn Met Ala Glu Trp Asp Gln Lys Glu
56 61 66 71

ctg ttc cca gtg gat gtg atg cgg aag gca gcc cag cta ggc ttc gga 354
Leu Phe Pro Val Asp Val Met Arg Lys Ala Ala Gln Leu Gly Phe Gly
72 77 82 87

ggg gtc tac ata caa aca gat gtg ggc ggg tct ggg ctg tca cgt ctt 402
Gly Val Tyr Ile Gln Thr Asp Val Gly Gly Ser Gly Leu Ser Arg Leu
88 93 98 103

gat acc tct gtc att ttt gaa gcc ttg gct aca ggc tgc acc agc acc 450
Asp Thr Ser Val Ile Phe Glu Ala Leu Ala Thr Gly Cys Thr Ser Thr
104 109 114 119

aca gcc tat ata agc atc cac aac atg tgt gcc tgg atg att gat agc 498
Thr Ala Tyr Ile Ser Ile His Asn Met Cys Ala Trp Met Ile Asp Ser
120 125 130 135

ttc gga aat gag gaa cag agg cac aaa ttt tgc cca ccg ctc tgt acc 546
Phe Gly Asn Glu Glu Gln Arg His Lys Phe Cys Pro Pro Leu Cys Thr
136 141 146 151

atg gag aag ttt gct tcc tac tgc ctc act gaa cca gga agt ggg agt 594
Met Glu Lys Phe Ala Ser Tyr Cys Leu Thr Glu Pro Gly Ser Gly Ser
152 157 162 167

gat gct gcc tct ctt ctg acc tcc gct aag aaa cag gga gat cat tac 642
Asp Ala Ala Ser Leu Leu Thr Ser Ala Lys Lys Gln Gly Asp His Tyr
168 173 178 183

atc ctc aat ggc tcc aag gcc ttc atc agt ggt gct ggt gag tca gac	690
Ile Leu Asn Gly Ser Lys Ala Phe Ile Ser Gly Ala Gly Glu Ser Asp	
184 189 194 199	
atc tat gtg gtc atg tgc cga aca gga gga cca ggc ccc aag ggc atc	738
Ile Tyr Val Val Met Cys Arg Thr Gly Gly Pro Gly Pro Lys Gly Ile	
200 205 210 215	
tca tgc ata gtt gtt gag aag ggg acc cct ggc ctc agc ttt ggc aag	786
Ser Cys Ile Val Val Glu Lys Gly Thr Pro Gly Leu Ser Phe Gly Lys	
216 221 226 231	
aag gag aaa aag gtg ggg tgg aac tcc cag cca aca cga gct gtg atc	834
Lys Glu Lys Lys Val Gly Trp Asn Ser Gln Pro Thr Arg Ala Val Ile	
232 237 242 247	
ttc gaa gac tgt gct gtc cct gtg gcc aac aga att ggg agc gag ggg	882
Phe Glu Asp Cys Ala Val Pro Val Ala Asn Arg Ile Gly Ser Glu Gly	
248 253 258 263	
cag ggc ttc ctc att gcc gtg aga gga ctg aac gga ggg agg atc aat	930
Gln Gly Phe Leu Ile Ala Val Arg Gly Leu Asn Gly Gly Arg Ile Asn	
264 269 274 279	
att gct tcc tgc tcc ctg ggg gct gcc cac gcc tct gtc atc ctc acc	978
Ile Ala Ser Cys Ser Leu Gly Ala Ala His Ala Ser Val Ile Leu Thr	
280 285 290 295	
cga gac cac ctc aat gtc cgg aag cag ttt gga gag cct ctg gcc agt	1026
Arg Asp His Leu Asn Val Arg Lys Gln Phe Gly Glu Pro Leu Ala Ser	
296 301 306 311	
aac cag tac ttg caa ttc aca ctg gct gat atg gca aca agg ctg gtg	1074
Asn Gln Tyr Leu Gln Phe Thr Leu Ala Asp Met Ala Thr Arg Leu Val	
312 317 322 327	
gcc gcg cgg ctg atg gtc cgc aat gca gca gtg gct ctg cag gag gag	1122
Ala Ala Arg Leu Met Val Arg Asn Ala Ala Val Ala Leu Gln Glu Glu	
328 333 338 343	
agg aag gat gca gtg gcc ttg tgc tcc atg gcc aag ctc ttt gct aca	1170
Arg Lys Asp Ala Val Ala Leu Cys Ser Met Ala Lys Leu Phe Ala Thr	
344 349 354 359	
gat gaa tgc ttt gcc atc tgc aac cag gcc ttg cag atg cac ggg ggc	1218
Asp Glu Cys Phe Ala Ile Cys Asn Gln Ala Leu Gln Met His Gly Gly	
360 365 370 375	
tac ggc tac ctg aag gat tac gct gtt cag cag tac gtg cgg gac tcc	1266
Tyr Gly Tyr Leu Lys Asp Tyr Ala Val Gln Gln Tyr Val Arg Asp Ser	
376 381 386 391	
agg gtc cac cag att cta gaa ggt agc aat gaa gtg atg agg ata ctg	1314
Arg Val His Gln Ile Leu Glu Gly Ser Asn Glu Val Met Arg Ile Leu	
392 397 402 407	
atc tct aga agc ctg ctt cag gag tag aaccc acacttggtc tggcctggtg	1366

Ile Ser Arg Ser Leu Leu Gln Glu *
408 413

```

ttcagtgcga ctgcagtcag tgttgagtgg tgccatgtgg gccgctctat tccaaaggaa 1426
tcatggatta gacccaaggg ctgagctcct ctagggcagg acctgcaccc tgtgtgttgg 1486
caccagcatc ggggtcttga ctggggcaga atccccagtg gaaccggaag agctggactg 1546
atgagaaaca tcagaagaac acatactacc ttgttttcct aatgccagaa ggttgaccag 1606
tgaagattca ccgtcaaacc atgaaagtcc tttcttggat ccactttatc ttgattagtc 1666
tgcattttac tagttcactg gatccctcct ctaggggcct ggggactttc actgatgctc 1726
ttcctgattc tagagcaaag gtgtgggaag gggaaatgga ggaatgccct cctgtctgtg 1786
tcgtttctctg tgccacagct acagatgcag aagggtttctc tggatagcac acctctgaat 1846
gtaaatcatg ataaaatgga tatttggaat cttactccta agctgtgatt taggggtgat 1906
ttctacttct ggactgcctc aatatcaagg gctgagactt ttgaattttg aatattcgtt 1966
gggtttcatg ttaagaagcc tgtggtctag gagtgcatt cagtgtttct tttcctgata 2026
aacactttga atattttttt tgtgtttttg tttccttttc tgaagctggt cctcctttta 2086
aatattttta atcacattga taaaatctat ccttcaccac ctctggttct actatagttg 2146
atttttattt taaatgttta attgtatttg attaaacact taactggatt ttggaataat 2206
aaaactctcg tccaatttgg cttttaaaaa aaaaaaa 2243

```

<210> 160
<211> 1014
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (141)..(986)

```

<400> 160
tcggcctgac ttcccggggtc gacgatttcg tcttccggct gtcaagctcc cggccgggct 60
gactcaagcg gaggcgcgcg gaacagtcgc cgaggcgatt cccgccagg ctctgtaac 120
cgccaggcag tggccccgcc      atg tcc cag ccc cgg acc cca gag cag gca 170
                        Met Ser Gln Pro Arg Thr Pro Glu Gln Ala
                        1                5

ctg gat aca ccg ggg gac tgc ccc cca ggc agg aga gac gag gac gct 218
Leu Asp Thr Pro Gly Asp Cys Pro Pro Gly Arg Arg Asp Glu Asp Ala
11                16                21                26

```

ggg gag ggg atc cag tgc tcc caa cgc atg ctc agc ttc agt gac gcc	266
Gly Glu Gly Ile Gln Cys Ser Gln Arg Met Leu Ser Phe Ser Asp Ala	
27 32 37 42	
ctg ctg tcc atc atc gcc acc gtc atg atc ctg cct gtg acc cac acg	314
Leu Leu Ser Ile Ile Ala Thr Val Met Ile Leu Pro Val Thr His Thr	
43 48 53 58	
gag atc tcc cca gaa cag cag ttc gac aga agt gta cag agg ctt ctg	362
Glu Ile Ser Pro Glu Gln Gln Phe Asp Arg Ser Val Gln Arg Leu Leu	
59 64 69 74	
gca aca cgg att gcc gtc tac ctg atg acc ttt ctc atc gtg aca gtg	410
Ala Thr Arg Ile Ala Val Tyr Leu Met Thr Phe Leu Ile Val Thr Val	
75 80 85 90	
gcc tgg gca gca cac aca agg ttg ttc caa gtt gtt ggg aaa aca gac	458
Ala Trp Ala Ala His Thr Arg Leu Phe Gln Val Val Gly Lys Thr Asp	
91 96 101 106	
gac aca ctt gcc ctg ctc aac ctg gcc tgc atg aag acc atc acc ttc	506
Asp Thr Leu Ala Leu Leu Asn Leu Ala Cys Met Lys Thr Ile Thr Phe	
107 112 117 122	
ctg cct tac acg ttt tgc tta atg gtg acc ttc cct gat gtg cct ctg	554
Leu Pro Tyr Thr Phe Ser Leu Met Val Thr Phe Pro Asp Val Pro Leu	
123 128 133 138	
ggc atc ttc ttg ttc tgt gtg tgt gtg atc gcc att ggg gtc gtg cag	602
Gly Ile Phe Leu Phe Cys Val Cys Val Ile Ala Ile Gly Val Val Gln	
139 144 149 154	
gca ctg att gtg ggg tac gca ttc cac ttc ccg cac ctg ctg agc ccg	650
Ala Leu Ile Val Gly Tyr Ala Phe His Phe Pro His Leu Leu Ser Pro	
155 160 165 170	
cag atc cag cgc tct gcc cac agg gct ctg tac cga cga cac gtc ctg	698
Gln Ile Gln Arg Ser Ala His Arg Ala Leu Tyr Arg Arg His Val Leu	
171 176 181 186	
ggc atc gtc ctc caa ggc ccg gcc ctg tgc ttt gca gcg gcc atc ttc	746
Gly Ile Val Leu Gln Gly Pro Ala Leu Cys Phe Ala Ala Ala Ile Phe	
187 192 197 202	
tct ctc ttc ttt gtc ccc ctg tct tac ctg ctg atg gtg act gtc atc	794
Ser Leu Phe Phe Val Pro Leu Ser Tyr Leu Leu Met Val Thr Val Ile	
203 208 213 218	
ctc ctc ccc tat gtc agc aag gtc acc ggc tgg tgc aga gac agg ctc	842
Leu Leu Pro Tyr Val Ser Lys Val Thr Gly Trp Cys Arg Asp Arg Leu	
219 224 229 234	
ctg ggc cac agg gag ccc tgc gct cac cca gtg gaa gtc ttc tgc ttt	890
Leu Gly His Arg Glu Pro Ser Ala His Pro Val Glu Val Phe Ser Phe	
235 240 245 250	

gac ctc cac gag cca ctc agc aag gag cgc gtg gaa gcc ttc agc gac 938
 Asp Leu His Glu Pro Leu Ser Lys Glu Arg Val Glu Ala Phe Ser Asp
 251 256 261 266

gga gtc tac gcc atc gtg gcc acg ctt ctc atc ctg gac atc tgg tga 986
 Gly Val Tyr Ala Ile Val Ala Thr Leu Leu Ile Leu Asp Ile Trp *
 267 272 277 282

ggacccccgcg tcacctgccc cagctatt 1014

<210> 161
 <211> 1893
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (289)..(1317)

<220>
 <221> misc_feature
 <222> (1)...(1893)
 <223> n = a,t,c or g

<400> 161
 cagggatgatg gatattctgca gaattcggct tactcactat agggctcgag cggccgcccc 60
 ggcaggtgca gaacagaaca ctttctcatg tccaggggtca gattacaaga gcactcaaga 120
 ctttactgac gaaaactcag gaaatcctct atcacaaaga ggtttggcaa ctaaactaag 180
 acattaaaag gaaaatacca gatgccactc tgcaggctgc aataactact acttactgga 240
 tacattcaaa ccctccagaa tcaacagtta tcaggttaacc aacaagaa atg caa gcc 297
 Met Gln Ala
 1

gtc gac aat ctc acc tct gcg cct ggg aac acc agt ctg tgc acc aga 345
 Val Asp Asn Leu Thr Ser Ala Pro Gly Asn Thr Ser Leu Cys Thr Arg
 4 9 14 19

gac tac aaa atc acc cag gtc ctc ttc cca ctg ctc tac act gtc ctg 393
 Asp Tyr Lys Ile Thr Gln Val Leu Phe Pro Leu Leu Tyr Thr Val Leu
 20 25 30 35

ttt ttt gtt gga ctt atc aca aat ggc ctg gcg atg agg att ttc ttt 441
 Phe Phe Val Gly Leu Ile Thr Asn Gly Leu Ala Met Arg Ile Phe Phe
 36 41 46 51

caa atc cgg agt aaa tca aac ttt att att ttt ctt aag aac aca gtc 489
 Gln Ile Arg Ser Lys Ser Asn Phe Ile Ile Phe Leu Lys Asn Thr Val
 52 57 62 67

att tct gat ctt ctc atg att ctg act ttt cca ttc aaa att ctt agt 537

Ile Ser Asp Leu Leu Met Ile Leu Thr Phe Pro Phe Lys Ile Leu Ser	
68 73 78 83	
gat gcc aaa ctg gga aca gga cca ctg aga act ttt gtg tgt caa gtt	585
Asp Ala Lys Leu Gly Thr Gly Pro Leu Arg Thr Phe Val Cys Gln Val	
84 89 94 99	
acc tcc gtc ata ttt tat ttc aca atg tat atc agt att tca ttc ctg	633
Thr Ser Val Ile Phe Tyr Phe Thr Met Tyr Ile Ser Ile Ser Phe Leu	
100 105 110 115	
gga ctg ata act atc gat cgc tac cag aag acc acc agg cca ttt aaa	681
Gly Leu Ile Thr Ile Asp Arg Tyr Gln Lys Thr Thr Arg Pro Phe Lys	
116 121 126 131	
aca tcc aac ccc aaa aat ctc ttg ggg gct aag att ctc tct gtt gtc	729
Thr Ser Asn Pro Lys Asn Leu Leu Gly Ala Lys Ile Leu Ser Val Val	
132 137 142 147	
atc tgg gca ttc atg ttc tta ctc tct ttg cct aac atg att ctg acc	777
Ile Trp Ala Phe Met Phe Leu Leu Ser Leu Pro Asn Met Ile Leu Thr	
148 153 158 163	
aac agg cag ccg aga gac aag aat gtg aag aaa tgc tct ttc ctt aaa	825
Asn Arg Gln Pro Arg Asp Lys Asn Val Lys Lys Cys Ser Phe Leu Lys	
164 169 174 179	
tca gag ttc ggt cta gtc tgg cat gaa ata gta aat tac atc tgt caa	873
Ser Glu Phe Gly Leu Val Trp His Glu Ile Val Asn Tyr Ile Cys Gln	
180 185 190 195	
gtc att ttc tgg att aat ttc tta att gtt att gta tgt tat aca ctc	921
Val Ile Phe Trp Ile Asn Phe Leu Ile Val Ile Val Cys Tyr Thr Leu	
196 201 206 211	
att aca aaa gaa ctg tac cgg tca tac gta aga acg agg ggt gta ggt	969
Ile Thr Lys Glu Leu Tyr Arg Ser Tyr Val Arg Thr Arg Gly Val Gly	
212 217 222 227	
aaa gtc ccc agg aaa aag gtg aac gtc aaa gtt ttc att atc att gct	1017
Lys Val Pro Arg Lys Lys Val Asn Val Lys Val Phe Ile Ile Ala	
228 233 238 243	
gta ttc ttt att tgt ttt gtt cct ttc cat ttt gcc cga att cct tac	1065
Val Phe Phe Ile Cys Phe Val Pro Phe His Phe Ala Arg Ile Pro Tyr	
244 249 254 259	
acc ctg agc caa acc cgg gat gtc ttt gac tgc act gct gaa aat act	1113
Thr Leu Ser Gln Thr Arg Asp Val Phe Asp Cys Thr Ala Glu Asn Thr	
260 265 270 275	
ctg ttc tat gtg aaa gag agc act ctg tgg tta act tcc tta aat gca	1161
Leu Phe Tyr Val Lys Glu Ser Thr Leu Trp Leu Thr Ser Leu Asn Ala	
276 281 286 291	
tgc ctg gat ccg ttc atc tat ttt ttc ctt tgc aag tcc ttc aga aat	1209
Cys Leu Asp Pro Phe Ile Tyr Phe Phe Leu Cys Lys Ser Phe Arg Asn	

292	297	302	307	
tcc ttg ata agt atg ctg aag tgc ccc aat tct gca aca tct ctg tcc				1257
Ser Leu Ile Ser Met Leu Lys Cys Pro Asn Ser Ala Thr Ser Leu Ser				
308	313	318	323	
cag gac aat agg aaa aaa gaa cag gat ggt ggt gac cca aat gaa gag				1305
Gln Asp Asn Arg Lys Lys Glu Gln Asp Gly Gly Asp Pro Asn Glu Glu				
324	329	334	339	
act cca atg taa aca aattaactaa ggaaatattt caatctcttt gtgttcagaa				1360
Thr Pro Met *				
340				
ctcgttaaag caaagcgcta agtaaaaata ttaactgacg aagaagcaac taagttaata				1420
ataatgactc taaagaaaca gaagattaca aaagcaattt tcatttacct ttccagtatg				1480
aaaagctatc ttaaaatata gaaaactaat ctaaactgta gctgtattag cagcaaaaca				1540
aacgacatcc aattgtcatg ctgcatgcaa aactacacag aattcatgtt ttgcagagtt				1600
ttgccaaaat gagtaatcat ataatattta ctgtaatttt taaaatacat tatcgttcac				1660
aattttattt tttcataatc cactaaggga agaacgatca attggatata atcttcttac				1720
caaaaaatga tagntaaaat gtatataata tctagtcccc taacccaaat ncttgaccta				1780
ttgggatact taataaaaaa ttaaagtaag tgggataccc caaagaaata ataactattt				1840
aactttttca tttattagcc aaaaacccta aggggattta aacctaattg gga				1893
<210>	162			
<211>	627			
<212>	DNA			
<213>	Homo sapiens			
<220>				
<221>	CDS			
<222>	(72)..(494)			
<220>				
<221>	misc_feature			
<222>	(1)...(627)			
<223>	n = a,t,c or g			
<400>	162			
atttggccct cgaggccaag aattcggcac gaggacacaa ctgtgttcac tagcaacctc				60
aaacagacac c atg gtg cac ctg act cct gag gag aag tct gcc gtt act				110
Met Val His Leu Thr Pro Glu Glu Lys Ser Ala Val Thr				
1	5	10		
gcc ctg tgg ggc aag gtg aac gtg gat gaa gtt ggt ggt gag gcc ctg				158

Ala Leu Trp Gly Lys Val Asn Val Asp Glu Val Gly Gly Glu Ala Leu	
14 19 24 29	
ggc agg ctg ctg gtg gtc tac cct tgg acc cag agg ttc ttt gag tcc	206
Gly Arg Leu Leu Val Val Tyr Pro Trp Thr Gln Arg Phe Phe Glu Ser	
30 35 40 45	
ttt ggg gat ctg tcc act cct gat gct gtt atg ggc aac cct aag gtg	254
Phe Gly Asp Leu Ser Thr Pro Asp Ala Val Met Gly Asn Pro Lys Val	
46 51 56 61	
aag gct cat ggc aag aaa gtg ctc ggt gcc ttt agt gat ggc ctg gct	302
Lys Ala His Gly Lys Lys Val Leu Gly Ala Phe Ser Asp Gly Leu Ala	
62 67 72 77	
cac ctg gac aac ctc aag ggc acc ttt gcc aca ctg agt gag ctg cac	350
His Leu Asp Asn Leu Lys Gly Thr Phe Ala Thr Leu Ser Glu Leu His	
78 83 88 93	
tgt gac aag ctg cac gtg gat cct gag aac ttc agg ctc ctg ggc aac	398
Cys Asp Lys Leu His Val Asp Pro Glu Asn Phe Arg Leu Leu Gly Asn	
94 99 104 109	
gtg ctg gtc tgt gtg ctg gcc cat cac ttt ggc aaa gaa ttc acc cca	446
Val Leu Val Cys Val Leu Ala His His Phe Gly Lys Glu Phe Thr Pro	
110 115 120 125	
cca gtt gca ggc ttg cct atc aga aag ttg gtg gct ggt tgt ggc taa	494
Pro Val Ala Gly Leu Pro Ile Arg Lys Leu Val Ala Gly Cys Gly *	
126 131 136 141	
tgccctggcc cacaagtaat caactaagcc tcgctttcct tgctggtcca atttccaatt	554
aaaaggttcc tttggttccc taagtccaaa tacttaaachn ggggggatata tattgaaagg	614
gccttgagaa tct	627
<210> 163	
<211> 2402	
<212> DNA	
<213> Homo sapiens	
<220>	
<221> CDS	
<222> (295) .. (1962)	
<400> 163	
gcccgttgta ccgccccgga attccccgggt cgaccacgc gtccgaccac gcgtacgccc	60
acgcgtgcgg ctcaaggcat ttgggaagtg caaaatgaca tgcaccccct ctggaggggc	120
gcacctttga agtcacctgg accaaggaaa ggccctgccc tgaaggctgg tcacttgacg	180
aggtaaaactc ccctctttga cttctggcca gggtttgtgc tgagctggct gcagccgctc	240

tcagcctcgc	tccggggcacg	tccggggcagcc	tccggggccctc	ctgcctgcag	gatc	atg	297
						Met	
						1	
ccc acc acc gtg gac gat gtc ctg gag cat gga ggg gag ttt cac ttt	345						
Pro Thr Thr Val Asp Asp Val Leu Glu His Gly Gly Glu Phe His Phe							
2 7 12 17							
ttc cag aag caa atg ttt ttc ctc ttg gct ctg ctc tcg gct acc ttc	393						
Phe Gln Lys Gln Met Phe Phe Leu Leu Ala Leu Leu Ser Ala Thr Phe							
18 23 28 33							
gcg ccc atc tac gtg ggc atc gtc ttc ctg ggc ttc acc cct gac cac	441						
Ala Pro Ile Tyr Val Gly Ile Val Phe Leu Gly Phe Thr Pro Asp His							
34 39 44 49							
cgc tgc cgg agc ccc gga gtg gcc gag ctg agt ctg cgc tgc ggc tgg	489						
Arg Cys Arg Ser Pro Gly Val Ala Glu Leu Ser Leu Arg Cys Gly Trp							
50 55 60 65							
agt cct gca gag gaa ctg aac tac acg gtg ccg ggc cca gga cct gcg	537						
Ser Pro Ala Glu Glu Leu Asn Tyr Thr Val Pro Gly Pro Gly Pro Ala							
66 71 76 81							
ggc gaa gcc tcc cca aga cag tgt agg cgc tac gag gtg gac tgg aac	585						
Gly Glu Ala Ser Pro Arg Gln Cys Arg Arg Tyr Glu Val Asp Trp Asn							
82 87 92 97							
cag agc acc ttt gac tgc gtg gac ccc ctg gcc agc ctg gac acc aac	633						
Gln Ser Thr Phe Asp Cys Val Asp Pro Leu Ala Ser Leu Asp Thr Asn							
98 103 108 113							
agg agc cgc ctg cca ctg ggc ccc tgc cgg gac ggc tgg gtg tac gag	681						
Arg Ser Arg Leu Pro Leu Gly Pro Cys Arg Asp Gly Trp Val Tyr Glu							
114 119 124 129							
acg cct ggc tcg tcc atc gtc acc gag ttt aac ctg gta tgt gcc aac	729						
Thr Pro Gly Ser Ser Ile Val Thr Glu Phe Asn Leu Val Cys Ala Asn							
130 135 140 145							
tcc tgg atg ttg gac cta ttc cag tca tca gtg aat gta gga ttc ttt	777						
Ser Trp Met Leu Asp Leu Phe Gln Ser Ser Val Asn Val Gly Phe Phe							
146 151 156 161							
att ggc tct atg agt atc ggc tac ata gca gac agg ttt ggc cgt aag	825						
Ile Gly Ser Met Ser Ile Gly Tyr Ile Ala Asp Arg Phe Gly Arg Lys							
162 167 172 177							
ctc tgc ctc cta act aca gtc ctc ata aat gct gca gct gga gtt ctc	873						
Leu Cys Leu Leu Thr Thr Val Leu Ile Asn Ala Ala Ala Gly Val Leu							
178 183 188 193							
atg gcc att tcc cca acc tat acg tgg atg tta att ttt cgc tta atc	921						
Met Ala Ile Ser Pro Thr Tyr Thr Trp Met Leu Ile Phe Arg Leu Ile							
194 199 204 209							

caa gga ctg gtc agc aaa gca ggc tgg tta ata ggc tac atc ctg att	969
Gln Gly Leu Val Ser Lys Ala Gly Trp Leu Ile Gly Tyr Ile Leu Ile	
210 215 220 225	
aca gaa ttt gtt ggg cgg aga tat cgg aga aca gtg ggg att ttt tac	1017
Thr Glu Phe Val Gly Arg Arg Tyr Arg Arg Thr Val Gly Ile Phe Tyr	
226 231 236 241	
caa gtt gcc tat aca gtt ggg ctc ctg gtg cta gct ggg gtg gct tac	1065
Gln Val Ala Tyr Thr Val Gly Leu Leu Val Leu Ala Gly Val Ala Tyr	
242 247 252 257	
gca ctt cct cac tgg agg tgg ttg cag ttc aca gtt gct ctg ccc aac	1113
Ala Leu Pro His Trp Arg Trp Leu Gln Phe Thr Val Ala Leu Pro Asn	
258 263 268 273	
ttc ttc ttc ttg ctc tat tac tgg tgc ata cct gag tct ccc agg tgg	1161
Phe Phe Phe Leu Leu Tyr Tyr Trp Cys Ile Pro Glu Ser Pro Arg Trp	
274 279 284 289	
ctg atc tcc cag aat aag aat gct gaa gcc atg aga atc att aag cac	1209
Leu Ile Ser Gln Asn Lys Asn Ala Glu Ala Met Arg Ile Ile Lys His	
290 295 300 305	
atc gca aag aaa aat gga aaa tct cta ccc gcc tcc ctt cag cgc ctg	1257
Ile Ala Lys Lys Asn Gly Lys Ser Leu Pro Ala Ser Leu Gln Arg Leu	
306 311 316 321	
aga ctt gaa gag gaa act ggc aag aaa ttg aac cct tca ttt ctt gac	1305
Arg Leu Glu Glu Glu Thr Gly Lys Lys Leu Asn Pro Ser Phe Leu Asp	
322 327 332 337	
ttg gtc aga act cct cag ata agg aaa cat act atg ata ttg atg tac	1353
Leu Val Arg Thr Pro Gln Ile Arg Lys His Thr Met Ile Leu Met Tyr	
338 343 348 353	
aac tgg ttc acg agc tct gtg ctc tac cag ggc ctc atc atg cac atg	1401
Asn Trp Phe Thr Ser Ser Val Leu Tyr Gln Gly Leu Ile Met His Met	
354 359 364 369	
ggc ctt gca ggt gac aat atc tac ctg gat ttc ttc tac tct gcc ctg	1449
Gly Leu Ala Gly Asp Asn Ile Tyr Leu Asp Phe Phe Tyr Ser Ala Leu	
370 375 380 385	
gtt gaa ttc cca gct gcc ttc atg atc atc ctc acc atc gac cgc atc	1497
Val Glu Phe Pro Ala Ala Phe Met Ile Ile Leu Thr Ile Asp Arg Ile	
386 391 396 401	
gga cgc cgt tac cct tgg gct gca tca aat atg gtt gca ggg gca gcc	1545
Gly Arg Arg Tyr Pro Trp Ala Ala Ser Asn Met Val Ala Gly Ala Ala	
402 407 412 417	
tgt ctg gcc tca gtt ttt ata cct ggt gat cta caa tgg cta aaa att	1593
Cys Leu Ala Ser Val Phe Ile Pro Gly Asp Leu Gln Trp Leu Lys Ile	
418 423 428 433	
att atc tca tgc ttg gga aga atg ggg atc aca atg gcc tat gag ata	1641

Ile Ile Ser Cys Leu Gly Arg Met Gly Ile Thr Met Ala Tyr Glu Ile	
434	439 444 449
gtc tgc ctg gtc aat gct gag ctg tac ccc aca ttc att agg aat ctt	1689
Val Cys Leu Val Asn Ala Glu Leu Tyr Pro Thr Phe Ile Arg Asn Leu	
450	455 460 465
ggc gtc cac atc tgt tcc tca atg tgt gac att ggt ggc atc atc acg	1737
Gly Val His Ile Cys Ser Ser Met Cys Asp Ile Gly Gly Ile Ile Thr	
466	471 476 481
cca ttc ctg gtc tac cgg ctc act aac atc tgg ctt gag ctc ccg ctg	1785
Pro Phe Leu Val Tyr Arg Leu Thr Asn Ile Trp Leu Glu Leu Pro Leu	
482	487 492 497
atg gtt ttc ggc gta ctt ggc ttg gtt gct gga ggt ctg gtg ctg ttg	1833
Met Val Phe Gly Val Leu Gly Leu Val Ala Gly Gly Leu Val Leu Leu	
498	503 508 513
ctt cca gaa act aaa ggg aaa gct ttg cct gag acc atc gag gaa gcc	1881
Leu Pro Glu Thr Lys Gly Lys Ala Leu Pro Glu Thr Ile Glu Glu Ala	
514	519 524 529
gaa aat atg caa aga cca aga aaa aat aaa gaa aag atg att tac ctc	1929
Glu Asn Met Gln Arg Pro Arg Lys Asn Lys Glu Lys Met Ile Tyr Leu	
530	535 540 545
caa gtt cag aaa cta gac att cca ttg aac taa gaagagag accgttgctg	1980
Gln Val Gln Lys Leu Asp Ile Pro Leu Asn *	
546	551 556
ctgtcatgac ctagctttga tggcagcaag accaaaagta gaaatccctg cactcatcac	2040
aaagcccata caactcaacc aaacttaccc ctgagcccta tcaacctagg tctacagcca	2100
gtggagtcta ttgtacactg tggaaaaata cccatggggac cagatcctgc caaattcttc	2160
cagctcactt tattctcagc attcctagga cattggacat tggttttctg gaggggtttt	2220
tttccatctt tgtatttttt taaatttgat tcttttcttt gcaatgctat ctaaccagaa	2280
tacatagggg aactgtgggc taggcaaaca aaatagaaaa aagtgtgaaa aacagtaaaag	2340
ttgggagagg agcatctatt ttcttaaaga aataaaacac ccaaaacaat aaaaaaaaaa	2400
aa	2402

<210> 164
 <211> 2029
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> (69)..(917)

<220>

<221> misc_feature

<222> (1)...(2029)

<223> n = a,t,c or g

<400> 164

```
ccggaattcc cgggtcgacc cacgcgtccg cccacgcgtc cgtggactct cagattcttt      60
actatgca atg ttg ggg gtg aat ccc cgc ttt gac tca gct tcc tcc agc      110
      Met Leu Gly Val Asn Pro Arg Phe Asp Ser Ala Ser Ser Ser
            1              5              10

tac tat ttg gac atg cac agc ctc ccc cat gtc atc aac cca gtg gag      158
Tyr Tyr Leu Asp Met His Ser Leu Pro His Val Ile Asn Pro Val Glu
      15              20              25              30

tcc cgg ctg gga tcc agt gct gcc tcc ttg tac cct gtg ctc aac ttt      206
Ser Arg Leu Gly Ser Ser Ala Ala Ser Leu Tyr Pro Val Leu Asn Phe
      31              36              41              46

cta ctc tac gtg cct gag ctt gca cac tca ccg ctg tac att cag gac      254
Leu Leu Tyr Val Pro Glu Leu Ala His Ser Pro Leu Tyr Ile Gln Asp
      47              52              57              62

aag gat ggc gct cca gtg gcc acc aat gcc ttc cat agt ccc cgc tgg      302
Lys Asp Gly Ala Pro Val Ala Thr Asn Ala Phe His Ser Pro Arg Trp
      63              68              73              78

ggt ggc att atg gta tat aat gtt gac tcc aaa acc tat aat gcc tca      350
Gly Gly Ile Met Val Tyr Asn Val Asp Ser Lys Thr Tyr Asn Ala Ser
      79              84              89              94

gtg ctg cca gtg aga gtc gag gtg gac atg gtg cga gtg atg gag gtg      398
Val Leu Pro Val Arg Val Glu Val Asp Met Val Arg Val Met Glu Val
      95              100              105              110

ttc ctg gca cag ttg cgg ttg ctc ttt ggg att gct cag ccc cag ctg      446
Phe Leu Ala Gln Leu Arg Leu Leu Phe Gly Ile Ala Gln Pro Gln Leu
      111              116              121              126

cct cca aaa tgc ctg ctt tca ggg cct acg agt gaa ggg cta atg acc      494
Pro Pro Lys Cys Leu Leu Ser Gly Pro Thr Ser Glu Gly Leu Met Thr
      127              132              137              142

tgg gag cta gac cgg ctg ctc tgg gct cgg tca gtg gag aac ctg gcc      542
Trp Glu Leu Asp Arg Leu Leu Trp Ala Arg Ser Val Glu Asn Leu Ala
      143              148              153              158

aca gcc acc acc acc ctt acc tcc ctg gcg cag ctt ctg ggc aag atc      590
Thr Ala Thr Thr Thr Leu Thr Ser Leu Ala Gln Leu Leu Gly Lys Ile
      159              164              169              174

agc aac att gtc att aag gac gac gtg gca tct gag gtg tac aag gct      638
Ser Asn Ile Val Ile Lys Asp Asp Val Ala Ser Glu Val Tyr Lys Ala
      175              180              185              190
```

gta gct gcc gtc cag aag tcg gca gaa gag ttg gcg tct ggg cac ctg	686
Val Ala Ala Val Gln Lys Ser Ala Glu Glu Leu Ala Ser Gly His Leu	
191 196 201 206	
gca tct gcc ttt gtc gcc agc cag gaa gct gtg aca tcc tct gag ctt	734
Ala Ser Ala Phe Val Ala Ser Gln Glu Ala Val Thr Ser Ser Glu Leu	
207 212 217 222	
gcc ttc ttt gac ccg tca ctc ctc cac ctc ctt tat ttc cct gat gac	782
Ala Phe Phe Asp Pro Ser Leu Leu His Leu Leu Tyr Phe Pro Asp Asp	
223 228 233 238	
cag aag ttt gcc atc tac atc cca ctc ttc ctg cct atg gct gtg ccc	830
Gln Lys Phe Ala Ile Tyr Ile Pro Leu Phe Leu Pro Met Ala Val Pro	
239 244 249 254	
atc ctc ctg tcc ctg gtc aag atc ttc ctg gag acc cgc aag tcc tgg	878
Ile Leu Leu Ser Leu Val Lys Ile Phe Leu Glu Thr Arg Lys Ser Trp	
255 260 265 270	
aga aag cct gag aag aca gac tgt gta cgt gat atc tga acactcctca	927
Arg Lys Pro Glu Lys Thr Asp Cys Val Arg Asp Ile *	
271 276 281	
cttcttcccc aggacatgat gagctacatt gggcccaaga ggacagcagt ggtgcggggg	987
ataatgcacc gggaggcctt taacatcatt ggccgcgcga tagtccaggt ggcccaggcc	1047
atgtctttga ctgaggatgt gcttgctgct gctctggctg accaccttcc agaggacaag	1107
tggagcgcgtg agaagaggcg gcctctcaag tccagcttgg gctatgagat caccttcagt	1167
ttactcaacc cagaccccaa gtcccatgat gtctactggg acattgaggg ggctgtccgg	1227
cgctatgtgc aacctttcct gaatgccctc ggtgccgctg gcaacttctc tgtggactct	1287
cagattcttt actatgcaat gttgggggtg aatccccgct ttgactcagc ttcctccagc	1347
tactatattg acatgcacag cctcccccat gtcacaaacc cagtggagtc ccggctggga	1407
tccagtgtg cctccttgta ccctgtgtc aactttctac tctacgtgcc tgagcttgca	1467
cactcaccgc tgtacattca ggacaaggat ggcgctccag tggccaccaa tgccttccat	1527
agtccccgct ggggtggcat tatggtatat aatgttgact ccaaaaccta taatgcctca	1587
gtgctgccag tgagagtcga ggtggacatg gtgcgagtga tggaggtgtt cctggcacag	1647
ttgcggttgc tctttgggat tgctcagccc cagctgcctc caaaatgcct gctttcaggg	1707
cctacgagtg aagggctaata gacctgggag ctagaccggc tgctctgggc tcggtcagtg	1767
gagaacctgg ccacagccac caccaccctt acctccctgg cgcagcttct gggcaagatc	1827
agcaacattg tcattaagga cgacgtggca tctgaggtgt acaaggctgt agctgccgtc	1887

cagaagtcgg	cagaagagtt	ggcgtctggg	cacctggcat	ctgcctttgt	cgccagccag	1947
gaagctgtga	catcctcacg	aaatcgtcga	cccgggaatt	ccggnccggt	cctgcaggcg	2007
acaggcttac	aatggcgagc	ct				2029